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INTERPOL Review of Forensic Biology and DNA, 2023-2025

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ABSTRACT

As a part of the 21st INTERPOL International Forensic Science Managers Symposium, this work explores the latest scientific developments, methodologies, and trends in forensic biology and forensic DNA analysis of biological evidence during the years 2023 to 2025 and builds upon previous INTERPOL DNA reviews. Almost 2000 references covering the three-year time range of this review were located via various online searches including use of Scopus, Web of Science, and PubMed. The scientific articles, which originated from more than 300 different journals, were curated in a Zotero reference manager database (see Supplemental File 1) and sorted into 15 topics and 116 sub-topics (see Supplemental File 2) under sections focused on advances in current practices (Section 3) and emerging technologies and research studies (Section 4). This triennial review describes 24 books or major reports, 20 special issues of journals on aspects of forensic DNA, 292 articles from 2 International Society for Forensic Genetics (ISFG) conference proceedings, and 70 guidance documents from 17 different organizations to assist in quality DNA testing. Publications were evaluated and sorted into 10 topics around advances in current practices and 5 topics related to emerging technologies and research studies. These topics, which are further sub-divided in a compiled list (see Supplemental File 2) included rapid DNA analysis; law enforcement DNA databases and ethics; forensic investigative genetic genealogy (FIGG); forensic biology and body fluid identification; DNA processing; DNA typing with short tandem repeat (STR) markers; DNA interpretation at the source or sub-source level of the hierarchy of propositions along with mixture interpretation using probabilistic genotyping software (PGS); DNA interpretation at the activity level along with aspects of DNA transfer, persistence, prevalence, and recovery (TPPR); statistics and population genetic data; human identification and kinship analysis; next-generation sequencing (NGS) and technology developments; forensic DNA phenotyping (FDP) and methylation; lineage markers (Y-chromosome, mitochondrial DNA, X-chromosome analyses); new markers and approaches (microhaplotypes, insertion/deletion markers, proteomics, microbiome, single-cell analysis, using environmental DNA, and biomarkers for diagnosis of sudden death, molecular autopsy, or post-mortem interval); and non-human DNA testing and wildlife forensics. Artificial intelligence (AI) tools for summarizing references were explored and utilized in performing this review of over 1900 publications.

1. Introduction

This review explores developments in forensic biology and forensic DNA analysis of biological evidence during the years 2023 to 2025 and builds upon previous INTERPOL DNA reviews conducted by the same author covering 2016 to 2019 [1] and 2019 to 2022 [1]. A few items from the latter half of 2022 were included if they were not present in the previous review [1].

Section 2 describes general resources related to biological evidence, such as books, major reports, conference proceedings, special issues of journals on forensic DNA, and published guidance documents to assist in quality control of DNA testing. Section 3 covers ten topics related to advances in current practices intended to benefit practitioners while Section 4 covers emerging technologies and research studies likely to be of interest to both practitioners and researchers.

Multiple searches, using the Scopus[1] (Elsevier), Web of Science[2] (Clarivate), and PubMed[3] (National Center for Biotechnology Information, National Institutes of Health) databases, were conducted at various

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[1] https://www.scopus.com/.
[2] https://clarivate.com/academia-government/scientific-and-academic-research/research-discovery-and-referencing/web-of-science/.
[3] https://pubmed.ncbi.nlm.nih.gov/.

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times up until October 2025 with "forensic" and "DNA" or "biology" and "2023 to 2025" as search options. Additional references were included through December 2025. For example, a Web of Science search on September 19, 2025 using "forensic DNA" or "DNA profiling" or "DNA typing" or "forensic genetics" or "short tandem repeat" for publication years 2023, 2024, or 2025 located 1959 total publications of which 169 were review articles. The thousands of articles that were returned with these searches were focused down to around 1550 items (including journal articles, reports, and book chapters) through visual examination of titles, authors, and abstracts and removing duplicates. For journals not indexed in online databases, such as *WIRES Forensic Science*, *Journal of Forensic Identification*, and *Forensic Genomics*, tables of contents for issues in 2023, 2024, and 2025 were examined to locate potentially relevant articles. Gathered information was stored in a Zotero[4] (Digital Scholar) reference manager database. An exported version of this database (in.RIS format) is provided as **Supplemental File 1**.

An analysis of 1748 journal articles and conference proceedings collected in the Zotero database used for this review found 305 unique journals, many of which only had a single publication on forensic biology or DNA. The top ten journals, with the number of articles collected shown in parentheses, were:

1. *Forensic Science International: Genetics* (250)
2. *International Journal of Legal Medicine* (110)
3. *Forensic Science International* (98)
4. *Journal of Forensic Sciences* (78)
5. *Genes* (70)
6. *Electrophoresis* (48)
7. *Australian Journal of Forensic Sciences* (41)
8. *Forensic Genomics* (40)
9. *Science & Justice* (39)
10. *Forensic Science International: Synergy* (34)

Proceedings of the International Society for Forensic Genetics (ISFG) Congresses published within the timeframe of this review include 126 articles (351 pages total) in volume 8 of the *Forensic Science International: Genetics Supplement Series* and 166 articles (1231 pages total) published by the University of Santiago de Compostella under a single digital object identifier (DOI).

1.1. A curated reference list sorted by categories

Reference article information stored in the Zotero database created for this review were exported from Zotero into the *Forensic Science International: Synergy* reference format. This full reference listing was then manually sorted by the author into 15 different topic areas considered appropriate to advances in current practices (see Section 3) or emerging technologies and research studies (see Section 4), based in part on groupings used in the author's previous INTERPOL DNA review [1]. These 15 topics (10 in Section 3 and 5 in Section 4) were further subdivided into 116 subtopics. The general grouping and specific subtopics were informed by the author's previous efforts (e.g. Refs. [1,2]) and artificial intelligence (AI) assisted sorting (see next section).

A combined 122-page file is provided as **Supplemental File 2** with references listed in the journal format in 9-point Calibri font. This file served as the basis for the AI-generated summary text created for each article (see next section).

In Supplemental File 2, each of the 15 topic areas begins with a subtopic titled "books, review articles, and guidance." More information on these general resources across all categories can be found in Section 2 of this review.

While references could potentially go into more than one category (including primary topics or sub-topics in some cases), each reference was included only once in the final list. A single exception was the proceedings of a 2024 National Academy of Sciences workshop on law enforcement use of probabilistic genotyping software, forensic DNA phenotyping, and forensic investigative genetic genealogy [3] that was included in each of in the "books, review articles, and guidance" sections for these three categories (see Supplemental File 2).

To aid in finding references within each category, articles were sorted alphabetically by the last name of the first author. Any references available online but missing final publication page numbers when this review was written were designated "(in press)" and highlighted in yellow. If available, the DOI was provided as part of the reference listing to enable a direct link to each publication.

1.2. Exploration and use of AI tools

Given the enormous task of working with almost two thousand reference items, several AI tools were explored to assist with the tasks of gathering, grouping, and organizing reference lists as well as summarizing articles.

The AI tools explored between March 2025 and December 2025 included Google Gemini (Deep Research) and Gemini Pro (Fast and Thinking Modes), Google AI, Scopus AI, Elicit, Scite AI, and free versions of Google Notebook LM, ChatGPT, and Perplexity. While some potential was seen with several of these tools when they were explored, none were able to independently accomplish all tasks desired to perform this extensive review.

AI reproducibility and accuracy were assessed through providing multiple tools with the same input as well as exploring responses to the same prompt over time with a single AI tool. AI-induced hallucinations were reduced or even eliminated by working with smaller datasets and requesting simpler tasks (e.g., summarizing a set of defined articles rather than attempting to find all articles on a particular topic). It is important to emphasize that the references in this review came from regular searches using Scopus, Web of Science, and PubMed to avoid any potential AI-induced hallucinations with reference details. Each reference citation was also checked by the author.

The outputs of various AI tools were found to be impacted by the specific prompt, the AI tool used, the available inputs accessible to the AI tool (e.g., open-access information vs. databases and articles behind paywalls), and the date the tool was used. Since AI tools as well as the information they can access are rapidly changing, it is expected that what the author experienced when conducting this research throughout 2025 will be quickly out of date.

Article summaries found in Sections 3 and 4 were generated using the following prompt with Gemini Pro (Thinking Mode) on December 10, 2025:

I am writing a scientific review of the forensic DNA literature for the past three years similar to what I did previously with this publication https://doi.org/10.1016/j.fsisyn.2022.100311. Summarize each article in the list below in one or two sentences referring to key data found within the summarized article and include a citation by author and year at the end of each sentence. Discuss the results directly without using a "First Author et al." format.

Put the information in paragraphs that are grouped by topic like this example [this can be any text written by the author in the desired voice, format, and structure; a portion of material for Section 4.5 is shown here]: ***Domesticated Animal DNA***. *Findings of the Canine DNA Recovery Project described efforts to optimize recovery methods for canine DNA in forensic contexts (Dawnay* et al. *2025). A qPCR assay was created to quantify canine autosomal DNA recovered from livestock attacks (Dawnay* et al. *2024). There were also publications on a multidisciplinary forensic approach to solving a fatal dog pack attack (Di Nunzio* et al. *2024) and the introduction of a panel of tetranucleotide STR markers capable of distinguishing between wolves and dogs for forensic identification (Hrebianchuk* et al. *2024). Validation studies have been reported for a 24-locus canine STR genotyping assay (Du* et al. *2023) and a novel 30-plex STR assay for canine*

[4] https://www.zotero.org/.

individual identification and parentage testing (Liu et al. *2024). Also published were a test to predict externally visible traits in dogs to assist in forensic investigations (Heinrich* et al. *2023), a description of the population genetics for 18 STR loci using the Canine Genotypes Panel 2.1 Kit on pure-bred dogs in Japan (Kunita* et al. *2024), a comparison of commercial dog breed kits with STR genotyping for identity determinations (Novroski* et al. *2023), a method was reported for sequencing the whole mitochondrial DNA of domestic dogs (Sugasawa* et al. *2023), and how annealing temperatures affect 16S rRNA gene-amplicon sequencing for analyzing the bacterial community on canine skin (Apostolopoulos* et al. *2023).*

List of articles to summarize: [pasted in references for each section from Supplemental File 2].

To produce additional summaries for each subsequent section within the same AI chat, the following prompt was used:

Please create a similar summary for these provided references: [paste in references for the next section].

Some minor text polishing was required to finalize the text used in Sections 3 and 4 of this INTERPOL DNA review. Readers can verify the accuracy of information provided as the full list of references cited in these sections can be found in each category of Supplemental File 2. For example, for the domestic animal DNA summary provided above in the AI prompt, the reference for a whole mitochondrial DNA sequencing method of domestic dogs (Sugasawa et al., 2023) is available on page 115 of Supplemental File 2. The curated information gathered and described within this review, in particular Supplemental File 2, should benefit searches and summaries performed with future AI tools.

2. General resources

General resources considered in this section include books and major reports published in 2023, 2024, and 2025 along with special issues in various journals related to forensic biology or forensic DNA, key conferences and published proceedings (including ISFG 2022 and 2024), and guidance documents intended to support quality assurance efforts in forensic DNA laboratories.

2.1. Books and major reports

Table 1 lists 24 books or major reports published during the period of this review relating to forensic biology and forensic DNA. Several of these books describe efforts using investigative genetic genealogy. At the bottom of Table 1, two National Institute of Standards and Technology Interagency Reports (NISTIRs) are listed that each contain more than 400 pages of content and provide recommendations and key takeaways on DNA interpretation. Both reports provide training material outlining principles that underpin biology, genetics, measurement science, interpretation, and statistical aspects of DNA mixture interpretation.

2.2. Special issues of journals

Over the past three years, multiple special issues on topics related to forensic biology and DNA were published in *Electrophoresis*, *Forensic Science International* (FSI), *Forensic Science International: Genetics* (FSIG), *Genes*, *International Journal of Molecular Sciences* (IJMS), and *Sensors* (Table 2). These 20 special issues were typically collated virtually rather than physically as invited articles were published online over a period of time and then bundled together virtually as a special issue. Some of these review articles or a set of special issue articles are open access (i.e., the authors paid a publication fee so that the article would be available online for free to readers).

2.3. Key conferences and published proceedings

A growing number of conferences are held around the world covering aspects of DNA testing and use in law enforcement investigations and courts of law. For example, the UK Royal Society and U.

Table 1
Forensic DNA books and major reports published from 2023 to 2025.

Book Title (Publisher, Year)	Author(s) or Editor(s)	Ref.
Forensic DNA Trace Evidence Interpretation: Activity Level Propositions and Likelihood Ratios (CRC Press, 2023)	Bas Kokshoorn, Duncan Taylor	[4]
Law, Practice and Politics of Forensic DNA Profiling: Forensic Genetics and their Technolegal Worlds (Routledge, 2023)	Victor Toom, Matthias Wienroth, Amade M'charek (editors)	[5]
Forensic DNA Analyses Made Simple: A Guide for the Curious (CRC Press, 2023)	O. Bagasra, E. McLean, M. Saffar	[6]
Forensic DNA Analysis: Methods and Protocols (Human Press, 2023)	Catherine Cupples Connon (editor)	[7]
Advancements in Forensic DNA Analysis (Springer, 2023)	Hirak Ranjan Dash, Kelly M. Elkins, Noora Rashid Al-Snan	[8]
Genetic Reconstruction of the Past: DNA Analysis in Forensics and Human Evolution (Oxford University Press, 2023)	Henry A. Erich	[9]
Forensic DNA Applications: An Interdisciplinary Perspective, Second Edition (CRC Press, 2023)	Dragan Primorac, Moses Schanfield (editors)	[10]
Forensic DNA Transfer (CRC Press, 2023)	Jane Moira Taupin	[11]
Fundamentals of Forensic Biology (Springer, 2024)	Avinash Puri, Nithyanandam Mahalakshmi, Tanya Chauhan, Alka Mishra, Preeti Bhatnagar (editors)	[12]
Next Generation Sequencing (NGS) Technology in DNA Analysis (Elsevier, 2024)	Hirak Ranjan Dash, Kelly M. Elkins, Noora Rashid Al-Snan (editors)	[13]
Evidentiary Value of DNA Profiling in Criminal Trials: Law & Forensics (Law & Justice Publishing, 2024)	Abhishek Sharma Padmanabhan	[14]
Forensic DNA Evidence: Science and the Law (The Rutter Group Criminal Practice Series) (Thomson Reuters, 2025)	Hon. Ming W. Chin (Ret.), Michael Chamberlain, Amy Rojas, Lance Gima	[15]
An Introduction to Forensic Genetics for Non-geneticists (CRC Press, 2025)	Antonio Amorim, Nadia Pinto	[16]
Advances in Forensic Biology and DNA Typing (CRC Press, 2025)	Anna Barbaro, Amarnath Mishra (editors)	[17]
Forensic Biology, Third Edition (CRC Press, 2025)	Richard Li	[18]
Forensic Serology (Elsevier Academic Press, 2025)	Shanan S. Tobe	[19]
I Know Who You Are (Random House, 2023)	Barbara Rae Venter	[20]
Revolutionizing Law Enforcement Investigations Through DNA Genealogy: Solving the Unsolvable Through Genetic Detective Work (self-published, 2024)	James E. Lefemine	[21]
The Complete Guide to FamilyTree DNA: Y-DNA, Mitochondrial, Autosomal and X-DNA (Genealogical Publishing Company, 2024)	Roberta Estes	[22]
Forensic Genealogy: Theory & Practice (National Genealogical Society, 2025)	Michael S. Ramage and Catherine B. W. Desmarais	[23]
The Forensic Revolution: IGG Investigative Genetic Genealogy (self-published, 2025)	Curtis C. Rogers, Jr.	[24]
Law Enforcement Use of Probabilistic Genotyping, Forensic DNA Phenotyping, and Forensic Investigative Genetic Genealogy Technologies: Proceedings of a Workshop (National Academies Press, 2024)	National Academies of Sciences, Engineering, and Medicine	[3]
Forensic DNA Interpretation and Human Factors: Improving the	Expert Working Group led by Melissa K. Taylor	[25]

(*continued on next page*)

Table 1 (*continued*)

Book Title (Publisher, Year)	Author(s) or Editor(s)	Ref.
Practice Through a Systems Approach (NISTIR 8503)		
DNA Mixture Interpretation: A NIST Scientific Foundation Review (NISTIR 8351)	John M. Butler, Hari Iyer, Rich Press, Melissa K. Taylor, Peter M. Vallone, Sheila Willis	[26]

Table 2
Special issues on forensic DNA topics during 2023-2025 (a few articles were published earlier). *issue had not yet closed when this table was created.

Journal	Special Issue Title (with hyperlinks to issue)	Issue Editor(s)	# Articles
Electrophoresis	Innovation in Forensic Analysis 2024	Athina Vidaki & Bruce McCord	15 research, 1 review, 1 editorial
FSI	23rd Meeting Collection for the International Association of Forensic Sciences (IAFS)	Claude Roux, Marie Morelato, Chris Lennard, Ali Ross	12 of 50 on DNA or body fluid ID
FSI	European Academy of Forensic Sciences (EAFS) 2022	Didier Meuwly	3 of 27 on DNA
FSIG	Forensic Genetics: Unde venisti et quo vadis?	Manfred Kayser	11 review, 1 editorial
FSIG	Ethics in Forensic Genetics	Eugenia D'Amato	6 research
FSIG	Advancing Justice: Insights from Exceptional Cases	Lourdes Prieto & Walther Parson	5 research, 1 report*
Genes	Advances in Forensic Molecular Genetics	Erin K. Hanson & Claire L. Glynn	8 research
Genes	Improved Methods in Forensic DNA Analysis	Marie Allen	8 research, 1 review
Genes	State-of-the-Art in Forensic Genetics	Chiara Turchi	13 research, 4 review
Genes	Identification of Human Remains for Forensic and Humanitarian Purposes: From Molecular to Physical Methods	Elena Pilli & Cristina Cattaneo	9 research, 1 report
Genes	Strategies and Techniques in DNA Forensic Inves tigations	Claus Børsting & Vania Pereira	5 research, 1 review
Genes	Genetic Tools and Techniques in Forensic Science—an In-Depth Look at the Process of Quantification of Forensic Samples	Ugo Ricci	5 research, 1 review, 1 report
Genes	Advanced Research in Forensic Genetics	Mauro Pesaresi	3 research
Genes	Advances in Forensic Genetics and DNA	Maria Saiz	1 research
IJMS	Molecular Biology in Forensic Science: Past, Present and Future	Francesco Sessa & Monica Salerno	8 research, 2 review, 1 editorial
IJMS	New Perspectives on Bi ology in Forensic Diagnosti cs	Isabella Aquila	5 research, 1 review
IJMS	The Contribution of Proteomics and Post-mortem Laboratory Investigations in Forensic Pathology	Isabella Aquila	1 research, 3 review, 1 editorial
IJMS	Molecular Biology in Forensic Science: Past, Present and Future, 2nd Edition	Francesco Sessa & Monica Salerno	4 research, 2 review
IJMS	Molecular Updates and Applications in Forensic Medicine	Eugenia Carnevali	2 research, 2 review
Sensors	Advanced Analysis and Sensing at the (Crime) Scene or Location of Interest)	Brigitte Bruijns & Roald M. Tiggelaar	6 research, 3 review

S. National Academy of Sciences jointly organized an October 2023 meeting titled "Science in the Interests of Justice" with a published summary of discussions that included some remarks on DNA mixture evidence, likelihood ratios, and presenting evidence ([27] see pp. 11-13, 22-26).

Two sets of proceedings for the biennial International Society for Forensic Genetics (ISFG) were published within the time window of this review: ISFG 2022 with 126 articles across 352 pages [28] and ISFG 2024 with 166 articles across 1253 pages [29]. In his role as ISFG President, the author wrote the introduction for the Congress Proceedings of ISFG 2022 [30] and ISFG 2024 [31]. The extended abstracts published in the ISFG proceedings contain a great deal of useful information, some of which may be published later in more extensive research articles. The American Academy of Forensic Sciences (AAFS) held three meetings with many forensic DNA presentations over the course of this review timeframe. The AAFS presentation abstracts are available[5] online.

The International Symposium on Human Identification (ISHI) no longer publishes proceedings[6] from their annual meetings and now shares information through a periodic *ISHI Report*[7] and blog.[8] A Gordon Research Conference (GRC) "Forensic Analysis of Human DNA" was held June 22-27, 2025, with discussions of cutting-edge research but no published proceedings. Topics in this GRC meeting[9] included techniques for challenging samples; characterization of -omics approaches; using RNA, peptides, and microbes; activity-level analysis and reporting; making the most of lineage analysis; inferring the age of stains, donors or post-mortem interval; progress in forensics through machine learning and AI; and single-cell analysis and microfluidics.

In March 2024, the U.S. National Academy of Sciences held a two-day workshop and published proceedings titled "Law Enforcement Use of Probabilistic Genotyping, Forensic DNA Phenotyping, and Forensic Investigative Genetic Genealogy Technologies" [3] that brought together experts on these topics along with ethics, privacy, and the law to consider implications in terms of public trust in law enforcement efforts. Presentation materials from this workshop are available[10] online.

2.4. Guidance documents

Numerous documentary standards and guidance documents related to forensic DNA have been published in English by various organizations around the world. Table 3 lists 70 such documents released in the past three years (2023 to 2025) from 17 organizations in the United States, United Kingdom, Australia, and the European Union. These guidance documents are briefly discussed in the following sections and are organized by date and organization.

2.4.1. FBI, SWGDAM, and other US DOJ activities

The Federal Bureau of Investigation (FBI) Laboratory funds the Scientific Working Group on DNA Analysis Methods (SWGDAM)[11] to serve as a forum for discussing, sharing, and evaluating forensic biology methods, protocols, training, and research. In addition to creating guidelines on various topics, SWGDAM, which meets semiannually in January and July, provides recommendations to the FBI Director on the

[5] See https://www.aafs.org/research/annual-conference-proceedings.
[6] For ISHI Conference Proceedings from 1998 to 2019, see https://www.promega.com/products/pm/genetic-identity/ishi-conference-proceedings/proceedings-index-home/.
[7] https://www.ishinews.com/the-ishi-report/.
[8] https://www.ishinews.com/blog/.
[9] https://www.grc.org/forensic-analysis-of-human-dna-conference/2025/.
[10] See https://www.nationalacademies.org/event/41774_03-2024_law-enforcement-use-of-probabilistic-genotyping-forensic-dna-phenotyping-and-forensic-investigative-genetic-genealogy-technologies-a-workshop-public-session.
[11] See https://www.swgdam.org/.

Table 3
Guidance documents related to forensic DNA published since the previous review [1]. Abbreviations: FBI (Federal Bureau of Investigation), SWGDAM (Scientific Working Group on DNA Analysis Methods), ANSI (American National Standards Institute), ASB (Academy Standards Board), OSAC (Organization of Scientific Area Committees for Forensic Science), UKFSR (United Kingdom Forensic Science Regulator), ENFSI DNA WG (European Network of Forensic Science Institutes DNA Working Group), ANZPAA NIFS (Australia New Zealand Policing Advisory Agency National Institute of Forensic Science), AABB (Association for the Advancement of Blood and Biotherapies), ISFG (International Society for Forensic Genetics), IACP (International Association of Chiefs of Police), ISO (International Organization for Standardization).

Organization	Publication Date	Guidance Document Title	Ref.
FBI	July 2025	Quality Assurance Standards for Forensic DNA Testing Laboratories (50 pages) with Quality Assurance Standards Audit for Forensic DNA Testing Laboratories (Excel file)	[32]
FBI	July 2025	Quality Assurance Standards for DNA Databasing Laboratories (38 pages) with Quality Assurance Standards Audit for DNA Databasing Laboratories (Excel file)	[33]
FBI	July 2025	Guidance Document for the FBI Quality Assurance Standards for Forensic DNA Testing and DNA Databasing Laboratories (effective July 1, 2025) (109 pages)	[34]
FBI	Mar 2025	Guide to All Things Rapid DNA (17 pages)	[35]
SWGDAM	Jan 2024	SWGDAM Resource Document: Forensic DNA Analysis – Team Approach (9 pages)	[36]
SWGDAM	Jan 2024	SWGDAM Interpretation Guidelines for Single Nucleotide Polymorphism (SNP) Analysis by Forensic DNA Testing Laboratories (30 pages)	[37]
SWGDAM	Sept 2024	SWGDAM Interpretation Guidelines for Mitochondrial DNA Analysis by Forensic DNA Testing Laboratories (15 pages)	[38]
SWGDAM	Sept 2024	Supplemental Information for the SWGDAM Interpretation Guidelines for Mitochondrial DNA Analysis by Forensic DNA Testing Laboratories (62 pages)	[39]
SWGDAM	Dec 2024	SWGDAM Guidelines for Missing Persons Casework (36 pages)	[40]
SWGDAM	Apr 2025	SWGDAM Guidelines for Reporting Likelihood Ratios (13 pages)	[41]
SWGDAM	Apr 2025	SWGDAM Guidelines for the Use of Probabilistic Genotyping with Autosomal STR Typing Results (26 pages)	[42]
SWGDAM	July 2025	Validation Guidelines for the Use of an Expert System with Forensic Samples (24 pages)	[43]
SWGDAM	Dec 2025	SWGDAM Position Statement on Formal Activity Level Reporting (ALR) (5 pages)	[44]
ANSI/ASB	Jan 2024	(ANSI/ASB Standard 123) Standard for Routine Internal Evaluation of a Laboratory's DNA Interpretation and Comparison Protocol	[45]
ANSI/ASB	Jan 2024	(ANSI/ASB Standard 154) Standard for Training on Testimony for Forensic Biology	[46]
ANSI/ASB	Feb 2024	(ANSI/ASB Standard 139) Reporting DNA Conclusions	[47]
ANSI/ASB	Feb 2024	(ANSI/ASB BPR 171) Best Practice Recommendations for the Management and Use of Quality Assurance DNA Elimination Databases in Forensic DNA Analysis	[48]
ANSI/ASB	May 2024	(ANSI/ASB Standard 180) Standard for the Selection and Evaluation of GenBank® Results for Taxonomic Assignment of Wildlife	[49]
ANSI/ASB	July 2024	(ANSI/ASB Standard 175) Standard for Interpreting, Comparing and Reporting DNA Test Results Associated with Failed Controls and Contamination Events	[50]
ANSI/ASB	June 2025	(ANSI/ASB Standard 216) Standard for Construction of Multilocus Databases	[51]
OSAC	Aug 2025	OSAC Technical Guidance Document 0009: Human Forensic DNA Reporting Appendix Exemplar (23 pages)	[52]
OSAC	Sept 2025	OSAC Wildlife Forensic Biology Process Map (57 pages)	[53]
NIST	Sept 2024	(SP1319) Strategic Opportunities to Advance Forensic Science in the United States: A Path Forward Through Research and Standards (50 pages)	[54]
NIST	Mar 2025	(SP1500-28) Informational Scientific Primers for Officers of the Court: Intended to Strengthen Use of Forensic Science Evidence (68 pages)	[55]
NIST	Sept 2025	(SP1500-33 A,B,C) Evidence Management Steering Committee Report: Opportunities to Strengthen Evidence Management Processes (90 pages), Results of the 2021 National Evidence Handlers Survey (142 pages), Expanded Bibliography (91 pages)	[56–58]
NIST	Dec 2025	(NISTIR 8589) Validation in Forensic Science: Guiding Principles for the Collection and Use of Validation Data (31 pages)	[59]
ASTM	2023	(ASTM-E2057-23) StandardSpecifications for Preparation of Laboratory Analysis Requests in Sexual Violence Investigations	[60]
ASTM	2024	(ASTM-E2917-24a) StandardPractice for Forensic Science Practitioner Training, Continuing Education, and Professional Development Programs	[61]
ASTM	2025	(ASTM-E1732-25) StandardTerminology Relating to Forensic Science	[62]
NTVIC	Feb 2023	NTVIC Policies and Procedures for Forensic Investigative Genetic Genealogy (FIGG)	[63]
NTVIC	Nov 2023	NTVIC Guidelines for Establishing Forensic Investigative Genetic Genealogy (FIGG) Programs	[64]
NTVIC	Dec 2025	NTVIC Updated Guidelines for Establishing Forensic Investigative Genetic Genealogy (FIGG) Programs	[65]
IGGAB	Apr 2024/ 2025	Investigative Genetic Genealogy – Professional Standards and Accreditation Requirements (17 pages)	[66]
IGGAB	Apr 2025	Investigative Genetic Genealogy – Code of Professional Ethics (8 pages)	[67]
UKFSR	Oct 2023	(FSR-GUI-0016) Guidance: Contamination Controls: Scene of Crime	[68]
UKFSR	Oct 2023	(FSR-GUI-0018) Guidance: DNA Contamination Controls: Laboratory	[69]
UKFSR	July 2024	(FSR-P-300) Guidance Protocol: Use of Casework Material for Validation Purposes: Issue 2	[70]

(*continued on next page*)

Table 3 (*continued*)

Organization	Publication Date	Guidance Document Title	Ref.
UKFSR	July 2024	(FSR-G-213) Guidance: Allele Frequency Databases and Reporting Guidance for the DNA (Short Tandem Repeat) Profiling: Issue 2	[71]
UKFSR	July 2024	(FSR-P-302) Guidance: DNA Contamination Detection: Issue 2	[72]
UKFSR	July 2024	(FSR-G-222) Guidance: DNA Mixture Interpretation: Issue 3	[73]
UKFSR	July 2024	(FSR-G-228) Guidance: DNA Relationship Testing Using Autosomal Short Tandem Repeats	[74]
UKFSR	July 2024	(FSR-G-200) Guidance: Expert Report Content: Issue 4	[75]
UKFSR	July 2024	(FSR-G-201) Guidance: Forensic Science Providers: Validation: Issue 2	[76]
UKFSR	July 2024	(FSR-G-224) Guidance: Proficiency Testing Guidance: DNA Mixture Analysis and Interpretation	[77]
UKFSR	July 2024	(FSR-G-223) Guidance: Software Validation for DNA Mixture Interpretation: Issue 2	[78]
UKFSR	Jan 2025	(FSR-GUI-0017) Guidance: DNA Contamination Controls: Forensic Medical Examinations	[79]
UKFSR	June 2025	Guidance: Forensic Science Activities: Statutory Code of Practice - Version 2	[80]
UKFSR	Jan 2025	(FSR-GUI-0015) Guidance: Methods Employing Rapid DNA Devices	[81]
UKFSR	Mar 2025	(FSR-GUI-0013) Guidance: Y-STR Profiling: Issue 2	[82]
ENFSI DNA WG	Dec 2022	ENFSI Best Practice Manual for Human Forensic Biology and DNA Profiling (50 pages)	[83]
ENFSI DNA WG	May 2023	ENFSI Guideline for Internal Validation/Verification of Various Aspects of the DNA Profiling Process (11 pages)	[84]
ENFSI DNA WG	Oct 2023	ENFSI Guideline for DNA Database Management Review and Recomm endations (94 pages)	[85]
ENFSI DNA WG	Oct 2023	ENFSI Guideline for DNA Contamination Minimization in DNA Laboratories (10 pages)	[86]
ANZPAA NIFS	Apr 2024	Principles for the Application of Forensic/Investigative Genetic Genealogy	[87]
ANZPAA NIFS	Sept 2024	Principles for Reporting Forensic Biology Evidence	[88]
ANZPAA NIFS	Dec 2024	Principles of Authentic Quality Culture in Forensic Science Service Provision	[89]
ANZPAA NIFS	June 2025	Guideline for the Validation of Forensic Science Methods (53 pages)	[90]
AABB	Jan 2024	Standards for Relationship Testing Laboratories, 16th Edition	[91]
ISFG DNA Commission	Jan 2024	Recommendations of the DNA Comm ission of the International Society for Forensic Genetics (ISFG) on short tandem repeat sequence nom enclature	[92]
FSI Genetics	July 2023	Editorial Considerations for Publication in *Forensic Science International: Genetics*	[93]
FSI Genetics	July 2025	Minimum FSI: Genetics requirements for publishing data on DNA transfer and recovery, given activities	[94]
INTERPOL	Nov 2023	Disaster Victim Identification Guide (110 pages with all annexes) Disaster Victim Identification Guide Annexure 8 Methods of Identification (5 pages)	[95]
IACP	2024	Resolution: Incorporation of Rapid DNA in Mass Disaster Response Plans	[96]
IACP	2024	Resolution: Promote Implementation of and Adherence to Forensic Science Standards	[97]
ISO 21043-Part1	June 2025	Forensic Sciences – Part 1: Vocabulary	[98]
ISO 21043-Part3	June 2025	Forensic Sciences – Part 3: Analysis	[99]
ISO 21043-Part4	June 2025	Forensic Sciences – Part 4: Interpr etation	[100]
ISO 21043-Part5	June 2025	Forensic Sciences – Part 5: Reporting	[101]

Quality Assurance Standards (QAS) used to assess U.S. forensic DNA laboratories involved in the National DNA Index System (NDIS) that perform DNA databasing and forensic casework. New versions of the QAS became effective July 1, 2025, along with forensic QAS audit and database QAS audit Excel files and an additional guidance document [34]. The 2025 QAS includes new sections on laboratory use of rapid DNA and rapid DNA partner agencies. In March 2025, the FBI revised their "Guide to All Things Rapid DNA" [35]. Since July 1, 2025, crime scene evidence analyzed with approved rapid DNA instruments can now be searched in the Combined DNA Index System (CODIS) when eligibility requirements have been met.

From 2023 to 2025, SWGDAM work products include guidelines for missing persons casework [40], for reporting likelihood ratios [41], for interpretation of single nucleotide polymorphism (SNP) typing results [37], for mitochondrial DNA analysis [38,39], for the use of probabilistic genotyping with autosomal STR typing results [42], and validation guidelines for the use of an expert system with forensic casework [43].

In January 2024, SWGDAM prepared a 9-page resource document to explain a commonly used team approach with forensic DNA analysis and how this might impact court testimony requests [36]. Survey responses by 94 laboratories to six questions from SWGDAM found that 65% employ a team approach where more than one laboratory staff member performs the steps involved to produce a DNA profile from a biological sample "to foster consistency, achieve efficiencies and to ensure quality work" [36].

In 2025, SWGDAM started a new Investigation Genetic Genealogy Committee to consider technical, quality assurance, and data privacy issues for the forensic science and law enforcement communities. This committee will likely build upon earlier work [102]. In December 2025, SWGDAM also released a position statement on formal activity level reporting (ALR) – that "in its present form, [formal ALR] is not suitable for use in the U.S. criminal justice system" and "SWGDAM will continue to monitor developments and make recommendations as necessary" [44].

The U.S. Department of Justice Uniform Language for Testimony and Reports (ULTRs)[12] for DNA, which includes autosomal DNA with probabilistic genotyping, mitochondrial DNA, and Y-chromosome short tandem repeat DNA, have not changed since 2022.

2.4.2. OSAC and ASB activities

The Organization of Scientific Area Committees for Forensic Science (OSAC)[13] is Congressionally funded and administered by the Special Programs Office within the National Institute of Standards and Technology (NIST). OSAC consists of a governing board and over 600 members and associates organized into seven scientific area committees

[12] https://www.justice.gov/olp/uniform-language-testimony-and-reports.
[13] https://www.nist.gov/organization-scientific-area-committees-forensic-science.

(SACs) and 22 subcommittees. The Biology SAC is divided into human and wildlife forensic biology activities. The Human Forensic Biology Subcommittee[14] focuses on standards and guidelines related to training, method development and validation, data analysis, interpretation, and statistical analysis as well as reporting and testimony for human forensic serological and DNA testing. The Wildlife Forensics Subcommittee[15] works on standards and guidelines related to taxonomic identification, individualization, and geographic origin of non-human biological evidence based on morphological and genetic analyses.

The Academy Standards Board (ASB)[16] is a wholly owned subsidiary of the American Academy of Forensic Sciences (AAFS) and was established in 2016 as a standards developing organization (SDO) under the American National Standards Institute (ANSI). After development, ANSI/ASB standards and best practice recommendations documents are considered for inclusion in the OSAC Registry to promote implementation of standards in forensic laboratories and advance the practice of forensic science. Single-page factsheets[17] are currently published to summarize the purpose, use, and contents of each published ASB document.

From 2023 to 2025, six standards and one best practice recommendation document were completed by ANSI/ASB and subsequently approved for inclusion on the OSAC Registry. These documents discuss conducting routine internal protocol evaluations [45], training for court testimony [46], reporting DNA conclusions [47], managing and using quality assurance DNA elimination databases [48], reporting DNA test results associated with failed controls and contamination events [50], performing genetic taxonomic assignment of wildlife [49], and constructing multi-locus population databases for wildlife forensics [51]. In August 2025, the OSAC Human Biology Subcommittee published a guidance document discussing "reporting statements, limitations, and caveats to accompany reports containing DNA results and conclusions" [52]. The Wildlife Forensic Biology Subcommittee also released a 57-page detailed process map covering steps in analysis and comparison of wildlife evidence, species identification, sex determination, geographic origin, and familial relationships [53].

In May 2025, the OSAC Human Forensic Biology Subcommittee revised their research and development needs[18] and organized them into 8 high priority and 3 medium priority needs compared to the 18 listed needs reported in the previous review three years ago (see Table 3 in Ref. [1]).

2.4.3. NIST publications

During the timeframe of this review, NIST issued several special publications (SP) that can be considered as general guidance documents (see Table 3).

NIST SP 1319 (published in September 2024) examined strategic opportunities to advance forensic science in the United States through research and standards [54]. These opportunities, which are not limited to the United States, center around four grand challenges related to (1) accuracy and reliability of complex methods and techniques for analysis of forensic evidence, (2) new methods and techniques for analysis of forensic evidence, (3) science-based standards and guidelines for forensic science practices, and (4) adoption and use of advanced forensic analysis methods, techniques, standards, and guidelines [54].

NIST SP1500-28 (released in March 2025) provided 17 informational primers (typically 2-pages in length) intended to provide short overviews on aspects of quality, statistics, and communication for officers of the court [55]. Topics covered include accreditation and certification, documentary standards, quality assurance versus quality control, method validation and method verification, metrological traceability, human factors, algorithms, performance monitoring of methods, people, and organizations, why certain items are selected for examination, general statistics, method performance statistics, statistical sampling, population statistics, probability and likelihood ratios, measurement uncertainty, frequency data, error rates, forensic science reports, and communicating limitations.

NIST SP1500-33 (finalized in September 2025) relates to evidence management and contains three parts assembled by a joint NIST and NIJ Evidence Management Steering Committee: (A) a 90-page committee report with recommendations for the retention, preservation, integrity, and disposition of evidence and property [56], (B) a 142-page summary of results from a 2021 national evidence handlers survey [57], and (C) a 91-page expanded bibliography of published resources found in the evidence management steering committee report [58]. The raw data from the survey was also published.

As cited in Table 1, two major NIST Interagency Reports (IRs) were published by NIST in 2024: one on human factors involved in DNA interpretation (NISTIR 8503 [25]) and the other a scientific foundation review of DNA mixture interpretation (NISTIR 8351 [26]). In December 2025, NIST researchers provided five guiding principles for the collection and use of validation data (NISTIR 8589 [59]).

2.4.4. ASTM

ASTM International, formerly known as the American Society for Testing and Materials, has a committee (E30)[19] working on forensic science topics. Three documents of relevance to forensic DNA were published in the past three years by ASTM E30: (1) standard specifications for requesting the scientific examination of physical evidence collected in sexual assault investigations [60], (2) standard practices for practitioner training and continuing education [61], and (3) standard terminology related to forensic science [62].

2.4.5. NTVIC and IGGAB

Guidance to support forensic investigative genetic genealogy efforts has come from two groups that have become active over the past three years.

The National Technology Validation and Implementation Collaborative (NTVIC) consists of volunteer members from U.S. forensic science laboratories, universities, and private technology and research companies with a "common vision to share existing resources to work together on validation and implementation projects to lessen the burden on individual forensic science and forensic medicine providers" [103]. The NTVIC, which launched in 2022, has published several articles in *Forensic Science International: Synergy* to describe its mission, vision, purposes, and first working group [103], policies and procedures for forensic investigative genetic genealogy (FIGG) [63], and guidelines for establishing FIGG programs [64,65]. As of September 2025, NTVIC[20] had representatives from 35 U S. states and the District of Columbia and established technical validation working groups or task groups in FIGG, firearm 3D imaging, rapid DNA, single-cell DNA, DNA activity level evaluation, and public policy evaluations.

The Investigative Genetic Genealogy Accreditation Board (IGGAB)[21] was founded in early 2022 and consists of the seven individuals representing academic and private efforts in this field. IGGAB's Advisory Board[22] involves subject matter experts in a broad range of IGG-related disciplines, including genetic genealogy, bioethics, legal, forensic

[14] https://www.nist.gov/organization-scientific-area-committees-forensic-science/human-forensic-biology-subcommittee.
[15] https://www.nist.gov/topics/organization-scientific-area-committees-forensic-science/wildlife-forensics-subcommittee.
[16] https://www.aafs.org/academy-standards-board.
[17] https://www.aafs.org/standards-resources-training/factsheets.
[18] https://www.nist.gov/osac/osac-research-and-development-needs.
[19] https://www.astm.org/membership-participation/technical-committees/committee-e30.
[20] https://sites.google.com/view/ntvic/.
[21] https://www.iggab.org/board.html.
[22] https://www.iggab.org/advisors.html.

science, bioinformatics, law enforcement and academia. In 2024 and 2025, the IGGAB published professional standards and accreditation requirements [66] and a code of professional ethics [67]. IGGAB also administers an IGG accreditation exam.

2.4.6. UK Forensic Science Regulator

The UK Forensic Science Regulator (UKFSR) oversees forensic science efforts in England, Wales, and Northern Ireland. In 2021, the Forensic Science Regulator Act passed by Parliament made the Code of Practice statutory beginning in October 2023. Version 2 of this Code of Practice (now 388 pages) [80] went into effect in October 2025. Table 3 lists 15 guidance documents pertinent to biological evidence from the UKFSR [68–82]. Some recent changes in the guidance documents accompanying the Code of Practice (i.e., those UKFSR documents in Table 3 with Issue 2, 3, or 4 in their title) appear to be editorial rather than substantive compared to previous versions.

2.4.7. European Union and ENFSI

The European Network of Forensic Science Institutes (ENFSI) DNA Working Group published four documents in the past three years: a best practice manual for human forensic biology and DNA profiling [83] as well as guidelines for internal validation/verification of various aspects of the DNA profiling process [84], DNA database management [85], and DNA contamination minimization in laboratories [86] (see Table 3).

2.4.8. Australia and New Zealand

During the past three years, the Australian New Zealand Policing Advisory Agency (ANZPAA) National Institute of Forensic Science (NIFS) published three short (1- or 2-page) documents considering key principles on applying investigative genetic genealogy [87], reporting forensic biology evidence [88], and providing an authentic quality culture in forensic science [89]. In June 2025, ANZPAA NIFS also shared guidelines for validation of forensic science methods [90] (see Table 3).

2.4.9. Other international efforts

The Association for the Advancement of Blood and Biotherapies (AABB)[23] published the 16th edition of their Standard for Relationship Testing Laboratories, which became effective on January 1, 2024. This documentary standard was developed by the AABB Relationship Testing Standards Committee and applies to laboratories accredited for paternity testing and other forms of genetic relationship assessment [91].

The International Society for Forensic Genetics (ISFG) DNA Commission[24] published one article during the timeframe of this INTERPOL review (see Table 3) relating to short tandem repeat sequence nomenclature [92]. This ISFG DNA Commission described five recommendations covering 1) sequence strings and a minimum reporting range, 2) additional sequence formats, 3) resources for researchers, bioinformaticians, and practitioners, 4) information on characterizing new STR loci, and 5) considerations for incorporating STR sequences and other new markers into investigative databases [92].

Forensic Science International: Genetics, the official journal of ISFG, provided guidance for authors and reviewers, which among other topics emphasized the importance of having "conclusions supported by a comprehensive set of open-access data and/or open-source software and/or other documentation to ensure that the work is accessible and useful to the broader community" [93]. With a goal to improve consistency in studies on DNA transfer, persistence, prevalence, and recovery (TPPR), editorial guidance was recently provided with a supplemental Excel template outlining the minimum information required for each sample in future analyses [94].

In November 2023, INTERPOL released their updated Guide to Disaster Victim Identification (DVI) with multiple annexes [95]. The Forensic Science Committee of the International Association of Chiefs of Police (IACP) provided two resolutions in 2024 that were accepted by the IACP membership regarding the use of rapid DNA in mass disaster responses [96] and promoting adoption of forensic science standards [97].

In June 2025, Technical Committee 272 of the International Organization for Standardization (ISO), which was created in 2012 to work on standardization and guidance in forensic science,[25] published four parts to ISO 21043 covering vocabulary [98], analysis [99], interpretation [100], and reporting [101]. These ISO 21043 standards are intended for all aspects of forensic science, not just biological evidence, and "represents a unique opportunity to unify and advance forensic science as a discipline, and to improve the reliability of expert opinions and trust in the justice system" [104].

3. Advances in current practices

This section contains information of primary use to law enforcement and practitioners and is focused on publications that describe advances in current practices. The following section (Section 4) contains information that is researcher-focused with emphasis on emerging technologies and research studies.

Most of the article summary text in both sections was written by AI (Gemini 3 Pro Thinking Mode) using the prompts described in Section 1.2 of this review. For the text of Sections 3 and 4, reference citations (author-year) refer to the sorted references listed in the specified sections found in Supplemental File 2. *This approach has been used (after consulting with the journal editor-in-chief) to avoid having a very long list of references at the end of this review article that the journal publisher would have to type set for publication.*

3.1. Rapid DNA analysis

Rapid DNA instruments that provide integrated "swab-in-profile-out" results in 90 min or less can be used in police booking station environments and assist investigations outside of a traditional laboratory environment.

Books, Review Articles, and Guidance. A systematic review published in January 2023 examined 8 ParaDNA, 21 RapidHIT, 12 ANDE, and 2 RapidHIT & ANDE articles available in 2022 or earlier, and determined that while impressive developments have occurred with these technologies, "there is still no portable device containing all the required steps available for fast analysis (under 1 h for a full STR profile) of real 'dirty' samples directly at the crime scene" (Bruijns et al., 2023). Options for improving forensic genetic workflows in small geographical areas were evaluated for cost-effectiveness (De La Chica et al., 2025). The FBI released a comprehensive guide covering all aspects of implementing rapid DNA analysis (Federal Bureau of Investigation 2025), while the UK Forensic Science Regulator published specific guidance for methods employing these devices (Forensic Science Regulator 2025). Detailed protocols for profile development using the Applied Biosystems RapidHIT ID System were documented (Foley 2023). The IACP Forensic Science Committee issued a resolution incorporating rapid DNA analysis into mass disaster response plans (IACP Forensic Science Committee 2024), and its specific utility for human identity determination was highlighted following the Maui wildfires (Novroski 2023). Additionally, a book chapter reviewed DNA sequencing and rapid DNA tests within the context of modern forensic tools (Singh & Rawtani 2023).

Results with Rapid DNA Instruments. Empirical studies have expanded the applications of rapid DNA instruments beyond standard reference samples. A field experiment introduced a rapid DNA analysis

[23] https://www.aabb.org/standards-accreditation/standards/relationship-testing-laboratories.

[24] https://www.isfg.org/DNA+Commission.

[25] ISO/TC 272 Forensic sciences: https://www.iso.org/committee/4395817.html.

procedure for crime scene samples outside the laboratory (de Roo et al., 2023). Two simplified tooth sample preparation methods were developed for conventional and RapidHIT ID workflows (Eaton et al., 2024). The processing of biological samples from simulated radiological terrorist events was evaluated using rapid DNA instruments (Frégeau & Laurin 2024). The RapidHIT ID system was applied for fast cell authentication via STR profiling (Koh et al., 2023). A comparative analysis of two rapid DNA technologies was conducted for blood and saliva-based samples (Laurin et al., 2023). The performance of two different RapidHIT ID cartridge types was compared for generating forensic leads (Lim et al., 2025). Results from the 2023 multi-laboratory study were reported for the I-Chip (Romsos et al., 2024) and the RapidINTEL Plus sample cartridge (Romsos et al., 2024). Subsampling blood swabs was identified as an efficient practice for RapidHIT ID analyses (Siatka et al., 2024). A simplified differential extraction method was developed to obtain investigative leads from sexual assault evidence using the RapidHIT ID (Tirado et al., 2025). Finally, the success rate of rapid DNA technology was evaluated for kinship analysis purposes (Ünsal Sapan et al., 2024).

Rapid Methods or Assays. Innovations in rapid testing extend to novel sensors and amplification techniques. A quartz tuning fork-based biosensor was developed for latent DNA detection at crime scenes (Alzahrani et al., 2025). A rapid ABO genotyping method was created using loop-mediated isothermal amplification (LAMP) and real-time PCR (Choi et al., 2024). A critical review examined the conjugation of visual enhancers in lateral flow immunoassays for forensic analysis (Dede & van Dam 2025). A Fusion-5 Filter-based microchip was introduced for efficient on-chip DNA extraction and PCR amplification (Nagpal & Kumar 2024). Field-adapted species identification was achieved by combining multiplex multienzyme isothermal rapid amplification with lateral flow dipsticks (Sun et al., 2024). Rapid human-specific DNA quantitation was demonstrated using a microfluidic amplification module at the point of care (Tan & Selden 2023). Strategies for proactive crime scene response to optimize investigations were discussed (Wickenheiser 2023), alongside a new service delivery model focusing on speed in the forensic laboratory (Wickenheiser & Knutson 2024). Additionally, a recombinase polymerase amplification assay was developed for the specific and rapid detection of human DNA (Zheng et al., 2023).

3.2. DNA databases and ethics

Forensic DNA databases can aid investigations by demonstrating connections between crime scenes, linking a previously developed DNA profile from an arrestee or convicted offender to biological material recovered from a crime scene, or aiding identification of missing persons through association of remains with biological relatives. Establishment of these databases requires significant investments over time to enroll data from crime scenes and potential serial offenders or unidentified human remains and relatives of missing persons. This section explores issues around national DNA databases, elimination databases, familial searching, and ethics related to database governance.

Books, Review Articles, and Guidance. The ENFSI DNA Working Group released comprehensive guidelines for DNA database management review and recommendations (ENFSI DNA Working Group 2023). A review discussed the specific utility of trace DNA within forensic science for both investigative and intelligence purposes (Hoffmann et al., 2024). Additionally, a chapter in a recent text provided a broad overview of forensic DNA databases (Omran 2025).

DNA Databases. The effectiveness of DNA banks in criminal investigations was measured in Brazil (Ataide & Sousa 2023). The usefulness of one-off DNA database searches was evaluated in Western Switzerland (Basset et al., 2025). A retrospective study analyzed the first implementation of the Fast DNA Identification Line (FIDL) automated workflow at the Netherlands Forensic Institute (Benschop et al., 2022). Quality management practices were reviewed for a Brazilian forensic DNA laboratory (Bezerra et al., 2025). A new model for an integrated forensic database was proposed for India (Das et al., 2024), while another study tested the efficacy of recent STR markers in the Indian population (Dixit et al., 2025). ProbRank was introduced as an efficient search method for complex mixtures using a quantitative likelihood ratio model (Hoogenboom et al., 2023). A proposal was made to build a DNA database to help identify children stolen in conflicts (Huston 2025). The impact of DNA databases on crime investigation was analyzed in Ukraine (Kostiuchenko et al., 2024). Public support for expanding DNA databases in South Korea was linked to police empowerment and legitimacy (Kuen et al., 2025). The potential of DNA databanks in Canada to provide information on the criminal behavior of unidentified individuals was explored (Lavergne et al., 2024). The Italian experience with DNA data banks was reviewed regarding facts and perception (Luparia et al., 2024). The establishment of a DNA fingerprinting database was detailed for the United Arab Emirates (Madi 2024). The impact of Brazil's convict genetic profile identification project was evaluated after five years (Minervino et al., 2024). Public awareness and willingness to establish a national forensic DNA and odontology database were assessed in Egypt (Moawad et al., 2025). Awareness and acceptance of storing DNA profiles in a forensic databank were assessed in Malaysia (Nawani et al., 2023). Empirical studies evaluated searching national databases with complex profiles using probabilistic genotyping (Nozownik et al., 2025). The "Prüm implementation" in the UK was cited as a success story of collaboration (Revoir et al., 2025). DNA profiling issues in India, such as sample preservation and legislation, were addressed (Sahajpal & Bhandari 2024). DNA databases were highlighted as a tool to improve the search for missing persons in Brazil (Silva Junior et al., 2022). The value of forensic DNA databases was discussed (Smith & Horne 2024), as well as their establishment in Africa (Smith & Horne 2024) and future directions for the continent (Smith et al., 2024). In the Sahel region of Africa, the need to update national security policy to support forensic DNA databases was emphasized (Zeye et al., 2024).

Elimination Databases. Best practice recommendations were published for the management and use of quality assurance DNA elimination databases (ANSI/ASB 171). The importance of including staff genetic profiles in these databases was highlighted (Bogas et al., 2025). Hungarian legislation regarding the implementation of an elimination database was reviewed (Nogel 2024). A comparative analysis of elimination databases across seven European countries was conducted (Nogel et al., 2025).

Familial Searching. Y-chromosomal kinship estimation was proposed to assist forensic familial searching (Claerhout et al., 2022). Regulatory frameworks for familial searching in Hungary were discussed (Nogel 2022). A new search tool was implemented for familial searches in the Israel criminal DNA database (Ram et al., 2023). The National Forensic DNA Database of South Africa was utilized for familial searching to aid in identifying missing persons (Singh et al., 2025). A report detailed the outcomes of Swedish familial searches from 2019 to 2024 (Widen & Ansell 2025).

Ethics and Database Governance. EU law concerning access to research biobanks for forensic purposes was analyzed (Aime et al., 2023). Legal ethics regarding double jeopardy and splitting cases were discussed (Akhtar 2024). The balance between law, medicine, and ethics in state genomic registries was examined in Ukraine (Akhtyrska & Kostiuchenko 2023). The intersection of behavioral genetics, big data, and the risk of future offending was explored (Alimardani et al., 2023). Stakeholder perspectives on humanitarian forensics and international kinship matching were surveyed (Amankwaa et al., 2025). Migration control and Britain's DNA profiling pilot project were historically analyzed (Bivins 2024). A code of conduct was published for Italian forensic geneticists (Buscemi et al., 2022). Limitations of forensic science in rape and murder cases in India were discussed (Charan & Manikyam 2023).

Ethical considerations for forensic genetic frequency databases were

reported (D'Amato et al., 2024) as were some ethical issues with next-generation sequencing (NGS) technology (DeAngelo & Elkins 2023). A contextual integrity approach was applied to genomic information (de Groot 2024). The importance of consent forms in creating DNA databases was emphasized (Jankova et al., 2022). The governance of international genomics collaborations was reviewed (Joly 2024). Ethical considerations for DNA profiling in India were compared with international guidelines (Khan & Mer 2024). Genetic privacy in the age of consumer applications was examined (Krimsky 2023). Individual privacy and the reporting of biological sex were discussed (Lynch et al., 2025). Biometric forensic identity databases in Europe were analyzed regarding privacy and criminal processes (McCartney et al., 2023). Lessons learned about consenting families for DNA banking were reported from the Sudden Unexpected Infant Death and Sudden Death in the Young Case Registry (MacLeod et al., 2024). The ethical implications of testing DNA found on privately owned family artifacts were explored (McKibbin et al., 2023). The role of managerialism in Irish DNA database policy was deconstructed (O'Connell 2025). Legislative provisions balancing rights and scientific advancement were reviewed (Oosthuizen et al., 2023). Comparisons of forensic procedure legislation across Australian jurisdictions were conducted (Oosthuizen et al., 2024). The precarious future of consumer genetic privacy was highlighted (Ram et al., 2025). U.S. DNA testing policies in the context of family immigration were reviewed (Sandhu 2025), and the legal conundrum of DNA profiling adoption in India was analyzed (Sankar 2024).

Ethical, legal, and social implications (ELSI) of forensic genetic investigations were broadly reviewed (Sessa et al., 2025). The IndiGen project's application in Indian criminal law was discussed (Sharma & Bhardwaj 2023). Ethical forensic practice in research on biomaterials was promoted (Smith & Horne 2024). The regulation of massively parallel sequencing was examined (Smith & Miller 2024). Ethical considerations of CRISPR-Cas technology in forensics were reviewed (Sobral et al., 2025). Legal and ethical issues of gene technology in criminal proceedings were discussed (Sun & Zhang 2023). The emergence of "carceral human rights" in South Africa was discussed (Tamarkin 2025). A volume addressed the law, practice, and politics of forensic DNA profiling (Toom et al., 2023). A call was made to agree on international governance principles for forensic DNA databases (Uberoi et al., 2024). "Noble cause casuistry" in forensic genetics was critiqued (Wienroth & McCartney 2024) as was the new "Forensic Genetics Assemblage" and its boundary-dissolving nature (Wienroth & Granja 2024). Biometric surveillance and the policing of the "crimmigrant other" were discussed (Wienroth & Amelung 2023). A reference database for populations in Burkina Faso was established (Zeye et al., 2024). Ethical reflections on secondary research using criminal investigation data were presented (Zieger & Scudder 2025), along with discussions on dealing with incidental findings (Zieger 2025).

3.3. Forensic investigative genetic genealogy

In recent years when national DNA databases fail to generate a lead to a potential person of interest, law enforcement agencies have started to utilize the capabilities of investigative genetic genealogy (IGG), also called forensic genetic genealogy (FGG), forensic investigative genetic genealogy (FIGG) or even investigative forensic genetic genealogy (iFGG) (Tuazon et al., 2024), as an approach to locate potential persons of interest in criminal or missing persons cases.

Books, Review Articles, and Guidance. The ANZPAA NIFS released principles for the application of FIGG (ANZPAA NIFS 2024), while the National Academies published workshop proceedings on law enforcement use of this technology (Committee on Law and Justice 2024). A guide was published to aid genealogical research using autosomal and lineage marker information (Estes 2024). Notices of action called for standards and certification in investigative genetic genealogy (Gurney et al., 2022, Gurney et al., 2023). Practical guides and case studies illustrated the "forensic revolution," including works on solving cold cases (Lefemine 2024, Rogers 2025) and a memoir on identifying the Golden State Killer (Rae-Venter 2023). Textbooks covered the theory and practice of forensic genealogy (Ramage & Desmarais 2025) and the application of next-generation sequencing (NGS) to cold cases (Smirnova & Elkins 2023). The nomenclature and definition of law enforcement use of genetic genealogy databases were clarified (Tuazon et al., 2024) and reviews highlighted how FIGG is expanding pedigree tracing (Wang et al., 2025) and the challenges involved (Yadav & Sharma 2023). The National Technology Validation and Implementation Collaborative (NTVIC) released and updated guidelines for establishing FIGG programs (Wickenheiser et al., 2023a, Wickenheiser et al. 2023b, Wickenheiser et al. 2025).

Public Perceptions and Trust of FIGG. The commercial dynamics of direct-to-consumer testing and law enforcement cooperation were examined (Bakken & Kaufmann 2025). Conferences addressed the interplay of relationship inference, database accessibility, and ethical concerns (Chauhan & Kumar 2024). Public perspectives on "opting in or out" of forensic kinship investigations were surveyed (Claerhout et al., 2024). Ethical considerations of familial searching were discussed within Canadian legislation (Clausius et al., 2023). National focus group studies and surveys in the U.S. assessed public trust (Dahlquist et al., 2025) and perspectives (Dahlquist et al., 2024). Citizen science was positioned as the root and future of forensic genetic genealogy (Granja 2023). A five-year update on U.S. public perspectives showed continued evolution in opinion (Guerrini et al., 2025). Social media insights were analyzed to gauge public sentiment (Huston et al., 2024). Public trust in forensic science was assessed by surveying 1342 individuals in Israel and was found to be related to trust in science and also trust in the police (Kaplan-Damary et al., 2025). The investigative and policy impacts of FIGG on identifying human remains were discussed (Lasyone et al., 2025). University students were surveyed regarding police use of genetic genealogy databases (Marlor et al., 2025). The legitimacy of FIGG was analyzed under Article 8 of the European Convention on Human Rights (Tuazon et al., 2025).

Legislation and Operational Aspects in Various Countries. The present state of FIGG use in criminal cases in Sweden was detailed (Ansell & Aili Fagerholm 2024), alongside specific use cases (Ansell & Fagerholm 2025a) and legislative discussions (Ansell & Fagerholm 2025b). Perspectives on the use of FIGG in Brazil were shared (Bonamin et al., 2022). The non-consensual collection and analysis of DNA was identified as a “legal lacuna” (i.e., a deficiency or gap in the law) in Australia (Shackel et al., 2025). The operationalization of the National DNA Program for Unidentified and Missing Persons demonstrated capability for human remains identification in Australia (Ward et al., 2024).

Examples of FIGG Cases Solved. Three cold cases in Norway were solved using FIGG (Aanes et al., 2025). The technique was successfully applied to unidentified human remains cases in Oregon (Greytak et al., 2022) and broader human remains identification efforts (Greytak et al., 2024). Use of FIGG in the November 2022 Idaho student homicide investigation was discussed as a pivotal moment for the field (Novroski 2023). An interview highlighted the pioneering use of FIGG by the Toronto Police Service (Novroski 2024).

Privacy Concerns and Database Representation. The effect of increased Latin American representation in databases for identifying remains was analyzed (Binder & Gurney 2024). A genetic portal for crime solvers was launched (Brainard 2023). Privacy prioritization and supportable hypothesis testing were advocated for (Budowle et al., 2024). Legal protections for accessing third-party research databases were examined (Chan et al., 2024). The case for "social privacy" in commercial genetic information was made (de Groot 2023). Private detection of relatives using homomorphic encryption was proposed (de Souza et al., 2024). The decline of 23andMe was analyzed for its implications on consumer genomics (Erlich & Zielinski 2025). Editorial commentary focused on fine-scale population structure (Guanglin et al., 2023). The privacy-performance tradeoff of reference testing was

modeled (Hu & Wein 2024). Legal bases for using data "manifestly made public" were critically examined in Europe (Kuru 2025). Balancing crime-solving with genetic privacy was explored (McGuire et al., 2023), alongside the convergence of genealogy and molecular diagnostics (Newsham 2024). Digital forensics was suggested as a support tool for addressing legal challenges (Nogel 2024). Australian privacy law was analyzed regarding offshore direct-to-consumer genetic data (Shackel & Smith 2025).

Technology Used and Validation Studies Performed. A molecular framework was proposed for enhancing quality control in forensic genome sequencing (Bates et al., 2025). A cost-benefit analysis supported the use of large SNP panels and high-throughput typing (Budowle et al., 2023), asserting genomics will reshape forensic science (Budowle et al., 2025). Whole-genome sequencing methods were explored for degraded DNA (Cady & Greytak 2022). The establishment of the FIGG Technology Validation Working Group was announced (Gamette & Wickenheiser 2023). Algorithms for inferring distant relationships from dense SNP data were improved (Lin et al., 2024), revolutionizing source attribution certainty (Mandape et al., 2024). Workflows like MixDeR were developed to enable FIGG investigations from DNA mixtures (Mitchell et al., 2022, Mitchell et al., 2025). Computational approaches allowed for identification from low-coverage shotgun sequencing data (Nguyen et al., 2023). Advanced relationship predictions were achieved with tools like Orogen (Nicholson 2022). The three main SNP chemistries used in forensic genetics were compared (Novroski 2025). Methods for generating profiles over seven years were assessed (Oefelein 2022). Forensic likelihood ratios were derived from low-coverage sequencing (Ouerghi et al., 2025). Forensic investigation approaches were reviewed (Padmanabhan & Sapna 2023). Imputation studies (Tillmar & Kling 2024) and comparative studies of statistical approaches (Tillmar & Kling 2025) refined distant relationship inference. Benchtop-scale sequencing was shown to identify distant relatives (Woerner et al., 2024). Microarray analysis tools without normalization were developed for degraded DNA (Yagasaki et al., 2023).

Kintelligence Kit. Developmental validation of the ForenSeq Kintelligence kit was completed (Antunes et al., 2024). Considerations for multiplexing libraries with negative controls were evaluated (Bali et al., 2024). A multi-generational study demonstrated the kit's efficacy in kinship analysis (Daniel et al., 2024), and outcomes were compared with the Infinium Global Screening Array (Hymus et al., 2024). Internal validation for FIGG application was performed (Peck et al., 2022). The kit was operationalized for Australian unidentified and missing persons casework (Watson et al., 2024) and evaluated against other panels (Watson et al., 2025).

3.4. Forensic biology and body fluid identification

Workflows with forensic examinations of biological evidence typically involve a visual examination of the evidence, a presumptive and/or confirmatory test for a suspected body fluid (e.g., the amylase assay for saliva), and DNA analysis and interpretation. Body fluid identification (BFID), in particular blood, saliva, semen, or vaginal fluid stains, provides valuable evidence in many investigations and can aid in the resolution of a crime.

Books, Review Articles, and Guidance. The ANZPAA NIFS released principles for reporting forensic biology evidence (ANZPAA NIFS 2024). New books discussing advances in forensic biology and serology were published (Puri et al., 2024, Barbaro & Mishra 2025, Tobe 2025) along with the third edition of a previously published textbook (Li 2025). Several reviews and book chapters discussed lateral flow assays (Bruijns et al., 2023), immunochromatographic blood detection (Cuttaia et al., 2024), NGS-based body fluid detection (Dash 2023), evaluation of body fluid evidence (Crawford & Jarman 2024), and general forensic biology (Kushwaha et al., 2023).

Forensic Biology and Body Fluid Identification (General). Research has focused on improving the detection and characterization of biological stains on various substrates. Pilot studies demonstrated the detection of blood, semen, and saliva on the underside of fabric to which it was deposited (Beveridge et al., 2024). Raman hyperspectral imaging characterized bio-fluid spots on cotton (Castellino et al., 2025). Microbial influence on ABO typing discrepancies was explored (Chakraborti & Ghosh 2024). A rapid ABO genotyping method using loop-mediated isothermal amplification (LAMP) was developed (Choi et al., 2024). Validation studies for molecular identification methodologies were conducted (Dias et al., 2022). RNA expression was investigated for cases of head trauma in an attempt to detect which part of the brain had been injured (Euteneuer et al., 2022). Combined DNA and mRNA analysis was applied in casework (Fagerholm et al., 2025). A sequencing assay incorporating coding region SNPs was developed (Jiang et al., 2025). The sensitivity of presumptive tests was evaluated (Idris & Goodwin 2022). Advanced molecular technologies characterized challenging traces (Larnane et al., 2025). Mitochondrial DNA copy number was proposed for distinguishing common body fluids or tissues (Li et al., 2024). Fabric composition's impact on visualization was assessed (Lisman et al., 2025). Stability of DNA and mRNA under different storage conditions was tested on saliva and vaginal swabs (Moore et al., 2025). A “reverse” workflow identified body fluids after DNA analysis (Porto et al., 2025). Microfluidic devices were developed for body fluid examination (Shukla et al., 2023). DNA content was quantified in various body fluids (Siuta et al., 2024). Handheld near-infrared spectroscopy was investigated for detection of blood, semen, and saliva stains (Varela Morillas & Frascione 2025). Raman spectroscopy of urine was explored as a possible method to distinguish individuals with different ancestral backgrounds (Vyas et al., 2024). Fabric and weather impact on body fluid identification were assessed (Zapico et al., 2022, Zapico et al., 2024).

Bloodstains (Including Menstrual Blood). Hyperspectral imaging enhanced blood detection (Al-Alimi & Al-qaness 2025). STR profiles were detected from degrading menstrual blood (Al-Hazani et al., 2023). ATR-FTIR spectroscopy was reviewed for bloodstain analysis (Al-Hetlani et al., 2025). D-dimer detection identified postmortem blood (Brodeur et al., 2025). Optical biosensors and aptamers were developed for human blood (Costanzo et al., 2024a, Costanzo et al., 2024b). Thermal exposure effects on DNA typing were researched (Di et al., 2025). A 4-plex methyl-sensitive restriction enzyme (MSRE)-PCR system identified menstrual blood (Hsu et al., 2025). Environmental insults on presumptive tests were evaluated (Idris & Goodwin 2025). Sensitivity of presumptive tests for swabbed stains was evaluated (Jaremko et al., 2024). Differentiation between knife wound and nosebleed blood was investigated (Konrad et al., 2023). A panel based on blood-specific CpG-linked SNP markers was developed (Li et al., 2024). Bayesian analysis was applied to bloodstain patterns (Meijrink et al., 2023). Insect excretions' effect on DNA quality was studied (Murphy et al., 2024). After stepping in fresh blood and then walking across various substrates including concrete, linoleum, and carpet, the amount and distribution of visible blood and chemiluminescence coming from the latent shoeprint bloodstains were documented along with performing DNA testing to show that DNA results were obtained past the point of visualization with luminol (Taylor et al., 2024). A fluorescent dye method was introduced for blood detection (Vajpayee et al., 2023).

Saliva Stains. DNA methylation markers were identified in buccal samples (Balamurugan et al., 2025). A multiplex PCR system was developed for salivary identification (Liang et al., 2023). Biomarker analysis was used to estimate saliva deposition methods (Ohta et al., 2023). Deep ultraviolet Raman spectroscopy detected oral fluid on fabric (Weber et al., 2025).

Semen Stains. Prostate-specific antigen (PSA) and Semenogelin tests were evaluated for effectiveness (Aler et al., 2025). Novel mRNA semen-specific markers were validated (Borges et al., 2025). A colorimetric sensor detected trace zinc in seminal fluid (de Oliveira S. Silva et al., 2025). A reverse transcription droplet digital PCR (RT-ddPCR) assay simultaneously identified saliva and semen (Lee et al., 2024). PSA

was found unsuitable for post-mortem rectal samples (Müller et al., 2025). Cryopreservation methods were compared (Namaa et al., 2024). High-resolution melting quantitative PCR (HRM-qPCR) methods were used to analyze semen stains in casework (Nogueira et al., 2022). Methods for rapid documentation of possible semen stains were described (Thong et al., 2025).

Sperm Cells. Advancements were reviewed for differentiating sperm from epithelial cells in sexual assault cases (Dash 2024). Approaches described in the literature included fluorescence-activated cell sorting (Fokias & Bekaert 2022), alkaline lysis methods (Forsberg et al., 2025), the Hy-liter system (Grosjean & Castella 2025), magnetic bead-based separation (Li et al., 2023, Wang et al., 2025), acoustic filtration devices to obtain sperm enrichment (Wan et al., 2024), and AI systems for automated sperm identification (Mobäck et al., 2025, Schunck & Ehinger 2025).

Using RNA Analysis. RNA sequencing identified individuals from low-template samples (Andersen et al., 2022). Multiplex RNA analysis identified organ tissues (Broderius et al., 2025). Combined messenger (mRNA) and microRNA (miRNA) analysis was explored to differentiate five common body fluids (Chen et al., 2023). Targeted RNA sequencing protocols were evaluated (Gosch & Courts 2025). Two European DNA Profiling Group (EDNAP) collaborative exercises explored mRNA profiling (Hänggi et al., 2025). Targeted S5 RNA sequencing identified fluids in mixtures (Hanson et al., 2023). Vaginal cells were differentiated using autofluorescence (Ingram et al., 2022). A colorimetric RT-LAMP assay targeted the long non-coding RNA X-inactive specific transcript (XIST) to confirm female samples (Kubo et al., 2024). Multiplex RT-qPCR identified saliva, blood, and semen (Kwak et al., 2025). Transfer RNA-derived small RNAs (tsRNAs) were explored for fluid identification (Li et al., 2025a). Nanopore-based mRNA sets were developed for peripheral blood, menstrual blood, saliva, semen, and vaginal secretions (Li et al., 2025b). A support vector machine model used 14 miRNAs for forensic body fluid classification (Li et al., 2025c). Target mRNA cSNP sequencing identified fluid donors (Liu et al., 2024, Liu et al. 2025a, Liu et al. 2025b). Endpoint and real-time PCR assays were compared for their capabilities with body fluid characterization (Lynch & Fleming 2025). RT-LAMP was compared to mRNA methods (Martin et al., 2025). Targeted sequencing combined mRNA and coding region SNPs (Neis et al., 2024). The classification reliability of a quadratic discriminant analysis model using 8 miRNA markers was assessed (Rhodes et al., 2023). Dutch court outcomes regarding mRNA were reviewed (Sijen & van den Berge 2025). Adipose and rectal mucosa markers were added to assays (van den Berge & Sijen 2022, van den Berge et al., 2025). Likelihood ratio systems were implemented (van den Berge et al., 2022). An mRNA assay was developed incorporating insertion-deletion markers (InDels) (Wang et al., 2024). Reference genes were screened for miRNA analysis (Wei et al., 2023). New miRNA markers distinguished saliva from vaginal secretion (Yang et al., 2025).

Using DNA Methylation. Methylation markers were validated for the Chinese Han population (Fang et al., 2023). High-resolution melt detected skin/sweat (Fernandez-Tejero et al., 2023). Collection methods affected saliva methylation (Ghemrawi et al., 2024). Sex-specific differences in saliva were analyzed (Govender et al., 2025). Enzyme conversion was explored (Huang et al., 2025). SNaPshot and massively parallel sequencing (MPS) were compared and standardized (Kim et al., 2024a, Kim et al., 2024b). Workflows were established for fluid identification (Konrad et al., 2023; Li et al., 2025). Epigenetic markers linked suspects to tissues (Mizrachi et al., 2025) and approaches for methylation-sensitive restriction enzyme (MSRE) PCR were expanded (Rothe et al., 2024). Markers were analyzed across clinical phenotypes (Silva et al., 2023). Compound markers identified blood donors (Tang et al., 2024). Random forest models identified mixtures (Wang et al., 2023). A fluorescent probe-based assay detected saliva (Watanabe et al., 2023). AI-driven feature selection screened CpGs using pyrosequencing (Zhao et al., 2025).

Using Microbial DNA. Machine learning was used to identify bacterial profiles (Kim et al., 2025). Combined approaches used microbial DNA and microRNAs (Lewis & Seashols-Williams 2024). Exposure to vaginal fluid changed microbial communities (Liao et al., 2023). Metatranscriptomic characterization was applied to forensic samples (Liu et al., 2024). Bacterial signatures were used to identify seven body fluids (Wohlfahrt et al., 2023). Multiplex systems identified fluids and skin (Yao et al., 2024). Lateral flow dipsticks detected specific bacteria (Yu et al., 2023). Environmental microbiota were found to interfere with identification of body fluids (Zhang et al., 2025).

Using Flow Cytometry and Cell Morphology. Imaging flow cytometry differentiated vaginal cells (Ingram et al., 2023) and classified epidermal, buccal, penile, and vaginal cells (Ross et al., 2024). Biomarkers were used with flow cytometry to detect body fluids (Tewari et al., 2023).

Estimation of Time Since Deposition. Semen detection techniques were advanced to determine time since deposition (Cisana et al., 2025). Fluorescence spectroscopy integrated time estimation into workflows (Elliott et al., 2025). Quantitative approaches assessed autofluorescence and morphology (Gentry et al., 2023). Transcriptomic analyses estimated deposition time (Gosch et al., 2022, Gosch et al., 2025). Cellular signatures were identified for trace DNA (Ingram et al., 2022). Time since saliva deposition influenced the ability to recover DNA profiles from a living individual (Ishikawa et al., 2024). Microbial community succession was used to infer time since deposition of saliva (Jin et al., 2024) and vaginal fluid (Ye et al., 2024). Body fluids should be identified before estimating time since deposition when using microbiomes (Zhang et al., 2024).

DNA Suitability of Hair. Hematoxylin staining increased DNA profile success from hair roots (Admire et al., 2023, Burnett et al., 2025). Deep learning was applied to hair analysis (Airlie et al., 2024). Nuclei shapes were characterized (Donfack et al., 2024). Emerging technologies assessed profiling capabilities (Haines et al., 2025). Nuclei count thresholds were revisited (Otterstatter et al., 2023). Nucleic acid dyes targeted suitable hair follicles (Palencia-Madrid et al., 2025).

Biological Sex Determination. Exfoliated cells from toothbrushes were used for biological sex identification (Alqarni et al., 2024). LAMP-based methods detected male DNA using multiple Y-chromosome assays (Burgos et al., 2022, Chunkul et al., 2025, Kubo et al., 2023a, Kubo et al., 2023b). DNA from teeth allowed sex determination (Dubey & Shah 2023, Prasad et al., 2024). Amelogenin analysis was used for testing enamel (Gamble et al., 2024) and biological material collected on toothpicks (Kurniawan et al., 2023). Genetic approaches were applied to pseudohermaphroditism (Lai et al., 2023). Privacy concerns were raised regarding sex disclosure (Lynch et al., 2025). Recombinase polymerase amplification detected male DNA from all tested human semen samples (Sukjai & Monthatong 2023). Genetic sexing was performed on subadult remains (Zupanič Pajnič et al., 2023).

Processing Sexual Assault Kits. ASTM Standard E2057-23 was updated regarding analysis requests in sexual violence investigations (ASTM Committee E30 on Forensic Sciences 2023). Victim notification protocols (Campbell et al., 2023) and "test all" mandates were examined (Pattavina et al., 2024). Issues around community-based advocacy (Campbell et al., 2024a) and institutional betrayal (Campbell et al., 2024b) were explored. Trauma-informed approaches were advocated (Campbell et al., 2025a), and survivors' testimony experiences were analyzed (Campbell et al., 2025b). mRNA profiling of vaginal swabs was studied (Chierto et al., 2023). Bioanalytical workflows in the UK were reviewed (Dawnay & Sheppard 2023). Case labeling was compared (Duncan et al., 2025). Male underwear evidence was highlighted as a potential sample source in alleged sexual assault investigations (Flanagan et al., 2024). Consumables were assessed (Gaskell et al., 2024), and environmental DNA contamination examined (Gaskell et al., 2025). A call to action was issued for forensic nurses (Glover 2023). Judicial concerns regarding immigrant victims were analyzed (Hashmi et al., 2025). Automated processing kits were developed (Hess et al., 2025). Contextual analysis increased conviction rates (Karolien & Antje 2024).

Automation processed backlogs in Brazil (Kortmann et al., 2024). Forensic aspects of condom evidence were reviewed (Nimi et al., 2024). Microscopical detection of spermatozoa was improved (Savage et al., 2024). Optimal timing for evidence collection from pediatric cases was determined to be less than 24 h (Wood et al., 2023).

3.5. DNA processing

The process of obtaining a DNA profile begins with collecting a biological sample and extracting DNA from it. Foundational and advanced resources continue to shape the field of DNA processing.

Books, Review Articles, and Guidance. A new textbook introduced forensic genetics concepts specifically for non-geneticists (Amorim 2025). A comprehensive volume detailed recent advances in forensic biology and DNA typing (Barbaro & Mishra 2025). Specific protocols were published for using QIAGEN's Investigator Quantiplex Pro Kit (Bonnette 2023a) and the Investigator 24plex QS and GO! amplification kits (Bonnette 2023b). Manual silica-based DNA extraction methods were detailed in a methods protocol collection (Connon 2023). A textbook covered broad advancements in forensic DNA analysis (Dash et al., 2023). The ENFSI DNA Working Group released a best practice manual for human forensic biology and DNA profiling (ENFSI DNA Working Group 2022). Protocols were provided for the manual and semi-automated use of the PrepFiler Forensic DNA Extraction Kit (Foley 2023), as well as for DNA purification from bloodstains and saliva on FTA cards (Hudson & Connon 2023). Methodologies were outlined for DNA quantitation using the Quantifiler Trio kit (Knight et al., 2023) and for the quantitative PCR of Alu repeats (Laveroni & Parks 2023). Organic extraction techniques using ethanol precipitation or centrifugal filter purification were described (Lewis 2023). A method for detecting latent DNA using a DNA-binding dye was detailed (Linacre & Petcharoen 2023). A critical review examined the current state and limitations of PCR in forensic science (McDonald et al., 2024). NIST released reports on opportunities to strengthen evidence management processes (NIST/NIJ Evidence Management Steering Committee 2025a), results from a national survey of evidence handlers (NIST/NIJ Evidence Management Steering Committee 2025b), and an expanded bibliography on evidence management (NIST/NIJ Evidence Management Steering Committee 2025c).

Crime Science Investigation and Sample Selection Decisions. Research into decision-making and triage has highlighted human factors and new screening technologies. Casework pressures and ambiguity aversion were shown to influence how forensic items are triaged (Almazrouei et al., 2025). Investigator decision-making regarding forensic evidence was analyzed in volume crime investigations (Brown et al., 2024). The benefits and limitations of forensic light sources were illuminated in a recent study (Finnis et al., 2023). A framework for rational decision-making regarding whether to test forensic biology samples was proposed (Gittelson & Taroni 2025). Potential DNA contamination introduced by laboratory consumables was demonstrated using fluorescein (Hymus et al., 2025). Reliability and bias were examined in the context of crime scene investigators' selection and prioritization of blood traces (Lidén & Almazrouei 2023). A nationwide study analyzed the usage of forensic genetic analyses in criminal cases in Denmark (Meyer et al., 2025). The efficiency paradigm of high-tech forensic methods was challenged by the persistent attraction of low-tech solutions (Vestad 2024).

Fingerprint and DNA Processing. The compatibility of DNA analysis with fingerprint visualization techniques remains a key research area. DNA typing was successfully performed on cyanoacrylate-fumed latent fingerprints using GlobalFiler and ForenSeq kits (Bodnar et al., 2024). Diamond Nucleic Acid Dye was combined with cyanoacrylate fuming to visualize latent DNA alongside fingermarks (Britton et al., 2024). DNA loss from latent prints due to fingerprint processing was quantified in a laboratory setting (Carlin et al., 2023). An optical biosensor using Diamond Nucleic Acid Dye was investigated for analyzing DNA and friction ridges (Czarnomska et al., 2024). A customized protocol was developed to generate STR profiles from latent fingerprints (Di Nunzio et al., 2022). The "Minimum Surface Requirement" metric was introduced to assess the suitability of fingerprints for STR profiling (Di Nunzio et al., 2025). DNA sampling and fingerprint development were shown not to be a zero-sum game when using DNA-free consumables (Gardiner et al., 2025). The effects of solvent-based adhesive removal on subsequent fingerprint and DNA analysis were evaluated (Gausterer et al., 2023). Two adhesive media were evaluated for the recovery of DNA from latent fingermarks (Kwok et al., 2023). Fingerprint enhancement techniques were assessed for their impact on forensic DNA recovery (Li et al., 2025). An optical sensor based on aggregation-induced emission was used to visualize fingerprints on porous objects with minimal DNA destruction (Liang et al., 2023). A fluorescence metal-organic framework was developed for enhanced latent fingermark development that is minimally destructive to DNA (Liang et al., 2024). Chemical and biological warfare agent decontaminants were shown to impact DNA profiling from blood and saliva (Radgen-Morvant et al., 2024). Two methods for recovering fingerprint DNA from adhesive tapes were compared (Silvia et al., 2023). An optimized workflow was described for obtaining STR results from archived latent fingerprints (Solomon 2023). A multidisciplinary exercise by ENFSI analyzed an alleged improvised explosive device (Zampa et al., 2025). Recent advances in enhancement techniques for fingerprints left in blood were reviewed (Zhang & Peng 2023).

DNA Stability and Storage. Studies have investigated how environmental factors and storage conditions affect DNA integrity. Exposure to gamma rays was shown to impact DNA quality and genetic traits in human blood samples (Ajlouni et al., 2024). A method using tendons and table salt was proposed for preserving human DNA (Birne et al., 2024). Vitreous humour was identified as a potential source of DNA for postmortem identification (Čanović et al., 2024). The effects of freezing, thawing, and long-term storage on forensic DNA extracts were reported (Forsberg et al., 2022). Degradation of DNA extracts stored under different conditions was analyzed (Gino et al., 2025). A longitudinal assessment compared DNA recovery from post-mortem whole blood stored in various tube types (Grobbelaar et al., 2025). Storage conditions in a museum were compared to fresh excavation for DNA preservation in skeletal remains (Jeromelj et al., 2025). A novel buffer was developed for the long-term preservation of DNA in biological material at room temperature (Kasu et al., 2024). DNA collection from swabs was assessed up to three months after deposition on different cloth materials (Medina-Paz et al., 2024). UV exposure was shown to affect DNA deposited on drug capsules (Nolan & Linacre 2025). Cutting-edge methods for preserving and storing forensic pathology tissue samples were reviewed (Prajapati et al., 2025). Long-term DNA stability on buccal 4N6FLOQSwabs was explored in simulated paternity cases (Rosso & Franzoni 2025). DNA damage was detected in stored blood samples (Schulze Johann et al., 2023). Storage conditions were evaluated for their effect on DNA from evidence retrieved from lake water (Shahzad et al., 2024). The effect of sunlight on the quality of DNA analysis from bloodstains was investigated (Sliskovic et al., 2024). DNA recovery was demonstrated from human remains submerged in aggressive household chemicals for 28 days (Snedeker et al., 2025).

DNA Collection and Sampling Methods. Optimization of sampling techniques is crucial for maximizing DNA recovery. Swabbing technique and duration were shown to affect forensic DNA recovery (Abdullah et al., 2023). Different cotton and nylon swabs were compared for performance in DNA recovery and storage (Alrahma et al., 2023). Adhesive tape was compared to swabbing for touch DNA collection using a direct PCR approach (Asiri et al., 2025). DNA was isolated from spots on old glass microscope slides (Baersch & Bhatia 2024). The microbial wet-vacuum system (M-Vac) was evaluated for sampling from rough, porous substrates (Blackmore et al., 2024). Limitations and challenges of swab-based DNA sampling were reviewed (Bruijns 2024). A cost-benefit analysis supported the use of nylon 4N6FLOQSwabs (Budowle et al.,

2022). Operational DNA recovery methods were compared, contrasting swabs versus tapelifts (Burmuzoska et al., 2022). The Pulse Lavage System was compared to forensic wet-vacuum collection (Chaudhry & Kavlick 2023). A holistic approach was proposed for the selection of forensic DNA swabs (Comment et al., 2023). A systematic review evaluated swab materials used in forensic DNA testing (Conte et al., 2025). DNA sampling success was compared from steering wheels and car seats in tropical Australia (Gardiner & Krosch 2023). Three DNA collection methods were compared on Nile Red fluorescent areas of porous substrates (Hinojosa et al., 2023). Six adhesive tapes were compared for efficient trace DNA recovery without transferring PCR inhibitors (Hymus et al., 2024). Three swabs and three wetting agents were evaluated for collecting DNA from non-porous surfaces (Krosch et al., 2025). DNA recovery from mini tapes was achieved using a simple extraction buffer and solid-phase reversible immobilization (SPRI) purification (Kuffel et al., 2024a). The impact of swabbing solutions on recovery from non-porous surfaces was assessed (Kuffel et al., 2024b). An applicator prototype was tested to facilitate forensic DNA recovery by tapelifting (Meakin et al., 2024). "Total Human DNA Sampling" was introduced for obtaining profiles from large areas (Neves & Zieger 2023). Cell counting was used to monitor swab efficiency (Nolan & Linacre 2024). Adding salmon sperm DNA was shown to increase sample recovery of human DNA from cotton swabs (Oechsle et al., 2024). Updated recommendations were provided for collecting biological samples in cases of sexual violence (Pelotti et al., 2025). An alternative DNA recovery approach, the DNA-Buster, was evaluated (Währer et al., 2023).

Trace DNA/"Touch DNA". Trace DNA analysis has focused on specific deposition scenarios and detection methods. Touch DNA success rates were investigated in vehicle sites for hit-and-run casework (Aidarous et al., 2025). Collection techniques were assessed for touch DNA on human skin following strangulation (Alketbi 2023). Enhancements were proposed for trace DNA recovery from disposable face masks (Alketbi & Goodwin 2025). Extraction and direct amplification methods were compared for touch DNA profiling (Alketbi et al., 2025). A cytochemical labeling technique was used for the in situ detection of cell-derived markers in invisible traces (Bastat et al., 2025). The impact of alcohol-based hand sanitizer on touch DNA was evaluated (Bini et al., 2023). Trace DNA recovery was explored from titania-coated self-cleaning substrates (Bonsu et al., 2023). The forensic significance of touch DNA was discussed (Devika et al., 2024). A modified lysis buffer and chitosan-coated magnetic beads were used to extract DNA from trace samples (Hu et al., 2023). Detection and analysis of latent DNA were reviewed (Linacre & Petcharoen 2022, Linacre 2024). Probative levels of touch DNA on tapelifts were predicted using Diamond Nucleic Acid Dye (Madden et al., 2024). The potential utility of trace DNA evidence in forensic investigations was reviewed (Neole 2024). The limit of detection for STR analysis was determined for touch DNA samples (Saamia et al., 2024). Sampling solutions and volumes were evaluated for collecting touch DNA from glass surfaces (Schulte et al., 2023). A commercially available hydrogel was tested as a novel DNA surface sampling tool (Sekowski et al., 2023). Touch DNA success rates were monitored in cases of volume crime in a German police lab (Söchtig et al., 2025). Precision sampling on plastic bag knots improved profiling of packer and holder contributions (Stefanović et al., 2024).

Recovering DNA from Fingernails and Other Substrates. Recovery methods have been optimized for challenging substrates. The effect of lip cosmetics on human STR profiling was investigated (Abboosh et al., 2023). Optimized recovery of DNA was achieved from embalmed human cadavers (Afrifah et al., 2023). Recovery of DNA from exhaled breath devices was optimized for human identification (Carrillo & Hughes 2025). DNA was recovered from a shoe upper during an investigation based on a bloody footprint impression (Daniel et al., 2023). Face masks were evaluated as forensic DNA evidence (Dash et al., 2023). The Cell Elution Method was evaluated for analyzing smoked cigarettes (Ekka et al., 2024). Approaches for analyzing DNA on illicit drugs were described (Griffin et al., 2022, Griffin et al., 2024). Forensic DNA recovery from post-mortem fingernail samples was optimized (Heathfield et al., 2025). The Maxwell RSC Xcelerate Kit was optimized for DNA recovery from formalin-fixed paraffin-embedded (FFPE) tissue (Lisman et al., 2025). Pretreatment methods were examined for DNA extraction from fingernails (Ochiai et al., 2022). STR profiling was performed from histological slides (Poór et al., 2022). Coffee cups were analyzed as forensic evidence using STR analysis (Saeed et al., 2023). DNA recovery was assessed from laundered clothing with semen stains washed at different temperatures (Sapan et al., 2023). Factors associated with foreign DNA detection beneath deceased's fingernails were identified (Sripong 2023). Protocols were compared for enhancing profile quality from FTA-deposited urine samples (Srisiri et al., 2022). DNA profiles were obtained from biological trace material on underwear and toothbrushes (Torres-Pérez et al., 2022). The role of fingernails in death investigation was reviewed (Wankhede 2024). A comparative study analyzed DNA samples from under-fingernail materials (Yüksel et al., 2025).

DNA Extraction Methods. Automation and novel chemistries are improving extraction efficiency. Two semi-automated extraction methods, Automate Express and Hamilton Microlab STAR, were compared (Altamimi et al., 2023). Simultaneous extraction of DNA, RNA, and protein was assessed for human remains (Castagnola et al., 2025). Strategies were tested to improve DNA analysis of formaldehyde-damaged tissues (Czado et al., 2023). Toxicological screening was performed on waste residues from DNA extraction processes (Di Candia et al., 2024). Commercial direct DNA extraction kits were assessed (Hymus et al., 2025). A new kit was designed for extracting DNA from blood samples (Jarallah et al., 2023). Binding buffer composition was optimized for magnetic bead extraction (Khan et al., 2024), and an iron oxide nanoparticle-based method was evaluated (Khan & Kaushik 2025, Khan et al., 2025). A protocol was optimized for extracting DNA from fingerprints (Loarce et al., 2025). Sample throughput was improved using the PrepFiler kit on a robotic workstation (O'Rourke et al., 2024). Successive DNA extractions from swabs were evaluated (Pickell et al., 2025). Nucleic acid purification was achieved through magnetic bead integration with microfluidic chips (Priya et al., 2024). Validation studies were performed on the EZ2 Connect Fx with the EZ1&2 DNA Investigator Kit (Scherer et al., 2022). A microchip was fabricated for DNA capture from blood (Sehgal et al., 2024). Chemical contamination in extracted DNA was shown to affect HLA typing results (Shirizadeh et al., 2025). Non-toxic solvents were proposed for formalin-fixed paraffin-embedded (FFPE) tissue deparaffinization (Soldati et al., 2025). The effect of extraction protocols on single-stranded DNA versus double-stranded DNA proportion and integrity was studied (Stoljarova-Bibb et al., 2025). Robotic extraction using the Qiagen BioSprint 96 was detailed (Ziencik 2023).

Differential Extraction. Methods for separating sperm from epithelial cells continue to be refined. A modified differential extraction protocol was used in a sexual assault case (Chaudhary et al., 2024). A protocol for differential extraction with purification was detailed (Forsberg & Ayoub 2023). The MACSprep forensic sperm microbead kit was compared to the Erase Sperm Isolation kit (Grosjean et al., 2023). A modified differential lysis used a combined enzymatic and alkaline approach (Hudson & Dawson Green 2024). Sperm mRNA screening via a reverse transcription-recombinase polymerase amplification (RT-RPA) assay was used for decision-making regarding differential extraction (Kubo et al., 2023). Differential extraction thresholds were utilized to deduce the existence of spermatozoa (Ridgley et al., 2024). An inter-laboratory comparison indicated high male DNA recovery using the SpermX method (Sgueglia et al., 2023). An affinity-free centrifugal microfluidic system was proposed for rapid differential extraction (Woolf et al., 2023).

DNA from Firearms and Fired Cartridge Cases. Maximizing yield from firearms remains a challenge due to DNA degradation and inhibition. Genetic profiling was performed from 9 mm fired cartridge cases

over 30 days (Alem et al., 2022). The impact of metal ions on forensic DNA analysis was explored (Bonsu et al., 2024). A chelation filtration method improved DNA recovery from fired cartridge casings (Crenshaw et al., 2024). The effects of copper and zinc ions on DNA profiling were compared (Czado et al., 2022), and recovery was evaluated from fired and unfired brass ammunition (Czado et al., 2024). Factors influencing DNA recovery from firearms were reviewed (Kaesler et al., 2023). Storage conditions were shown to impact DNA yield from ammunition cartridges (McElhoe et al., 2023). The proportion of DNA from the owner versus a brief handler of a firearm was examined (Oefelein et al., 2023). Relevant sampling areas on firearms were identified for reconstructing shooting scenarios (Onofri et al., 2025). Trace DNA recovery rates from firearms were analyzed using casework data (Prasad et al., 2023). Three DNA extraction methods were compared for fired and unfired ammunition (da Rocha Marques et al., 2022). The amount of DNA found inside firearm barrels were analyzed relative to muzzle-to-target distance (Schyma et al., 2024). The potential for DNA loss during collection and packaging of fired cartridge cases was assessed (Stella et al., 2025). The effects of gunshot residue on STR PCR inhibition were investigated (Westring et al., 2025).

DNA from Teeth, Bones, and Hair. Protocols for hard tissues have focused on demineralization, automation, and difficult samples. Preservation substrates were compared for efficient DNA recovery in bone under field conditions (de Arellano Sánchez et al., 2023). The role of dental pulp in DNA fingerprinting was reviewed (Bansal & Gaikwad 2023). Extraction of DNA from human teeth was optimized using lye under different conditions (Castagnola et al., 2025). Deciduous teeth were used as a reference sample to identify some human remains (Chávez-Briones et al., 2023). Raman spectroscopy and lipid analysis were assessed for decomposed human bones (Corrêa et al., 2024). Skeletal remains exposed to extreme conditions were typed without pulverization (Della Rocca et al., 2025). Sampling methods in odontogenetics were reviewed (Dineja 2023). A new extraction method was evaluated on bone samples from a WWII mass grave (Di Stefano et al., 2024). Automatic extraction from bone was validated for the EZ2 Connect instrument (Doniec et al., 2024). A case report highlighted the importance of DNA profiling from teeth (Eriksen et al., 2023). Extraction methods for human hard tissue were systematically reviewed (Finaughty et al., 2023). Patellae were identified as a valuable source of DNA (Geršak et al., 2025). Alternative high DNA-yielding bone types were searched for in aged skeletal remains (Golob et al., 2024). Five DNA extraction methods were compared for degraded skeletal remains (Haarkötter et al., 2023a), and petrous bone/tooth were compared to femur/tibia (Haarkötter et al., 2023b). Bone extraction through demineralization was detailed (Iorio & Cooley 2023), while another study explored recovery without demineralization (Iyavoo & Goodwin 2022). Environmental factors affecting DNA preservation in petrous bones were compared (Kravanja et al., 2025). DNA preservation was compared between permanent and deciduous teeth (Leskovar & Pajnič 2023), and between petrous bones and metacarpal epiphyses (Leskovar et al., 2024). Nuclear SNP profiles were derived from human hair shafts (Lewis et al., 2022). Dental calculus was analyzed for its evidential value (Lisman et al., 2023). Enhanced ancient DNA extraction was applied to human remains for capillary electrophoresis (CE) analysis (Liu et al., 2025). DNA and protein analyses of hair were reviewed (Liu et al., 2023). Quantitative color analysis of burned bone was used to predict DNA quality (Macias et al., 2024). DNA recovery was assessed from teeth in a semi-natural marine environment (Malana et al., 2025). Optimal skeletal elements for DNA testing in routine practice were evaluated (Otagiri et al., 2024). Extraction methods were compared for telogen hair samples (Petersen et al., 2025). Diagnostic models predicted DNA recovery from incinerated teeth (Rahmat et al., 2023). Low-cost bone and teeth processing methods were evaluated for automated extraction (Rancourt et al., 2023). Advancements in extracting genetic material from hard tissues were reviewed (Rehman et al., 2025). Factors affecting DNA degradation in teeth were reviewed (Salazar et al., 2025a) and studied under extreme ante-mortem conditions (Salazar et al., 2025b). DNA recovery was determined from teeth exposed to acids (Sapan & Karaboğa 2025). The InnoXtract method was validated for bone, teeth, and rootless hair (Sinha et al., 2023) and optimized for skeletal samples (Snedeker et al., 2023). Downstream processing methods were investigated for challenging skeletal samples (Snedeker et al., 2025). A protocol without liquid nitrogen was developed for bones and teeth (Stan et al., 2024). Bead-beating homogenization was used for burnt bone and teeth (Varrathyarom et al., 2022). Dental pulp and cementum were compared for identification (Wei et al., 2023). A temperature-driven method was assessed for efficiency in human remains (Zapico et al., 2024). An automated extraction method was developed for small quantities of bone powder (Zupanič Pajnič et al., 2023).

DNA Quantitation and Degradation Assessment. Accurate quantitation and degradation assessment are critical for downstream success. A book chapter covered DNA quantitation methodologies (Abuidrees & Hadi 2025). An emission-based probe was developed for detecting and quantifying DNA and RNA (Adak et al., 2024). A framework was proposed for qPCR modeling of low copy number samples (Asogawa 2022). Simultaneous quantification of human, dog, and cat DNA was advanced (Bae et al., 2025). The Investigator Quantiplex Pro RGQ Kit was assessed at half volumes (Barbaro et al., 2025). DNA degradation implications in forensic casework were reviewed (Bhoyar et al., 2024). Tin contamination was found to cause qPCR overestimation (Bonsu et al., 2023). DNA profiles were degraded to specific levels using UV exposure (Cabral de Almada et al., 2024). Differential amplification efficiency was used to assess DNA degradation (Chierto et al., 2024). Optimal STR profile setup was predicted from Quantifiler Trio data (Dupont et al., 2022). A protocol for DNA degradation in genetic applications was published (Ewers & Parson 2025). A custom qPCR assay was designed to simultaneously quantify human and microbial DNA (Foster et al., 2024). Reverse transcription yield was evaluated using droplet digital PCR (Gao et al., 2024). Genomic multicopy loci targeted by current assays were examined (Jäger 2024). Total human DNA was quantified in sexual assault mixture samples to estimate whether a sample was likely to yield an autosomal- or Y-STR profile (Llamocca et al., 2025). DNA was quantified in dried blood and saliva-tinged blood compared to fresh blood (Manjunathan et al., 2024). A multiplex qPCR assay was validated for simultaneous nuclear and mitochondrial DNA quantification (Melchionda et al., 2025). Performance parameters were established for the Qubit 1X dsDNA HS Assay (Naidoo et al., 2025). Calculating mitochondrial DNA quantity from nuclear qPCR results was compared to direct measurement in aged bones (Obal et al., 2023). The usefulness of qPCR data for sample pre-assessment was discussed (Onofri et al., 2024). Real-time PCR quantification was examined in detail (Ricci et al., 2024). DNA concentration and purity were assessed on dental floss (Rizky et al., 2025). Limitations of the Quantifiler Trio-HRM assay for mixture identification were assessed (Smith et al., 2024). High-resolution melt curve assays were integrated into commercial quantification kits (Smith et al., 2025). Human DNA quantification was evaluated for predicting profiling success in historical bone (Thomas et al., 2023). A Quantifiler Trio-based HRM screening assay was used for accurate single source versus mixed prediction (Torres et al., 2023). The NuMY qPCR assay was developed to simultaneously target human autosomal, Y-chromosomal, and mitochondrial DNA (Xavier et al., 2023).

Direct PCR Amplification and PCR Improvements. Direct amplification and PCR enhancements are streamlining workflows. The Amplicon RX post-PCR clean-up kit was used to enhance trace DNA recovery (Aljanahi et al., 2025). Direct STR amplification was performed on human foetal tissues using FTA cards (Ani et al., 2024). Primerless PCR was explored for rescuing highly degraded DNA (Ashankyty 2023). Nicking endonuclease dependent amplification was developed for trace DNA (Bi 2025). An Ampliseq microhaplotype panel was adapted to nanopore sequencing through direct PCR (Casanova-Adán et al., 2023). The PCR inhibitory effect of hair dye constituents was assessed (Dash

et al., 2025). A theoretical framework (McDonald et al., 2024a) and practical application (McDonald et al., 2024b) were developed for a machine-learning 'smart' PCR thermocycler. A practical guide to PCR was published (McKinzie & Myers 2023). Molecular fracture of DNA chains after PCR heating cycles was investigated (Serpieri & Franchi 2024). Direct amplification of body fluids was achieved using Micro-FLOQ direct swabs (Shadoff et al., 2024). A protocol was developed to improve touch DNA analysis using direct STR amplification (Snyder et al., 2025). Post-PCR purification methods were evaluated for low input DNA (Steele et al., 2024). The role of PCR inhibitors and facilitators was reviewed (Vajpayee et al., 2023). Nanoparticle-assisted PCR was explored for forensic implications (Vajpayee et al., 2025). A recombinase polymerase amplification was developed for rapid detection (Zheng et al., 2023).

Quality Control to Avoid Contamination Strategies to monitor and remove contamination are essential for integrity of a laboratory's results. A high-performance PCR assay system was designed to clean carry-over contamination (Fu 2025). Chlorine wipes were tested for efficient DNA removal from laboratory surfaces (Kampmann et al., 2022). Contamination testing was conducted during the renovation of post-PCR laboratories (Petersen et al., 2022). The effect of vectors and pretreatment methods on DNA typing efficiency was compared (Xu et al., 2025).

3.6. DNA typing with short tandem repeat markers

DNA typing with short tandem repeat (STR) markers is the primary method used for DNA analysis following collection of DNA evidence and its extraction from biological samples. This section also includes historical information and efforts with training, quality assurance, and validation studies.

Books, Review Articles, and Guidance. ANZPAA NIFS published guidelines for the validation of forensic science methods (ANZPAA NIFS 2025). The ASB DNA Consensus Body completed ANSI/ASB Standard 154 regarding training on testimony for forensic biology (ASB DNA Consensus Body 2024). ASTM Standard E2917-24a provided updates for practitioner training and continuing education (ASTM Committee E30 on Forensic Sciences 2024), and ASTM Standard E1732-25e1 shared standard terminology relating to forensic science (ASTM Committee E30 on Forensic Sciences 2025). Introductory texts, such as *Forensic DNA Analyses Made Simple*, aim to make the field accessible (Bagasra et al., 2023), while other works delve into advanced topics like nuclear DNA markers (Barbaro 2025). Efforts towards a common body of knowledge were discussed, highlighting valuable publications and previous INTERPOL DNA reviews (Butler 2025). The legal context of forensic DNA evidence was explored in a new book (Chin W. et al., 2025). Several chapters in *Forensic DNA Analysis: Methods and Protocols* [7] covered laboratory processes (Cupples Connon 2023a) and low-volume STR amplification options (Cupples Connon 2023b). Advancements in forensic DNA analysis were detailed in a dedicated volume (Dash et al., 2023). A human verification system based on DNA biometrics was proposed (Dawood et al., 2023). The ENFSI DNA Working Group released guidelines for internal validation (ENFSI DNA Working Group 2023a) and DNA contamination minimization (ENFSI DNA Working Group 2023b). The FBI updated quality assurance standards for forensic laboratories (Federal Bureau of Investigation 2025a), DNA databasing laboratories (Federal Bureau of Investigation 2025b), and provided a guidance document for these standards (Federal Bureau of Investigation 2025c). The UK Forensic Science Regulator issued guidance on validation (FSR-G-201-Forensic Science Regulator 2024), contamination controls at crime scenes (FSR-GUI-00016-Forensic Science Regulator 2023), during medical examinations (FSR-GUI-0017-Forensic Science Regulator 2025), and in the laboratory (FSR-GUI-0018-Forensic Science Regulator 2023). Protocols were also released for using casework material for validation (FSR-P-300-Forensic Science Regulator 2024) and detecting DNA contamination (FSR-P-302-Forensic Science Regulator 2024). Protocols for DNA amplification using PowerPlex Fusion systems were detailed (McCaughan & Lenz 2023). Conventional STR technology was reviewed for analyzing biological transfer evidence (McClintock 2023). The evidentiary value of DNA profiling in criminal trials was examined (Padmanabhan 2024). An interdisciplinary perspective on forensic DNA applications was provided in a second edition text (Primorac & Schanfield 2023). The Royal Society reported on science in the interests of justice (The Royal Society 2023). DNA analysis in forensic investigations was summarized in a clinical and pathological context (Syndercombe-Court 2024). Protocols for the GlobalFiler PCR Amplification Kit were also published (Williams et al., 2023).

Historical Information. Historical perspectives on forensic genetics provide context for current practices. Pioneering DNA fingerprinting pilot programs on Britain's borders were analyzed (Bivins 2023). The investigative purposes of DNA testing were reviewed, focusing on perpetrator profiling and kinship analysis (Branicki 2024). The role of DNA in criminal indictments in Israel was examined (Buchnik et al., 2023). A profile of Bruce Budowle detailed his forensic odyssey (Budowle 2023), and the history of short tandem repeats as the "currency" of forensic genetics was described (Budowle & Sajantila 2024). An ecological understanding of wrongful convictions in the U.S. was presented (Crump 2024). The future of DNA forensics was discussed in the context of its 40-year history (Dash & Al-Snan 2025). Advancements in generating investigative leads and eliminating innocents were reviewed (Dash et al., 2024). The significance of DNA in forensic science was summarized in a textbook chapter (Dixit et al., 2023). Highly cited forensic scientists in the United States were identified (Jones 2023). A 25-year review of Hungarian court decisions shed light on DNA evidence contamination issues (Kovács et al., 2022). The history of the use of biological and botanical evidence was reviewed (Ladd et al., 2024). Wrongful convictions and claims of misleading forensic evidence were analyzed (Morgan 2023), with lessons drawn for improving forensic science (Morgan 2024). Interviews highlighted the roles of biomedical communication (Novroski 2023) and massively parallel sequencing pioneers (Novroski 2024). Legal considerations for accepting new forensic methods were discussed (Palmbach & Shutler 2024). A personal tribute honored Professor Peter Matthias Schneider (Phillips 2023). A judicial perspective on forensic science was offered (Rakoff & Liu 2023). The establishment and future prospects of forensic DNA technology in India were reviewed (Sahu et al., 2024). An overview of historical developments in forensic DNA analysis was provided for a book on forensic botany (Shutler 2024). Forensic DNA expert evidence was examined in the South African context (Smith et al., 2025). A bibliometric analysis covered forty years of research in forensic genetics (Stasi et al., 2023). A personal perspective traced the evolution from early DNA diagnostics to high-resolution genomics (Syvänen 2024). A historical review of legal medicine journals covered the period from 1948 to 1969 (Wirth et al., 2023). Finally, the fifteen-year journey of the Asian Forensic Sciences Network was chronicled (Yap & Cheng 2024).

Training, Quality Assurance, and Validation Studies. Training models and quality management systems are crucial for operational excellence. A five-phase model consisting of input, preparation, execution, feedback, and assessment (IPEFA) was introduced as an initiative for online training by the International Society for Forensic Genetics (Benschop et al., 2025). Two independent reviews addressed operational matters and reform recommendations for Forensic Science Queensland (Budowle 2025, Wright et al., 2025) along with the strengths and limitations of ISO/IEC 17025 conformance (Doyle 2024) and some lessons learned from the Queensland DNA inquiry (Walvisch et al., 2025). DNA analysts' experiences with human factors were captured in a snapshot study (Dawson et al., 2025). A collaborative model was proposed to standardize forensic DNA education (Elkins 2025). A survey assessed forensic DNA biology training in U.S. laboratories (Elkins et al., 2025). Strategies for minimizing DNA contamination were reviewed (Gall 2024). A survey explored practice and perceptions regarding quality issue management and disclosure (Heavey et al., 2025). Quality management systems in India and the UK were

compared (Joseph et al., 2025). Cleaning protocols in forensic genetic laboratories were discussed (Kampmann et al., 2024). QR code technology was used to introduce hands-on genotyping to medical students (Lai et al., 2023). Editorial considerations for publication in *Forensic Science International: Genetics* were outlined (Kayser et al., 2023). A multiplex assay was validated for detecting HIV-1, HBV, and human STRs on CE systems (Liu et al., 2025). A primer on understanding "error" in forensic sciences was published (Martire et al., 2024). Student-driven research evaluated the SeqStudio Genetic Analyzer for educational use (McGregor et al., 2025). A guide to ISO 21043 was presented from the perspective of forensic data science (Morrison et al., 2025). A software package was developed for designing and interpreting validation studies (Riman et al., 2025). NIST developed a forensic DNA research-grade test material (Romsos et al., 2025, Vallone et al., 2025) and made updates to Standard Reference Material (SRM) 2391 d, a PCR-based DNA profiling standard (Steffen et al., 2022). Documentation and disclosure of contamination events were discussed (Rudin et al., 2025). A bioluminescence assay was applied to assess PCR carryover contamination (Satoh et al. 2024). The Scientific Working Group on DNA Analysis Methods released validation guidelines for using expert systems with forensic samples (SWGDAM 2025), and five validation principles were provided by NIST scientists in December 2025 (Swofford 2025). A new risk management culture was implemented in a forensic genetics laboratory (Silva et al., 2025). STR profiling was assessed for combating COVID-19 insurance fraud (Srisiri et al., 2025). Co-detection of RNA virus and STR type on capillary electrophoresis was explored (Xu et al., 2023). Outcomes of the ENFSI 2022 multidisciplinary collaborative exercise were reported (Zampa et al., 2024).

Studies on Capillary Electrophoresis Instruments. Evaluations of CE platforms ensure reliable genotyping. Innovations in the SeqStudio Flex Genetic Analyzers were detailed (Aumsuwan et al., 2022). The SeqStudio was compared to the 3500 Genetic Analyzer (Griffin et al., 2024) and comprehensively investigated for forensic DNA typing (Keefe et al., 2025). The GA118-24B Genetic Analyzer was assessed with internal validation studies (Qu et al., 2024). Internal validation was also performed for the SeqStudio for human identification (Soldati et al., 2023).

STR Markers and Kits. Research on STR markers has focused on nomenclature, variation, and population comparisons. Nomenclature was harmonized for D6S474 and DYS612 (Bodner et al., 2024). The incorporation of STR sequences into STRBase was discussed (Borsuk et al., 2025). Compatibility between VeriFiler Plus and PowerPlex 21 profiles was assessed (Cooper 2025). Novel DIP-STRs were identified from whole-genome sequencing data (Damour et al., 2023). Amplification of specific loci was successful from DNA isolated from a ring (Furqoni et al., 2023). Bioinformatic methods predicted 5′ ends of primer sequences in STR kits (Kutsuwada et al., 2025). A SNP-STR analysis system was developed for Japanese people (Ohuchi & Mimasaka 2025). An ambiguous sequence-based allele of SE33 was reported (Sathirapatya et al., 2022). Genome-wide STR variation was characterized in 6487 human genomes (Shi et al., 2023). Sequencing and characterizing short tandem repeats in the human genome were reviewed (Tanudisastro et al., 2024). Comparisons were made between Japanese and Han Chinese populations for 261 autosomal STR loci (Yamamoto et al., 2022).

STR Kit Validation Studies. Validation studies confirm the robustness of commercial STR kits and custom assays. The Investigator ESSplex SE QS Kit was validated at half volumes (Barbaro et al., 2024). Internal validation was completed for the Investigator 26Plex QS kit (Cardoso et al., 2025). Forensic STR kits were evaluated for their tolerance to PCR inhibitors (Cho et al., 2024). The GlobalFiler PCR protocol was validated at half-volume (Cseppentő et al., 2025). Developmental validation was performed for the PowerPlex 35GY System (Graham et al., 2024). The GlobalFiler IQC PCR amplification Kit was used for low-input samples on the Magelia platform (Larnane et al., 2024). Developmental validation was reported for the Microreader 23HS Plex ID System (Li et al., 2024) and a 25 loci miniSTR system (Li 2025). The NGM Detect Kit was assessed at half-volume (Magonyi et al., 2024). The impact of inhibitors on biological samples was evaluated in a pilot study (Mosuro et al., 2025). Validation studies were conducted for the 6-dye SF25 PCR amplification kit (Shrivastava et al., 2023) and the Ingenomics AutoProfiler STR system (Sharma et al., 2025). A comparison and internal validation were performed for GlobalFiler, VeriFiler, and Investigator 24Plex kits (Tezel 2024). The PowerPlex 35GY System was evaluated on the Spectrum Compact CE System (Qu et al., 2024). Developmental validation was completed for the NeoTyper autosomal STR kit (Verma et al., 2024) and the Microreader 36 A ID System (Wang et al., 2025).

STR Artifacts, Variant Alleles, and Tri-Allelic Patterns. Anomalous STR results provide insights into genetic variation and potential pitfalls. A flanking region deletion at D19S433 caused genotyping discrepancies between CE and NGS (Carbó-Ramírez et al., 2025). STR isoalleles were detected in capillary electrophoresis (Carnevali et al., 2025). Amplification failure of Amelogenin X was caused by a rare mutation in the primer-binding region (Chang et al., 2023). Allelic drop-out of sequenced autosomal STRs was explored (Foley et al., 2024). A rare case of type II tri-allelic inheritance was demonstrated at multiple loci (Gavale et al., 2024). A rare allele 29 at D2S1338 was observed in the Bulgarian population (Iliev et al., 2023). A variant causing null alleles in parentage testing was identified by Sanger sequencing (Jiang et al., 2023). Cross-species amplification from non-human primate DNAs was noted in commercial kits (Nakagawa et al., 2024). Unusual phenomena were reported in DNA profiling of over 12,000 individuals (Prommakrit et al., 2025). Discordance of Penta D ×.4 microvariant alleles was found between different kits (Rye & Hymus 2024). Microbial DNA co-amplification caused a misconstrued peak at D7S820 (Saeed et al., 2024a). A true heterozygote variant was misjudged as a tri-allele due to neighboring effects (Saeed et al., 2024b). Unique tri-allelic patterns were reported in casework in Pakistan (Saeed et al., 2024c). Technical-legal implications of allelic inconsistencies between commercial kits were discussed (Sánchez et al., 2025). STR chimerism was reported following bone marrow transplantation (Shotivaranon et al., 2022). A novel SNP mutation causing drop-out alleles was identified in a paternity test (Wang et al., 2024). Rare alleles were analyzed at five STR loci (Wang et al., 2023). Genetic inconsistency at D6S1043 was linked to a microdeletion at 6q15 (Wu et al., 2023). Variant alleles and tri-allelic patterns were observed in the Albanian population (Zaimi & Xhetani 2023).

STR Markers and Potential Disease Connections. Recent research has explored the intersection of forensic markers and medical genetics. A probabilistic model was explored for identifying individual tumor tissue (Hu et al., 2024). Microsatellites used in forensics were found to be enriched for trait-associated variants (Link et al., 2023). A scoping review examined STR marker alterations in cancerous tissues (Omar et al., 2024). STR instability was unveiled in a colorectal cancer formalin-fixed paraffin-embedded (FFPE) sample (Soldati et al., 2025). STRIDE-DB was introduced as a database for exploring STR instability and phenotypic relevance (Uppili & Faruq 2024). Finally, forensic applications and the privacy implications of forensic STR loci and schizophrenia were explored (Yang et al., 2024).

3.7. DNA interpretation at the sub-source or source level

Due to the sensitivity of modern testing methods, DNA interpretation is most often conducted at the sub-source level in the hierarchy of propositions (see Ref. [26]). At this level, findings may assist investigators in answering questions of *who* deposited the cell material, whether attribution for the result can be made to a specific cell type (i.e., source level) or simply to the DNA if no attribution can be made to a specific cell type (i.e., sub-source level). For more than a decade, probabilistic genotyping software (PGS) has been used to assist with interpreting DNA mixtures, and artificial intelligence tools are being explored to assist with automatically distinguishing STR alleles from

artifacts [26].

Books, Review Articles, and Guidance. In 2024, the ASB DNA Consensus Body released standards for the internal evaluation of interpretation protocols (ANSI/ASB 123), reporting DNA conclusions (ANSI/ASB 139), and handling failed controls and contamination events (ANSI/ASB 175). NIST published a comprehensive scientific foundation review of DNA mixture interpretation (Butler et al., 2024). Proceedings from a National Academies workshop addressed the law enforcement use of probabilistic genotyping and related technologies (Committee on Law and Justice 2024). Methods for likelihood ratio calculation using LRmix Studio were detailed (Foley 2023). The UK Forensic Science Regulator issued guidance on proficiency testing for mixture analysis (FSR-G-224-Forensic Science Regulator 2024), software validation (FSR-G-223-Forensic Science Regulator 2024), and general mixture interpretation (FSR-G-222-Forensic Science Regulator 2024). OSAC released Technical Guidance Document 0009 as an exemplar for human forensic DNA reporting (OSAC Human Forensic Biology 2025) and an assessment guide for the ASB Standard 040 (OSAC Human Forensic Biology 2022). SWGDAM published updated guidelines for using probabilistic genotyping (SWGDAM 2025a) and reporting likelihood ratios (SWGDAM 2025b). Additionally, a NIST report focused on improving forensic DNA interpretation through a systems approach to human factors (Taylor and Expert Working Group 2024).

DNA Interpretation in General. Microchimerism was reviewed as a potential complicating factor in forensic science (Arslan 2025). The relationship between back stutter and double back stutter rates was investigated (Asogawa 2025). The necessity of Y-STR loci DYS570 and DYS576 in the PowerPlex Fusion 6C panel for mixture analysis was questioned (Ausania et al., 2025). Previous casework data were utilized to aid decision-making in interpretation (Benschop et al., 2022). The concept of "scientific imperialism" in judicial settings was critiqued (Biedermann & Kotsoglou 2025). The ISO 21043 standard was welcomed as a global benchmark for interpretation (Berger 2025). Case studies demonstrated solutions for interpreting trace amounts of degraded DNA mixtures (Chen et al., 2024). Body-wide chimerism and mosaicism were identified as primary causes of ABO discrepancies (Dauber et al., 2024). The accuracy of mixture analysis was found to decrease for groups with lower genetic diversity (Flores et al., 2024). Droplet digital PCR was used to discover unbalanced mixtures and evaluate mixing ratios (Fu et al., 2025). Bayesian inference was used to evaluate the effect of aging on stutter ratios (Inokuchi et al., 2023). The importance of optimizing thresholds was emphasized (Simon & Smith 2024). STR typing was performed on skin swabs from individuals after allogeneic hematopoietic stem cell transplantation (von Máriássy et al., 2023).

AI Efforts to Assist in DNA Interpretation. Artificial intelligence and machine learning are increasingly being integrated into interpretation workflows. A critical review examined machine learning applications in forensic DNA profiling (Barash et al., 2024). The need for interpretable algorithmic forensics was highlighted (Garrett & Rudin 2023). AI applications in forensic biology were detailed in a book chapter (Gupta et al., 2024). Ethical and security challenges, including bias and adversarial attacks, were discussed (Marsico & Amigo 2025). Deep learning approaches for DNA profiling were replicated and evaluated (Sangiovanni et al., 2025). Current applications and future perspectives of AI in forensic genetics were reviewed (Sessa et al., 2024). A narrative review discussed AI in the context of identifying the deceased (Siwan et al., 2025). Explainable AI was applied to allele identification in challenging electropherograms (Tan et al., 2025). Artificial neural network classification was combined with probabilistic genotyping to remove the need for analytical thresholds (Taylor & Buckleton 2023). A "lights-out" (fully automated) analysis workflow was proposed for no-suspect crime samples (Taylor & Abarno 2023). AI-driven human identification from skeletal remains was demonstrated (Valsecchi et al., 2023). Efforts to make AI accessible for forensic DNA profile analysis were described (de Wit et al., 2026).

Estimating the Number of Contributors. Accurately determining the number of contributors (NoC) remains a critical step in mixture analysis. The impact of considering different numbers of contributors on identification problems was analyzed in real casework mixtures (Costa et al., 2025). A simple Excel-based tool, eNoC, was introduced to improve NoC assignment (Thomson et al., 2022).

DNA Mixtures with Probabilistic Genotyping Software. Probabilistic genotyping software (PGS) is central to modern mixture interpretation. The value of mixture-to-mixture comparisons was assessed in an operational context (Basset et al., 2024). A DNA decision support tool was evaluated to bridge expertise and data-driven approaches (Benschop et al., 2025a). An automated workflow using PGS-based database searching provided fast reports for investigative leads (Benschop et al., 2025b). The exonerating power of "what isn't there" in mixture evidence was discussed (Brenner 2025). Primary differences between EuroForMix and STRmix were diagnosed (Buckleton et al., 2024a), and inconsistencies in forensic decisions were further discussed (Buckleton et al., 2024b). The impact of drop-out on likelihood ratios was evaluated using continuous approaches (Caglià et al., 2025). Developmental validation studies were conducted on a new version of STRmix for interpreting next-generation sequencing (NGS)-generated profiles (Cheng et al., 2023). Differences in results from the same software were analyzed (Costa et al., 2022). EuroForMix was validated at the Brazilian Federal Police for complex profiles (Duarte et al., 2025). A three-person mixture was solved using a sample from a relative (Gómez et al., 2025). Two widely used PGS systems in the US were compared (Greenspoon et al., 2024). A maximum likelihood ratio algorithm was proposed for three-contributor mixtures (Guo et al., 2024). Random forest regression predicted LR values for database searching (Hu et al., 2025). Whole-genome amplification improved contributor assignment in touch DNA mixtures (Hwa et al., 2025). An STR mixture analysis and resolution tool (SMART) was introduced for mixture interpretation (Ji et al., 2025). Commentary addressed uncertainty in PGS for low-template DNA (Thompson 2023, Kalafut et al., 2024, Perlin et al., 2024). Uncertain assumptions in DNA evidence evaluation were addressed (Kruijver et al., 2023). An R-shiny package, KongohPlus, was developed for MCMC-based software (Manabe et al., 2025). Calibration and discrimination performance were evaluated for "low" LRs (McCarthy-Allen et al., 2024) and for DNAStatistX (McCarthy-Allen et al., 2025). LRs from PGS were compared across different assays and instruments (McNevin & Barash 2024). EuroForMix was re-evaluated for deconvolution and weight-of-evidence computing (Minervino et al., 2025). Ambiguity and contested expertise in probabilistic profiling were analyzed sociologically (Pullen-Blasnik et al., 2024). A collaborative study assessed the precision of Markov chain Monte Carlo (MCMC) algorithms (Riman et al., 2024). LRs from EuroForMix and STRmix were compared for two- and three-contributor profiles (Saccente et al., 2025). The infringement of the presumption of innocence by evaluative probabilistic reporting was debated (Sallavaci 2025). LRs from STR sequencing and CE were compared for complex mixtures (Sidstedt et al., 2025). A guiding principle was proposed to identify the best supported propositions in mixture interpretation (Slooten et al., 2025). Similarities and differences between MPS and CE data were analyzed for their impact on LR calculations (van der Gaag et al., 2025). Compound likelihood ratios were investigated (Wivell et al., 2023), and mixture detection performed using Demixtify (Woerner et al., 2024).

Interlaboratory Studies on DNA Mixtures. Collaborative studies have highlighted variability and consensus in mixture interpretation. An interlaboratory comparison evaluated PGS parameters and performance (Boodoosingh et al., 2024). The DNAmix 2021 study provided a dataset on laboratory policies and procedures (Brinkac et al., 2023), revealing variation in assessments of suitability and number of contributors (Hicklin et al., 2023) and in interpretations and statistical analyses (Hicklin et al., 2025). Propositions used to assess mixtures were analyzed in an FSWG-ISFG interlaboratory comparison (Samie et al., 2025).

Low-Template DNA Interpretation. Strategies for low-level DNA focus on thresholds and sensitive detection methods. Analytical thresholds were optimized using insights from multi-laboratory negative controls (Chen et al., 2024). Interpretation considerations were outlined for low-level profiles following MinElute purification (Cooper et al., 2024). Amplification thresholds were optimized for low template DNA (Ido et al., 2025). Whole transcriptome shotgun sequencing identified individuals from low-template (LT) blood samples (Jepsen et al., 2024). Modifications for LT-DNA trace analysis were evaluated for efficiency (Parys-Proszek et al., 2022).

Communicating Forensic Findings Effective communication of complex statistical results to lay audiences remains a challenge. Mock juror evaluations of conclusion formats were explored (Bali & Martire 2025). Commentary was provided on joint recommendations for biostatistical evaluation (Berger et al., 2024). German project groups published recommendations on biostatistical evaluation with fully continuous models (Hahn et al., 2023, Templin et al., 2023) and mixture deconvolution using EuroForMix (Schiller et al., 2025). Finally, researchers investigated whether explaining the meaning of likelihood ratios improves lay understanding (Thompson et al., 2025).

3.8. DNA interpretation at the activity level

When investigators want to explore *how* or *when* an individual's DNA became associated with a crime scene, they may attempt to evaluate the evidence given activity-level propositions. This approach, sometimes referred to as evaluative reporting, is dependent on many variables including probabilities of DNA transfer, persistence, prevalence, and recovery (TPPR). This topic is an active area of research and was discussed in the two 2024 NIST reports [25,26].

Books, Review Articles, and Guidance. Guidance documents and texts are increasingly focusing on the interpretation of DNA evidence at the activity level. German recommendations were published for forensic expertise regarding indirect DNA transfer and its consideration in court proceedings (Förster et al., 2023). Minimum requirements for publishing data on DNA transfer and recovery given activities were established (Gill et al., 2026). A comprehensive book detailed interpretation of trace forensic DNA evidence using activity-level propositions and likelihood ratios (Kokshoorn & Taylor 2023). A literature review covered indirect DNA transfer and its forensic implications (Sessa et al., 2023). Another text focused specifically on forensic DNA transfer (Taupin 2023). The benefits and limitations of nucleic acid persistence were also reviewed (Żarczyńska et al., 2023).

Studies on Shedder Status. Understanding individual variation in shedding DNA is crucial for activity-level interpretation. Popular shedder tests were compared to determine the best assessment method (Ali et al., 2025). The efficacy of Diamond nucleic acid dye-stained cell counting was evaluated for forensic applications (Goray et al., 2024). The consistency of shedder status was assessed under various experimental conditions (Jansson et al., 2024). A meta-analysis investigated the individual propensity to shed skin material in the context of trace analysis (Koch et al., 2025). Touch DNA viability on various substrates was examined relative to different shedder levels (Saamia et al., 2024). An interaction timeline was used to investigate factors related to shedder status (Taylor et al., 2025).

DNA Transfer Study Design. Innovative experimental designs are improving the study of transfer mechanisms. An experimental design and qPCR assay were developed to identify primary, secondary, and tertiary DNA transfer (McCrane & Mulligan 2023, McCrane & Mulligan 2024). Methods were determined for sampling background areas to provide the greatest support for a person of interest in a target sample (Reither et al., 2024). A cellular target was developed and characterized for tracking transfers of biological traces (Sauvagère et al., 2025).

DNA Transfer Dynamics and Scenarios. Research has explored DNA transfer in diverse scenarios to aid casework interpretation. The impact of deposition area and time on touch DNA collected from fabric was studied (Alketbi & Goodwin 2022). DNA transfer was tracked in a social setting (Cahill et al., 2024). Glove-mediated transfer was investigated in burglary simulations (Carrara et al., 2023) and forensic casework (Mehta and Alketbi 2025). A case of contamination by indirect transfer in a sexual assault case was reported (Castella et al., 2025). Male DNA transfer and survival under female victim fingernails were tracked in a scratch simulation (Damour et al., 2025). Male DNA transfer onto female underwear was examined in simulated non-sexual social interactions versus digital penetration (Doole et al., 2023). Indirect transfer mechanisms of semen were evaluated under varying conditions (Finnis et al., 2024). DNA transfer during a slap and punch was analyzed (Galea et al., 2025). Saliva-derived secondary transfer on fabric was studied under varying conditions (Gegar et al., 2024). Parallel strategies using DNA and scanning electron microscopy analysis were applied to transfer and recovery of DNA and metal particles (Giorgetti et al., 2024). Garment cleaning protocols were tested for loss and re-location of traces (Gléonec et al., 2024). Self- and non-self-DNA were analyzed on hands and sleeve cuffs (Henry & Zieger 2024). Microbiota marker transfer from hand to knife was preliminarily studied (Karadayı et al., 2024). DNA transfer between items within an evidence package was assessed (Lee & Syn 2025), as was transfer on drug packages in simulated settings (Li et al., 2025) and in packaging generally (Stella et al., 2022). DNA transfer in washing machines was analyzed with different detergents (Lozano-García et al., 2025). Recovery methods were compared for worn hooded sweatshirts before and after use by a second wearer (Meakin et al., 2024). DNA accumulation and transfer were measured within an operational forensic exhibit storeroom (Mercer et al., 2023). DNA consistent with the known owner was quantified on law enforcement-owned firearms (Oefelein et al., 2025). Trace DNA transfer on a credit card was evaluated using Bayesian networks (Onofri et al., 2023). Transfer to drug packaging and knives in houses was studied (Reither et al., 2023). Transfer between contacting surfaces when both have DNA on them was investigated, with a subsequent corrigendum issued (Sallows et al., 2025). The impact of liquid antibacterial soap and hand sanitizer on transfer was studied (Sessa et al., 2024). Degradation of bloodstains on fabric caused by washing was analyzed (Stojanović et al., 2024). DNA on interior door handles was examined (Tièche et al., 2022). After resumed use by the owner, DNA transfer and persistence were studied in an office space that had been visited by an intruder (Zacher et al., 2022, Zacher et al., 2024).

Animal-Mediated DNA Transfer. Animals can act as vectors for human DNA transfer. The presence of human DNA on cats was investigated (Monkman et al., 2022), as well as their role in human DNA transfer (Monkman et al., 2025a). Human DNA on household dogs and its bi-directional transfer were studied (Monkman et al., 2023, Monkman et al., 2025b). Video analysis of human-animal interactions was explored for forensic identification use (Monkman et al., 2024). Transfer and persistence of owner DNA on domestic pets were also analyzed (Oefelein et al., 2025).

Environmental Factors Impacting DNA Persistence. Studies have assessed how environmental conditions affect DNA stability on various substrates. A long-term study investigated trace DNA persistence on non-metals (Arsenault et al., 2025). The impact of temperature and humidity on semen persistence was evaluated (Beveridge et al., 2025). Substrate characteristics were shown to impact biological material collection and persistence (Hughes et al., 2024). Persistence of touch DNA was studied under different storage conditions (Kaesler et al., 2023). DNA transfer and persistence were examined on non-porous surfaces submerged in spring water (Korzik et al., 2023). Persistence of cellular material after water exposure was analyzed (Nolan et al., 2023). Invisible biological traces were detected in relation to substrate physicochemical properties (Recipon et al., 2024).

Interlaboratory Data. Large-scale collaborative projects are seeking to standardize activity-level methods. The ENFSI ReAct project reported results from a large consortium investigation (Gill et al., 2025a) and characterized DNA recovery data from 23 laboratories given activity-

level propositions (Gill et al., 2025b). Accounting for interlaboratory data variability was discussed when performing evaluations given activities (Taylor et al., 2025).

Activity Level Evaluations. Case reports and surveys illustrate the practical application of activity-level interpretation. Activity-level propositions were applied in a murder case in Austin, Texas (Buckleton 2025) and Boston (Kalafut et al., 2025). Published recommendations for reporting the value of biological findings were discussed (Buckleton et al., 2025a). Interpreting DNA under fingernails given activity level propositions was explored (Buckleton et al., 2025b). A conjunctive analysis examined the role of context in homicide investigations involving DNA (Chamberlain et al., 2024). Serum cortisol and StAR gene expression were evaluated as biomarkers for the nature of sexual acts (Dash et al., 2025). Education and interpretation challenges were compared between source and activity issues (Hicks et al., 2025). Reporting practices for activity-level issues in the Netherlands were described (Kokshoorn & Luijsterburg 2023). Alternate hypotheses involving the transfer and persistence of saliva beneath fingernails were explored (Matte et al., 2023). Baselines for background DNA in new underwear were established for evaluative reporting (Oefelein et al., 2024). A global survey assessed evaluative reporting on DNA evidence with regard to activity-level propositions (Prinz et al., 2024). Commentary was provided on a Texas Forensic Science Commission report regarding a complaint about activity-level evaluation (Roy 2025). Bayesian networks were used to evaluate DNA results in a fatal car accident to determine the identity of the driver (Samie et al., 2025). Barriers to global adoption of forensic evaluative reporting were identified (Stacey et al., 2025). Sensitivity analyses in activity-level evaluations were treated practically (Taylor et al., 2024a). Finally, site-to-site DNA transfer on packaged exhibits was accounted for in evaluations (Taylor et al., 2024b).

3.9. Statistics and population genetic data

This section summarizes efforts over the previous three years in population genetics related to forensic DNA and STR allele frequency population data.

Books, Review Articles, and Guidance. Guidance documents and other texts have reinforced the statistical framework for DNA evidence. The UK Forensic Science Regulator published guidance on allele frequency databases and reporting for STR profiling (Forensic Science Regulator 2024). To strengthen the use of forensic science evidence, informational scientific primers were created for officers of the court (Jones et al., 2025). A review discussed how statistics, including likelihood ratios and graphical models, can aid forensic science (Xu & Vinci 2024).

Statistical Methods and Population Genetics. Research has refined statistical models and addressed ethical and practical challenges in population genetics. A qualitative assessment explored forensic scientists' perceptions of statistical models, sequence data, and ethical implications (Aalbers et al., 2023). Sequence-based population structure and inbreeding estimates were analyzed for forensic STR markers (Aalbers & Weir 2024). Recent statistical innovations in human genetics were reviewed (Balding & Speed 2025). Genomic diversity of Alu insertion polymorphisms was studied in native British and South Asian migrant populations (Beaumont et al., 2023). Foren-STR, a tool for rapid calculation of forensic parameters, was introduced (Castillo-Ortiz et al., 2025). The impact of parameter variation on forensic genetic evidence quantification was assessed (Costa et al., 2025). Minimal SNP sets were identified for record-matching with CODIS STR profiles (Gjorgjieva & Rosenberg 2025), and record-matching was achieved with fragmentary genomic SNP data (Kim & Rosenberg 2023). The use of Bayes factors to limit forensic testimony was discussed (Kadane & Nordgaard 2024). Population-specific theta values were estimated for sequence-based STR profiles (Liu et al., 2024). Complex genetic variation was characterized in nearly complete human genomes (Logsdon et al., 2025). The transition of STRs from historical loci to population databases in the NGS era was examined (Uguen et al., 2024). The effects of genetic linkage were determined when combining STR and SNP loci for kinship testing (Yang et al., 2024).

STR Allele Frequency Population Data. Population genetic data have been reported for diverse groups globally, enhancing reference databases. Guidance on population sampling for highly polymorphic STR loci was revisited (Aalbers & Gettings 2026). The impact of religious inbreeding on genetic structure was studied in Lebanon (Abbas et al., 2023), alongside population substructure assessments (El Andari et al., 2023) and sequence-based allele frequencies (Riman et al., 2023). Data for non-CODIS STR loci were published for Saudi Arabia (Alsafiah & Goodwin 2022). Informed consent practices for population studies were reviewed with a call for harmonization (Bodner & Parson 2025). Genetic ancestry was analyzed in Ecuador for Montubios rural populations (Burgos et al., 2025) and Afro-descendants (Burgos et al., 2022), as well as general population structure (Flores-Espinoza et al., 2022). A reference database for 24 STR loci was established for Argentina (Caputo et al., 2023).

In China, studies covered the Guizhou Gelao minority (Chai et al., 2024), 94 populations based on population structure estimates (Dai et al., 2023), the Guizhou Tujia ethnic minority (Li et al., 2023), the Shandong Han population (Liu et al., 2023), the Handan Han population (Wang et al., 2023), the Wuhu Han population (Yang et al., 2024), and the Hainan Han population (Zou et al., 2024). The impact of population size on genetic analysis parameters was investigated (Dash et al., 2025). Genetic analysis of the Moroccan population was performed based on 23 autosomal STRs (El Ossmani et al., 2025). Forensic parameters were reported for Western Mexico (García-Aceves et al., 2025) and Mexico City (Salinas-Pineda et al., 2024). STRAF 2 software was released with improvements for population data analysis (Gouy & Zieger 2025). Population studies were conducted in Northwest Iran (Haddadan et al., 2024). The Investigator 24plex GO! kit was evaluated for South African populations (Heathfield et al., 2024), and a GlobalFiler dataset was created for Southern Africa (Kasu et al., 2022). The comprehensive landscape of non-CODIS STRs in global populations was described (Huang et al., 2024). Genetic diversity was unveiled in English and Irish populations using SureID kits (Iyavoo et al., 2023) and compared to identify disparities (Perry et al., 2023). STR genotyping was performed for Arabs residing in Russia (Jaber et al., 2025). Allele frequencies were statistically integrated from several organizations (Jeong et al., 2024).

A genetic study of the Ghanaian population used 15 autosomal STR loci (Kofi et al., 2023). Allelic frequencies and tri-allelic patterns were identified in the Gabonese population (Lendoye et al., 2023). Novel STR loci were characterized in the Sierra Leone population (Liu et al., 2024). A PowerPlex Fusion 6C study examined a mestizo population from Mexico City (López-Armenta et al., 2024). A genetic database was established from a Spanish Civil War population (López-Parra et al., 2025). DNA polymorphism was studied in Mentawai populations (Manela et al., 2023). STR loci were evaluated in South and West Indian populations (Mathiyazhagan et al., 2023) and North and East Indian populations (Mathiyazhagan et al., 2024). A dataset was created for the Hawrami population in Iraq (Mohammad et al., 2025), and variation was assessed across 6 Iraqi cities (Sabbah et al., 2023). Genetic variation was analyzed in Peruvian populations (Neyra-Rivera & Budowle 2022, Ramirez et al., 2025, Ramos et al., 2025). Characterization was performed for the Sikh population of Sri Ganganagar (Ostwal et al., 2025), the Brahmin population of Rajasthan and Haryana (Sharma et al., 2023), and the Sikkim population in the Central Himalayas (Priyank et al., 2024). Population data were published for the Romanian population (Popoiu et al., 2025). Genetic variability was assessed in Austroasiatic-speaking populations from Thailand (Prakhun et al., 2024). Allele frequencies and forensic data were reported for Northeast Brazil (Santos et al., 2023). Genetic diversity was analyzed in the Russian Federation using PowerPlex CS7 (Semikhodskii et al., 2023) and Investigator HDplex (Semikhodskii et al., 2024). Genome-wide STR variation was

characterized in 6487 human genomes (Shi et al., 2023). Polymorphism and structure were analyzed for a Han-Chinese population from Luzhou (Song et al., 2023). Genetic variation was studied among siblings of Madurese living in Surabaya (Yudianto et al., 2023). A reference database was created for populations in Burkina Faso (Zeye et al., 2024). Finally, data were published for the Tawahka ethnic group in Honduras (Zuniga et al., 2025).

STR Allele Sequence Data. Massively parallel sequencing is providing high-resolution allele data. An overview of autosomal STRs and SNPs was provided for a Norwegian population (Agudo et al., 2024). High-resolution genotyping of 58 STRs was performed in Northern Han Chinese (Guo et al., 2023) and Northeastern Xibe populations (Guo et al., 2024). Forensic implications of a new microvariant allele at Penta E were discussed (Kocsis et al., 2023). Variability of 27 STR loci was assessed for the Republic of Belarus (Kotova et al., 2023). A sequence-based Rwanda population study provided insights into demographic history (Miao et al., 2024). A combined panel of 107 STRs and 292 SNPs was sequenced in the Han Chinese population (Sun et al., 2025). Population genetic analyses of an Eastern Chinese Han population were done using the ForenSeq DNA Signature Prep Kit (Tao et al., 2024). Sequence-based data for five STRs were reported for a Northeast Italy population (Turrina et al., 2025). Parallel sequencing of 170 STR and 132 SNP markers was performed using the FGID kit (Zhen et al., 2024).

3.10. Human identification and kinship analysis

Human remains identification can be important for many applications including identifying victims of war or mass disasters and missing persons casework. This work often relies on using kinship analysis with reference samples from close biological relatives. Methods to distinguish monozygotic twins or perform prenatal paternity testing continue to be developed. Some forensic investigations have also employed human DNA recovered from mosquitoes, leeches, and bed bugs.

Books, Review Articles, and Guidance. Guidance for human identification has been updated across various contexts. The Association for the Advancement of Blood and Biotherapies (AABB) released the 16th edition of standards for relationship testing laboratories (AABB Relationship Testing Standards Committee 2024). A review covered the computational analysis of human skeletal remains in ancient and forensic genetics (Childebayeva & Zavala 2023). Interdisciplinary approaches were proposed for identifying remains and missing persons (Dahal et al., 2023). Current and emerging solutions for identifying "genealogically bewildered" individuals were reviewed (Dash & Patel 2025). A comprehensive volume addressed the recovery, analysis, and interpretation of burnt human remains (Ellingham et al., 2023). Genetic reconstruction of the past and its application to forensics were discussed (Erlich 2023). The UK Forensic Science Regulator issued guidance on DNA relationship testing using autosomal STRs (Forensic Science Regulator 2024). INTERPOL updated its Disaster Victim Identification Guide (INTERPOL 2023). A bibliometric analysis traced global trends in kinship analysis from 1960 to 2023 (Liu et al., 2024). Methods for forensic human identification were reviewed within the context of smart healthcare (Mohamed et al., 2023). The history and present state of DNA profiling for identification were summarized (Panneerchelvam & Nor 2023), along with identification practices in India (Patra et al., 2023). SWGDAM released guidelines for missing persons casework (Scientific Working Group on DNA Analysis Methods 2024). Recommendations were provided for identifying altered human remains using standard and emerging technologies (Senst et al., 2023). DNA profiling from burnt remains was detailed (Zapico & Stone-Gordon 2023).

Human Remains Identification for War Victims and Others. Identification efforts for war victims and mass graves remain a critical application. Case reviews highlighted human identification through forensic skeletal analysis (Adserias-Garriga et al., 2024). Large consortia reported on identifying victims of the Spanish Civil War (Arroyo-Pardo et al., 2025, Baeta et al., 2025). A large-scale forensic search was conducted for remains of fallen soldiers from the American Revolutionary War (Bigman et al., 2023). Family reunification was achieved for survivors of the Armero-Tolima natural disaster in Colombia (Cuervo et al., 2022). Identification challenges in Iraq were discussed (Farhan et al., 2025). Skeletal remains of Baron Pasquale Revoltella were examined with various genetic markers (Fattorini et al., 2023). Ancient human remains from an Italian medieval site were analyzed (Gianfreda et al., 2025). The Korean War Identification Project's expanding scope was detailed (Go et al., 2023), including genetic identification studies (Zhang et al., 2024) and ancestry analysis of cremated remains (Oh & Park 2022). NGS and CE were compared for analyzing human remains (Kokotas et al., 2025). Polish World War II victims, including a pilot (Lisman et al., 2023a) and an unknown soldier (Lisman et al., 2023b), were identified. The political struggle over declaring missing soldiers dead using DNA technology was analyzed historically (Liu 2025). Forensic archaeology identified a fallen World War I soldier in France (Meucci Duly et al., 2024). The remains of the German outlaw Schinderhannes were identified (Parson et al., 2025). A 30-year review covered identification efforts in Croatia and Bosnia and Herzegovina (Primorac et al., 2024). WWII victims in Crete were identified using ancient DNA approaches (Psonis et al., 2024). Lessons learned from management of the forensic DNA identification operation following the October 7, 2023 attacks in Israel were described (Ram et al., 2025). Identification success rates were analyzed for Spanish Civil War mass graves (Sanchis-Gimeno et al., 2024). A forensic approach was applied to remains from an Italian cemetery collapse into the sea (Tettamanti et al., 2022). DNA techniques were evaluated for human remains from historic shipwrecks (Watherston & McNevin 2024).

Methods and Sample Types. Optimization of methods for challenging samples continues. Identification methods were compared between Brazil and the United States (Bastos Vieira et al., 2025). A multidisciplinary approach identified skeletal remains from Sandy Point, Australia (Blau et al., 2024). Elemental and microbial evidence were used as a "forensic footprint" in relocated remains (Bolhofner et al., 2025). Fingernails were identified as an optimal DNA source for decomposed bodies in seawater (Della Rocca et al., 2024). Mass spectrometry mRNA typing identified single hair shafts (Fan et al., 2025). A multidisciplinary approach profiled a single tooth and fingernail sample (Hulst et al., 2025). A sampling strategy was recommended for World War II victims in Slovenia (Inkret et al., 2025). Humeri pair matching was studied on a large scale (LeGarde 2025). RNA polymorphism was used for hair shaft identification (Liu et al., 2023). Advances in commingled human remains analysis were reviewed (Palmiotto et al., 2024). Cranial bone mutilation victims were identified using a combined approach (Priyatna et al., 2024). High-throughput SNP multiplex NGS was evaluated for human remains identification (Radecke et al., 2023). Innovations in human identification by the French Gendarmerie were reviewed (Sauvagère et al., 2023). Ancient DNA was recovered from a 20,000-year-old pendant (Sterling 2023). Y-STR analysis was successful on highly degraded skeletal remains (Zhang et al., 2024).

Missing Persons Casework. Missing persons investigations face unique challenges. Genetic data recovery from remains on the Western Balkan migration route was discussed (Barbarić & Horjan-Zanki 2023). Kinship SNP microarrays were used for identification in the absence of two generations (Biagini et al., 2025). NGS mitogenomes and phenotyping identified a newborn abandoned in a dumpster (Bini et al., 2025). A family reference DNA database was established for missing Australian service members (Connell et al., 2025). Efforts were reported with identification of human remains in a unique mummification case (Flouri et al., 2024). A software tool was tested to aid prioritization in selecting potential family reference samples to verify incomplete pedigrees (Iungman et al., 2022). Alternative workflows were proposed for identifying transnational missing persons (Kaplan et al., 2023). A case of dog scavenging on an elderly animal hoarder was described (Kmetiuk et al., 2023). The missing person problem was analyzed through information theory (Marsico et al., 2024). A study from Hesse, Germany, found that

DNA examinations were performed in 40% of human bone finds with 81% of these yielding STR profiles (Ohlwärther et al., 2024). Forensic genetic programs for missing person identification in humanitarian contexts were reviewed (Orozco 2025). Physical and molecular anthropology were combined to profile unidentified migrants (Pilli et al., 2023). Public and family support for providing DNA in long-term missing persons cases was surveyed (Russell et al., 2023a), identifying main concerns and policy implications (Russell et al., 2023b). Challenges of migrant mortality accounting in Texas were discussed (Siegert et al., 2024). The Australian approach to unidentified and missing persons was detailed (Ward 2022, Ward 2024). Kinship testing techniques were reviewed (Watson et al., 2024). A two-decade-old murder was solved using a collagen peptide mass spectrometry fingerprinting technique ("ZooMS") and ancient DNA methods (Xu et al., 2023).

Disaster Victim Identification (DVI). DVI protocols are adapting to mass casualty events. Challenges were identified by Australian practitioners (Adamovic et al., 2023). Stable isotope analysis was reviewed for identifying unknown decedents (Chesson et al., 2024). Ethnographic observation highlighted challenges in 21st-century DVI (Easthope 2023). SNP assays were reviewed for cost, time, and performance in DVI (Gettings et al., 2024). Forensic archaeology and anthropology contributions were reviewed to aid sample selection for DNA testing (Hanson & Fenn 2024). Deep learning-based STR analysis was applied to mass casualty incidents (Khalid & Khamiss 2024). Forensic medicine challenges were discussed following the October 7, 2023 attacks in Israel (Kuge et al., 2024). The association between DNA and odontology was systematically reviewed (Lopez Toribio et al., 2024). Forensic odontology's role was specifically detailed (Miller 2024). Efforts to identify the dead in the October 7, 2023 terror attack at the Israel-Gaza border were described (Mor et al., 2024). Recommendations on storage of biological samples were made based on the "Mass Grave Project" (Sguazzi et al., 2025). The feasibility of cell-free DNA for DVI was assessed (Worrapitirungsi et al., 2024). A simple postmortem sampling method was proposed for efficient DVI (Zgonjanin et al., 2025).

Software Tools and Computational Methods for Kinship Analysis. Software and statistical models are improving kinship inference. Multistep mutations in STRs were analyzed for their perception as single-step events (Antão-Sousa et al., 2022). Bayesian networks were validated for the GENis missing person module (Chernomoretz et al., 2022). Posterior parameters were analyzed from paternity tests in Mexico (García-Aceves et al., 2023). A deep neural network model was developed for paternity testing (Khalid & Nafea 2023). FamLink2 was introduced for likelihood computations in pedigrees with linked markers (Kling et al., 2025). Mutational analysis of 23 STRs was based on trio paternity testing in Korea (Lee et al., 2024). Easykin, an online tool for kinship testing, was developed (Li et al., 2023). A general approach for combining non-genetic and genetic data was proposed (Marsico & Egeland 2025). Computations for relationship inference using low-coverage sequencing were improved (Mostad et al., 2023). Paternity testing using 21 STRs was reported in Rwanda (Ndungutse et al., 2023). Software options for likelihood ratio calculations were explored for low-template DNA paternity cases (Riem et al., 2025). Uncertainties in different kinship scenarios were evaluated (Rockenbauer et al., 2025). The impact of theta correction in siblings testing was assessed (Tièche et al., 2025). Identification value of STRs was determined for indigenous peoples of Russia (Vagaitseva et al., 2024). M-FISys software was optimized for complex family pedigrees (Vinueza-Espinosa et al., 2025). Complex kinship inferences were made using combined STRs and microhaplotypes (Wei et al., 2025). Pedigree likelihood formulae based on founder symmetry were assessed (Yang 2023). The efficiency of common markers for parentage identification involving close relatives was evaluated (Zhang et al., 2023).

Complex Paternity/Kinship Cases. Complex biological relationships and scenarios require specialized analysis. The medicolegal concerns of "three-parent babies" were discussed (Chitara et al., 2025). Null alleles caused interpretative problems in a paternity case where close biological relatives refused to provide reference DNA samples (A. Di Nunzio et al., 2022). Deconvolution rules were used to solve a complex case involving a chimeric child (C. Di Nunzio et al., 2022). The impact of additional STR loci on paternity test accuracy was studied (Fontanil et al., 2025). Ethical challenges of the Amelogenin sex test were reviewed (Gabriele et al., 2023). Informativity of X-STRs was analyzed in real kinship cases (García-Aceves et al., 2025). Heterozygosity reduction was observed in children of closely related parents (Iyavoo et al., 2022). Aborted fetal material was analyzed in sexual assault cases (Jusic et al., 2023). Massively parallel sequencing of human leukocyte antigen (HLA) genes was used to assess relatedness in deficiency parentage testing (Kouniaki et al., 2024). The effect of uniparental disomy in parentage testing was examined (Ma et al., 2024). Chain of custody was highlighted as a vital component in kinship cases involving close relatives (Mishra & Raina 2024). Paternity exclusions were characterized in Honduras (Molina et al., 2023). A paternity case was solved using formalin-fixed paraffin-embedded tissue (Song et al., 2023). Common mutations in parentage testing were analyzed in Zimbabwe (Thelingwani et al., 2024).

New or Improved Methods for Kinship Analysis. High-throughput and novel marker systems are advancing kinship determination. A dense SNP PCR multiplex was applied for high-throughput kinship using NGS (Antunes et al., 2022). NGS-based SNP genotyping was evaluated for second- and third-degree kinship (Asari et al., 2025). Bi-allelic autosomal SNPs were effective for parentage testing in Taiwan (Chen et al., 2024). A novel approach used the physical length of genetically shared regions (Cho et al., 2024). High-density SNP microarrays were assessed for pairwise kinship with degraded DNA (Chu et al., 2023). Genome-wide and targeted sequencing were compared (Colucci et al., 2025), and 1993 SNP loci were applied to pairwise kinship identification (Cui et al., 2023). Considerations for implementing MPS into routine analysis were outlined (Davenport et al., 2025). A likelihood ratio framework was proposed for inferring close kinship from dynamically selected SNPs (Ge et al., 2025). The Precision ID GlobalFiler NGS STR panel v2 was used for single exclusion paternity cases (Gouveia et al., 2025). A high-throughput SNP assay was assessed for closed scenario kinship (Kiesler et al., 2025). Testing efficacy of SNP microarrays was enhanced for distinguishing pedigrees (Mo et al., 2025). A software program, correctKin, was optimized for inferring relatedness from low-coverage ancient genomes (Nyerki et al., 2023). Extended kinship inference was evaluated using STRs and SNPs (Watson et al., 2025a) and the impact of information loss was assessed (Watson et al., 2025b). Efficiency of complex kinship identification was improved by adding markers and reference individuals (Wen et al., 2025). Novel SNP markers were identified for the Korean population (Youn et al., 2023). Kinship probability in ancient skeletons was improved using identity SNPs and MPS (Zupanič Pajnič et al., 2023).

Distinguishing Monozygotic Twins and Prenatal Paternity Testing. Identifying identical twins and non-invasive prenatal testing are key frontiers. Strategies to solve the "twin paradox" were reviewed (Aourangzaib et al., 2024). Genetic markers for noninvasive prenatal paternity testing were reviewed (Carrara & Hall 2025). Early noninvasive prenatal paternity testing was achieved by targeted fetal DNA analysis (Damour et al., 2023). DNA methylation was used to identify monozygotic triplets (El-Hossary et al., 2024). Isoalleles and flanking SNPs were analyzed to distinguish monozygotic twins (Fonseca & Fridman 2022, Fonseca et al., 2025, Fridman et al., 2025). Microbiota information and genetic algorithms improved distinguishing power (Fu et al., 2023). A theoretical base was established for non-invasive prenatal paternity testing (Gao et al., 2023). Fetal DNA extraction techniques were compared (Guevara-Ramírez et al., 2025). DNA identification of monozygotic twins was reviewed (Hwa et al., 2024). DNA methylome profiling identified individuals in a twin pair (Kim et al., 2023). Rare mitochondrial genome differences were explored (Liu et al., 2023). Progress in personal identification of monozygotic twins was summarized (Liu et al., 2025). Immune repertoire sequencing

distinguished twins' blood samples (Meng et al., 2023). A SNP-based approach was developed for non-invasive prenatal paternity testing (Qu et al., 2024). NGS was used to differentiate twins (Skrant et al., 2023). Single-nucleotide variants were used for twin discrimination (Sun et al., 2024). A case was reported in dizygotic twins of heteropaternal superfecundation, which is the fertilization of two oocytes by different spermatozoa within the same ovulatory cycle (Timasheva & Tuktarova 2025). A monozygotic twin was identified as a donor in a mixed stain case (van der Gaag et al., 2025). Circular RNA expression profiles were used to distinguish twins (Wang et al., 2024). MicroRNA profiling differentiated twins in peripheral blood (Wang et al., 2025). Heteroplasmy of mtDNA was used for discrimination through probe capture enrichment (Zhong et al., 2023).

Human DNA in Mosquitoes, Leeches, and Bed Bugs. Vectors can serve as sources of human DNA evidence. STR profiling identified humans from mixed mosquito blood meals (Ahmed et al., 2023). Human STR profiles were generated from blood ingested by leeches (Knapp et al., 2024). The "bistro" R package was developed for vector bloodmeal identification (Lapp et al., 2024). Tropical bed bugs were used for human profiling (Lim & Ab Majid 2023) and a protocol was established (Lim & Ab Majid 2024). Bed bugs were reviewed as undercover agents in forensic investigations (Meiklejohn et al., 2025). Human DNA profiles were obtained from mosquito blood meals in Thailand (Suwannakart et al., 2024). Sex-typing of ingested blood was performed using the amelogenin gene (Talebzadeh et al., 2023). Mitochondrial genes and Alu elements detected human DNA in mosquito blood meals (Talebzadeh et al., 2023). Exogenous DNA was detected from the gut of a Neotropical carrion beetle (Toni et al., 2023).

4. Emerging technologies and Research studies

New technologies to aid forensic DNA typing are constantly under development. This section explores recent activities with next-generation DNA sequencing, DNA phenotyping for estimating a sample donor's age, ancestry, and appearance, lineage markers, other markers and approaches, and non-human DNA and wildlife forensics. This material is expected to be of value to researchers and those practitioners looking to future directions in the field.

4.1. Next-generation sequencing and technology developments

Next-generation sequencing (NGS), also known as massively parallel sequencing (MPS) in the forensic DNA community, expands the measurement capabilities and information content of a DNA sample beyond the traditional length-based results with STR markers obtained using capillary electrophoresis (CE) methods.

Books, Review Articles, and Guidance. Several comprehensive texts and reviews have recently addressed the implementation of NGS in forensics. A transition from capillary electrophoresis to NGS was advocated to meet the need for higher throughput analysis (Al-Snan 2023a), and the specific utility of NGS-based microRNA analysis for forensic applications was detailed (Al-Snan 2023b). An overview of current platforms highlighted the technological advancements facilitating these shifts (Barbaro 2023), while specific applications for analysis of hairs with roots demonstrated success rates of 96% to 98% using modified protocols (Benitez & Elkins 2023). Chapters have also covered the application of NGS for autosomal STRs (Berry 2023) and the necessary validation procedures for implementing NGS in casework laboratories (Bispo Santos Silva 2023). Policy considerations and forensic applications of NGS were reviewed to address the legal framework (Browne & Freeman 2024), alongside protocols for processing biological samples for NGS analysis (Coticone & Garcia 2023). Textbooks published in this period included *Next Generation Sequencing (NGS) Technology in DNA Analysis* (Dash et al., 2024) and *Advancements in Forensic DNA Analysis* (Dash et al., 2023). A survey of Southeast Asian laboratories revealed that while only 8 of 19 respondents currently use MPS, 10 of the remaining non-users plan to adopt it within five years (Estrella et al., 2025). The potential of long-read sequencing was explored, with results showing the ability to phase 87% of protein-coding genes (Ferreira et al., 2025). Other works focused on the ForenSeq DNA Signature Prep Kit methods (Foley 2023) and a global snapshot of opinions on NGS usage (Foley and Oldoni 2023). Reviews also covered pyrosequencing methodologies (Ghemrawi et al., 2023) and the challenges of introducing massively parallel sequencing into the UK market (Hartshorne et al., 2024). Further reviews discussed third-generation sequencing progress (Hu et al., 2024), the forensic relevance of SNP analysis (Malhotra & Sehgal 2023), and the analysis of challenging samples (Messaoudi 2023). The role of artificial intelligence in NGS was examined (Ouanes 2023), alongside the opportunities and barriers for implementing NGS and SNP microarrays in routine practice (Pedroza Matute & Iyavoo 2025). Future trends were identified in the use of compound genetic markers (Shabalala et al., 2025) and the application of nanopore sequencing (Tytgat & Van Nieuwerburgh 2023).

Library Preparation, Enrichment, and Quality Control. Efforts to improve data quality and recovery from difficult samples have led to several methodological optimizations. An enhanced error suppression strategy was developed that achieved a background error rate of less than 4.4×10^{-5} per base pair (Chen et al., 2025). For highly burned skeletal remains, targeted enrichment of whole-genome SNPs indicated that teeth subjected to temperatures below 350 °C provided the highest DNA yields (Emery et al., 2024). Genome-wide hybridization capture enrichment was tested on six degraded bones from the Spanish Civil War, yielding results comparable to autosomal STR analysis but with additional insights (Haarkötter et al., 2025). A study on DNA quality for whole genome library preparation was conducted (Jansson et al. 2024), and an evaluation of DNA extraction and library building methods was performed to prepare for shotgun sequencing (Kampmann et al., 2025). Optimization of crude buccal swab lysates for the ForenSeq kit involved dilution and purification steps, which improved success rates in samples where 93% initially showed inhibition (Martin & Heathfield 2025). A workflow for dual nucleic acid co-extraction allowed for the integrated sequencing of both DNA and RNA (Miao et al., 2025). Automation was addressed with the development of a workflow for ForenSeq library preparation (Scherer et al., 2025), and the Agilent 2100 Bioanalyzer was applied as a quality control instrument for NGS (Senst et al., 2024).

Sequencing STR Markers. The transition to sequence-based STR genotyping has required new standards and software tools. Guidelines for submitting data to STRSeq were updated (Borsuk et al., 2022), and unique molecular identifiers were used to improve allele calling in low-template mixtures (Crysup et al., 2023). Secondary structure predictions of autosomal STR alleles were analyzed using NGS data (Dash & Ranga 2024), and comparisons between massively parallel sequencing and capillary electrophoresis for trace DNA were reported (Dierig et al., 2024). The ISFG DNA Commission published recommendations on STR sequence nomenclature (Gettings et al., 2024). Studies characterized the amplification of STR markers in multiplex polymerase chain displacement reactions (Huang et al., 2023) and developed support systems like STRategy for collecting and analyzing NGS data (Kulthammanit et al., 2023). Sequence variations in flanking regions were characterized for 21 autosomal and 21 Y-chromosome STR markers (Li et al., 2024), and the GeneMarker HTS software was utilized for allele identification with variant tolerance (Luo et al., 2022). Software for analyzing rare and common STR variation was compared using human genome sequences (Oketch et al., 2024), and concordance between length- and sequence-based STRs was evaluated (Sathirapatya et al., 2023). Ultrasensitive sequencing utilizing SiMSen-Seq and unique molecular identifiers was described (Sidstedt et al., 2024). The era of long-read sequencing for tandem repeats was highlighted (Tandem repeats 2024), and the shift from historical loci to population databases was discussed (Uguen et al., 2024). New tools included TRcaller for ultrafast variant genotyping (Wang et al., 2023) and STRsensor for computationally efficient allele-typing (Zhang et al., 2025).

MPS Kit Development and Validation Studies. Validation studies for commercial and custom MPS kits have demonstrated their robustness and sensitivity. A forensic evaluation of the ForenSeq DNA Signature Prep Kit in a Mexican admixed population compared DNA primer sets A and B (Aguilar-Velázquez et al., 2025), and the ForenSeq MainstAY assay was examined for forensic use (Cabrejas-Olalla et al., 2025). Developmental validation was completed for the IDseek OmniSTR global autosomal STR profiling kit (de Jong et al., 2025). Sequencing of human autosomal STR orthologs was shown to provide individual and species identification in African great apes (Fedele et al., 2024). Automation was developed for the PowerSeq CRM Nested Assay (Galusha et al., 2025), and the STRSeqTyper122 kit was tested with massively parallel sequencing (Guo et al., 2024). Comparisons of the ForenSeq Signature Prep and MainstAY kits with traditional capillary electrophoresis were performed (Hymus et al., 2024), and the internal validation studies for the Precision ID GlobalFiler NGS STR panel v2 focused on mixtures and low template DNA (Kocsis et al., 2025). A novel 193-plex MPS panel integrating STRs and SNPs was introduced for individual identification (Liu et al., 2024). The Precision ID GlobalFiler panel was also evaluated for identity and ancestry applications (Pedroza Matute & Iyavoo 2024) and systematically tested using single-source and mixed samples (Sharma & Wurmbach 2024). Stochastic thresholds were calculated for MPS platforms (Stephens et al., 2022), and the developmental validation of the ForenSeq MainstAY kit demonstrated the detection of 99.2% of expected alleles in mixtures with minor contributions as low as 10 pg (Stephens et al., 2023). Further validation of the IDseek OmniSTR kit included the use of reverse complement PCR (van der Gaag et al., 2025). Case-specific applications included verifying a loss of heterozygosity at the D8S1179 locus (Wang et al., 2023) and genotyping formalin fixed skeleton samples with the ForenSeq DNA Signature Prep Kit and MiSeq FGx Sequencing System (Yang et al., 2024).

Sequencing to Aid DNA Mixture Interpretation. NGS technology has been applied to resolve complex DNA mixtures. NGS was utilized to analyze mixed DNA samples (Kara et al., 2024), while sequencing-induced artifacts in NGS STR data were characterized (Liu et al., 2024). Massively parallel sequencing improved individual identification in mixtures of unrelated or related contributors (Liu et al., 2024). Probabilistic genotyping was evaluated for low-pass DNA sequencing (Mandape et al., 2022), and cost-effective NGS-based STR typing was reported to improve the analysis of minor, degraded, and inhibitor-containing samples (Poethe et al., 2023). Additionally, publicly available forensic DNA sequence mixture data were developed to support interpretation efforts (Romsos et al., 2025).

SNP Markers and Methodology. Methodologies for single nucleotide polymorphism (SNP) analysis have expanded. Shotgun DNA sequencing was used for human identification with dynamic SNP selection (Andersen et al., 2025). The legal impact of these technologies was highlighted by a U.S. serial killer case that opened the door to using cutting-edge DNA data in courts (Bourzac 2025). Normalization based on read count distribution was proposed to maximize NGS potential (Brennan et al., 2023), and a SNP-STR haplotype panel was evaluated for genotype imputation (Chen et al., 2023). Flanking region variation in forensic identity SNPs was characterized using MPS (Davenport et al., 2023), and troubleshooting challenges for NGS were discussed (D'Orio et al., 2023). The SNPtotree method was introduced to resolve the phylogeny of SNPs on non-recombining DNA (Köksal et al., 2023). Probabilistic genotyping methods were developed for low DNA concentrations (Nielsen et al., 2022) and enhanced with symmetric multinomial logistic regression (Nielsen et al., 2025). The evolution of SNP use in forensic genetics was reviewed (Novroski & Cihlar 2022), and SWGDAM released interpretation guidelines for SNP analysis (Scientific Working Group on DNA Analysis Methods 2024). Capture baits were generated for targeted sequencing (Sundararaman et al., 2023), and a hybridization capture-based hereditary panel was evaluated (Xiong et al., 2025).

SNP Population Data and Specific Applications. Population-specific data and applications for SNPs were reported for diverse groups. An "FD Multi-SNP Mixture Kit" was analyzed for human complex mixtures (Chen et al., 2024). Genotyping of 58 STRs and 94 identity-informative SNPs (iiSNPs) was performed in Mexican-Mestizos from Jalisco (García-Aceves et al., 2025), and 94 iiSNPs were characterized in Northern Han Chinese (Guo et al., 2024). A study of 124 SNPs in a Myanmar population used the Precision ID Identity Panel (Joo et al., 2023). Population data for 94 iiSNPs were released for four U.S. population groups (Kiesler et al., 2022) and expanded to calculate a match probability of 1.7×10^{-38} (Kiesler et al., 2023). Targeted sequencing of high-density SNPs was conducted for the Chinese Korean ethnic group (Lan et al., 2023), and the NimaGen IDseek OmniSNP kit was used for population genetic analysis (Mandape et al., 2024). Characterization of 94 iiSNPs was also reported for a Northeastern Italian population (Saccardo et al., 2025). Trisomy 21 was disclosed using STR and SNP markers typed by the MiSeq FGx system (Turrina et al., 2022). Identity-informative markers were characterized in an Australian population with European ancestry (Watson et al., 2025), and 124 SNPs and microhaplotypes were analyzed in Koreans (Yang et al., 2023). Benchmarking for genotyping and imputation was performed using degraded DNA across diverse populations (Zavala et al., 2025).

SNP Panel Evaluation, Validation, and Proficiency Testing. Quality assurance and inter-laboratory comparisons for SNP panels were the focus of several studies. Results from the GHEP-ISFG proficiency testing program covered STR, Y-STR, and mtDNA markers (Fernández et al., 2025). An internal quality assessment and error investigation for SNP microarray testing was conducted following an ESWG-ISFG trial (Iyavoo et al., 2025). Reference materials were investigated for SNP typing with the FORCE panel (Kotchey et al., 2025). Three massively parallel sequencing platforms were compared for SNP genotyping (Li et al., 2023), and an inter-platform evaluation was performed for the MPSplex large-scale tri-allelic SNP panel (Ruiz-Ramírez et al., 2025). An interlaboratory exercise was established to create proficiency testing for sequencing forensic STR and SNP markers (Sadam et al., 2025). Unique molecular indices were applied to an extensive forensic SNP panel to improve accuracy (Staadig et al., 2023), and commercial kits for NGS-based analysis were reviewed (Unsal Sapan 2023).

SNP Arrays. High-throughput SNP arrays have been developed and validated for forensic use. The Infinium HTS iSelect Custom microarray panel "Rita" was developed (Pedroza Matute et al., 2024) and validation studies with the custom BeadChip assay showed over 95% marker success (Pedroza Matute and Iyavoo 2025). The Illumina Infinium Assay using the Global Screening Array was evaluated, showing call rates exceeding 99% for control samples (Russell et al., 2023). Additionally, the SNP + tool was introduced to predict dropout rates in SNP arrays (Sastre et al., 2023).

Other Technologies for STR Typing. Emerging technologies beyond standard NGS have been applied to STR typing. EasySSR, a web application for large-scale microsatellite mining, was released (Alves et al., 2023). Nanopore direct sequencing was explored for forensic STRs, SNPs, and methylation markers in a single assay (de Bruin et al., 2025). Statistical methods were applied to discriminate STR genotypes using high-resolution melt curve data (Cloudy et al., 2024). A perylene-oligonucleotide fluorescence assay was used for STR profiling (Hernández Bustos et al., 2023), and a digital microfluidic approach was developed for processing multi-source sexual assault samples (Elsayed et al., 2024). High-fidelity targeted profiling of microsatellites was achieved (Loh et al., 2024), and a pilot validation of on-field STR typing using MinION nanopore sequencing was conducted (Luo et al., 2024). The NASTRA tool was developed for accurate analysis of STR markers by nanopore sequencing (Ren et al., 2024). Real-time PCR using QueSTR probes was reported for STR genotyping (Škevin et al., 2023, Škevin et al., 2025). A review of microfluidic approaches to nucleic acid analysis was published (Turiello et al., 2023). Applications of nanopore sequencing in forensic genetics were discussed including the use of

QNome technology (Yang et al., 2024) and the rapid identification of an 18-STR long amplicon panel using portable devices (Zhang et al., 2025).

4.2. DNA phenotyping and methylation

Methods for forensic DNA phenotyping (FDP) have been explored to predict ancestry, appearance, and age of the individual who is the source of biological evidence under investigation. In addition to age prediction, DNA methylation analysis has been used for lifestyle prediction, such as smoking habits.

Books, Review Articles, and Guidance. A comprehensive review detailed computational methods and tools for identifying phenotypically informative SNPs to bridge the gap from genetic association to forensic prediction (Abbatangelo et al., 2023). Investigative DNA testing protocols were described with a focus on describing the perpetrator for forensic purposes (Branicki 2024). Chapters in recent texts have explored the integration of forensic DNA phenotyping (FDP) within the NGS era (Carratto et al., 2023) and the specific application of NGS-based epigenetic markers for forensic analysis (Ghai 2023). The National Academies of Sciences, Engineering, and Medicine published proceedings from a workshop addressing law enforcement use of probabilistic genotyping, FDP, and forensic investigative genetic genealogy (Committee on Law and Justice 2024). Ethical and social critiques highlighted that FDP may lead to privacy breaches and bias through abstract assessments of rights (Coquet & Terrado-Ortuño 2023). A survey of police officers examined their knowledge and operational views regarding FDP, revealing gaps between technological capabilities and investigative understanding (Gareau-Léonard et al., 2025). The utility and risks of FDP were analyzed through the views of forensic geneticists in Europe (Granja & Machado 2023). Other reviews focused on FDP using NGS technologies (Haidar et al., 2023) and the sociological implications of measuring and categorizing human variation in terms of race (Hopman 2023). Further sociological analysis suggested that these technologies require rethinking the use of technological innovations in policing (Hopman & Bleumink 2023). Technical advancements allowed for a multisample approach in phenotyping chronological old skeletal remains using MPS (Inkret et al., 2023). Recent advances in predicting appearance, ancestry, and age were synthesized to update the field on current capabilities (Kayser et al., 2023). Current trends and challenges in FDP were discussed with a focus on future directions (Navarro-López & de Pancorbo 2025), and the Oxford Nanopore Sequencing system was evaluated for its utility in FDP applications (Sapan et al., 2024). A review of SNP panels, genotyping techniques, and prediction models provided a technical overview of the field (Terrado-Ortuño & May 2025). Finally, insights into forensic biogeographical ancestry inference highlighted recent trends in global population analysis (Wen et al., 2023).

Ancestry Prediction. Methodologies for ancestry inference have expanded to include specific regional and haplogroup analyses. A haplogroup-based methodology using Y-STR data was developed to assign individuals to geographical regions (Afkanpour et al., 2024). Machine learning approaches, specifically partial least squares-discriminant analysis (PLS-DA), were applied to improve biogeographical ancestry prediction (Alladio et al., 2022). A custom hybridization enrichment panel was created to simultaneously infer biogeographic ancestry, hair and eye color, and Y chromosome lineage (Bardan et al., 2023). Large-scale selection of highly informative microhaplotypes was conducted to enhance ancestry inference and population-specific informativeness (de Barros Rodrigues et al., 2025). Genetic and linguistic origins of the Palenque population in Colombia were traced back to African roots (Beatriz et al., 2025). The genetic landscape of phenotyping markers was mapped among Mediterranean populations (Becher et al., 2024), and the power and limitations of inferring genetic ancestry were critically examined (Bird et al., 2025). Autosomal STRs were explored for their utility in inferring continental biogeographical ancestry (Casanova-Adán et al., 2025) and estimated in the sequencing era (Devesse et al., 2023). A panel of 165 ancestry-informative SNPs was used to resolve the ancestry of South Brazilians (Felkl et al., 2023). A scientific plea for legal regulation on predicting biogeographical origin was published in German (Fleckhaus et al., 2025). The inclusion of flanking SNPs was shown to advance the use of the Yb8 Alu dimorphism for assessing ethnicity (Kass et al., 2024).

Genetic relationships were analyzed between two sub-populations within the Akan ethnic group in Ghana (Kubi & Goodwin 2025). Genome-wide association studies identified rs17822931 as a key ancestry-informative marker in the Han Chinese population (Li et al., 2023). A proof-of-principle study demonstrated the potential of Mini-Hap biomarkers for ancestry inference using QNome nanopore sequencing (Liu et al., 2024). The utility of ancestry informative markers (AIMs) and their applications were reviewed (Mekhfi et al., 2024), and the GenoGeographer Admixture Module was updated with new AIMs population data (Mogensen et al., 2022). Admixture proportions in Peruvian Mestizo populations were analyzed using an Insertion Deletion multiplex (Neyra-Rivera et al., 2025). Y-STR and mitochondrial DNA markers were tested for ancestry prediction of World War II victims from a Slovenian mass grave (Obal et al., 2024). A new panel using variable selection and PLS-DA was developed to assess ancestry via MPS technology (Pilli et al., 2023).

Comparative evaluations were performed for the MAPlex, Precision ID Ancestry Panel, and VISAGE Basic Tool (Resutik et al., 2023). The VISAGE Enhanced Tool was developed and evaluated for combined appearance and ancestry prediction (Ruiz-Ramírez et al., 2023). Biogeographical ancestry was analyzed using the ForenSeq DNA Signature Prep Kit alongside multiple prediction tools (Salvo et al., 2024). Salivary microbiome signatures were investigated for their potential to distinguish between Polish and Serbian populations (Skonieczna et al., 2025). XGBoost was demonstrated as a reliable machine learning tool for predicting ancestry using autosomal STR profiles (Šorgić et al., 2025). A data clustering approach was used to pinpoint STR alleles for ethnic inferencing (Syukriani & Hidayat 2023). The ForAPP pipeline was introduced for the interpretation of ancestry informative markers (van der Gaag et al., 2022). Finally, a study in an Australian population characterized sex-chromosome, phenotype-informative, and ancestry-informative markers (Watson et al., 2025).

Appearance Prediction. Research into externally visible characteristics (EVCs) has refined predictions for eye, hair, and skin color, as well as facial morphology. The accuracy of eye and hair color prediction using the ForenSeq kit was evaluated in Mexican Mestizos from Monterrey City (Aguilar-Velázquez et al., 2023). Advancements in human face prediction from DNA were reviewed (Alshehhi et al., 2023). Face phenotypes in the Rio Grande do Sul population were analyzed in relation to *MC1R* variants and age (Bettim et al., 2024). Genes and variants specifically associated with eye color prediction were detailed (Brancato et al., 2023). Genetic predictions of eye and hair color were assessed in the Danish population (Cabrejas-Olalla et al., 2025). A review addressed the genetic challenges of creating a "DNA portrait" (Chemeris et al., 2024). Genome-wide association scans revealed novel loci for facial traits (Cho et al., 2023) and utilized polygenic scores for height estimation in Koreans (Cho et al., 2024). Phenotypic characteristics were profiled from three- or four-hundred year old human remains (Elkins et al., 2022). Additional predictions for EVCs were reported using the ForenSeq and Imagen kits (Elkins et al., 2023), though these methods sparked commentary regarding their validation and interpretation (Kayser 2024, Wendt 2023). FDP was successfully applied to predict eye, hair, and skin color in highly decomposed bodies (Fabbri et al., 2023). Profiling and phenotyping were achieved from non-standard samples like tobacco sticks and fingernails with polish (Fazio et al., 2025). Genetic polymorphisms associated with freckles were analyzed for phenotypic prediction (Fridman et al., 2022). Remarkably, human DNA recovered from *Lucilia sericata* larvae allowed for the prediction of eye and hair color (Deymenci et al., 2024).

The PyroMark Q48 Autoprep was evaluated with the HIrisPlex-S

system in an Italian population (Gentile et al., 2022). Facial hair-associated SNPs were evaluated in a pilot study on a male Pakistani Punjabi population (Jawad et al., 2023). The morphology and genetics of scalp and facial hair were investigated for phenotype prediction (Kataria et al., 2023). Machine learning models were applied to predict eye color in Latin American populations (Martínez et al., 2025). A quasi-landmark mesh was used to decode the upper facial region from DNA (Navarro López et al., 2025), and associations between SNPs and facial morphology were explored in a Spanish population (Navarro-López et al., 2025). Assays were evaluated for predicting ear morphology (Noreen et al., 2023) and hair color in the Argentine population (Nowik et al., 2025). A targeted amplicon sequencing panel of 50 SNPs was developed for EVCs and behavior (Park et al., 2024). Signal precision was enhanced for SNaPshot genotyping of IrisPlex targets (Patil & Patel 2025). Skin color prediction was focused on Asian populations, specifically in Thailand (Perez Palomeque et al., 2025). The Irisplex system was used for eye color prediction on skeletal remains from the past 30 years (Rafati et al., 2023) and tested in populations from the Malakand Division (Rahat et al., 2023) and Shangla Valley, Pakistan (Rahat et al., 2023). Associations were found between copy number variations in the *OCA2-HERC2* locus and eye color (Salvo et al., 2022a), and long-distance haplotyping of these variants was performed (Salvo et al., 2022b). Specific associations were identified between variants in the *OCA2-HERC2* region and blue eye color in *HERC2* rs12913832 AA and AG individuals (Salvo et al., 2023). A "Biological identikit" SNP panel was developed for FDP and ancestry (Sguazzi et al., 2022). Eye and forehead structure were determined to assist in facial morphology prediction (Simsek et al., 2025). Forensic intelligence utilization of phenotypic information was discussed in the context of "Kafka's beautiful eyes" (Taylor et al., 2024). The IrisPlex system was evaluated for the Serbian population (Vukovic et al., 2023). A dataset named BioKinVis was created for facial kinship verification (Yu et al., 2024). Finally, the association between DNA methylation and human height was modeled for predictive purposes (Wang et al., 2024).

Age Prediction. Epigenetic age estimation has seen significant activity, particularly using DNA methylation (DNAm) markers across various tissues. Legal age estimation was explored using DNA methylation (Boullón-Cassau et al., 2025), and models were refined to account for sex-specific differences and non-linear correlations in adults and minors (Carlsen et al., 2023). A review highlighted the path to age estimation through DNA methylation (Castagnola et al., 2024), while specific correlations were found between CpG island methylation of the *hTERT* promoter and age (Cui et al., 2023). Droplet digital PCR was used to predict age from blood using three methylation markers (Dias & Manco 2024). Transcriptomic signatures were also assessed, with mRNA markers selected for age estimation in blood stains (Dørum et al., 2024, Hänggi et al., 2025). A semen-specific DNA methylation model was developed that proved robust under environmental challenges (Er et al., 2024). A systematic review examined the *ELOVL2* gene for age determination (Faress et al., 2023, Paparazzo et al., 2023). Epigenetic-based age prediction models were developed for blood samples (Filoglu et al., 2024) and compared between Middle Eastern and Central European populations to assess biogeographic influence (Fleckhaus et al., 2023). Methylation patterns in fingernails and toenails were utilized for age determination (Fokias et al., 2023), with subsequent improvements to the toenail model (Fokias et al., 2023).

Costal cartilage was used to develop an epigenetic age predictor with a simultaneous somatic tissue differentiation system (Freire-Aradas et al., 2023) and for disaster victim identification (Jung et al., 2024). DNA methylation analysis was applied to burnt human remains (Grignani et al., 2025). An inter-laboratory evaluation validated the VISAGE enhanced tool for blood and buccal cells (Heidegger et al., 2025). Method-specific differences in detecting DNA methylation status were analyzed to determine whether models could be integrated (Hong & Shin 2023). Progress in the field was reviewed (Huang et al., 2023, Naue 2023), and male-specific age prediction models were created using Y-chromosome methylation in blood (Ji et al., 2024, Jiang et al., 2023) and Y-chromosome loss in leukocytes (Song et al., 2023). Collaborative exercises evaluated protocols using the PyroMark platform (Kampmann et al., 2024). Quality control of bisulfite-treated DNA was emphasized for semen samples (Kotková et al., 2025), and genome-wide markers were identified for semen-based age estimation (Li et al., 2025, Xiao et al., 2023). A five-locus multiple regression model was applied to buccal swabs (Marcante et al., 2024).

Epigenetic clocks were discussed in the context of aging-related diseases (Margiotti et al., 2023). ATR-FTIR spectroscopy of fingernails was proposed as an alternative method for age determination (Mitu et al., 2025). Nanopore sequencing was used to estimate the short-term age of bloodstains (time since deposition) (Nakanishi et al., 2024). Pilot studies and collaborative evaluations established the accuracy of methylation-based assays in the Italian population (Onofri et al., 2023, Onofri et al., 2025). Changes in methylation of *ELOVL2* and *ZYG11A* were observed in dental samples (Pinprasert et al., 2024). A multiplex amplicon sequencing assay was introduced to quantify markers for four epigenetic clocks (Pośpiech et al., 2023). Pyrosequencing data from saliva and buccal swabs were evaluated (Poussard et al., 2023), and a 10-CpG panel was developed via stepwise conditional epigenome-wide association study (Qian et al., 2025). Longitudinal changes were analyzed with the MethylationEPIC BeadChip (Refn et al., 2023), and an 11-CpG panel for blood was independently evaluated (Refn et al., 2025). Fluorescence spectroscopy was applied to human semen stains for age estimation (Santikulthani et al., 2025). Quantification of degradation levels was combined with age estimation in bisulfite-converted DNA (Shiga et al., 2024). Methylation of *ELOVL2*, *PRKG2*, and *EDARADD* genes were used to estimate age in Indonesian adolescents ages 11 to 20 (Soedarsono et al., 2024). Comparison of technologies for blood, buccal, saliva, and semen samples was conducted (Sutter et al., 2025). Machine learning algorithms were applied to small sets of methylation sites in blood (Varshavsky et al., 2023; Yamagishi et al., 2024). Finally, models were improved by combining sex chromosome and autosomal markers (Wan et al., 2025).

Metabolomics for Lifestyle Prediction. Epigenetic markers are increasingly used to infer lifestyle habits. Tobacco and alcohol consumption habits were inferred from DNA methylation analysis of blood (Ambroa-Conde et al., 2024). A comprehensive study predicted sex, age, height, body mass index (BMI), smoking status, and lipid-lowering drug use using epigenetic markers and plasma proteins (Llobet et al., 2023). Analysis of epigenetic clocks linked slower aging to factors such as yoga, sleep, education, reduced meat intake, and coffee consumption (Noroozi et al., 2024). Untargeted metabolomics were used to discover lifestyle biomarkers in human hair (Pego et al., 2024). DNA methylation at the *AHRR* gene was identified as a master predictor of smoke exposure and a biomarker for sleep and exercise (Pośpiech et al., 2024), and was also used in buccal cells to predict smoking status (Pośpiech et al., 2025). Massively parallel sequencing was utilized for targeted methylation analysis to predict smoking habits (Vidaki et al., 2023).

DNA Methylation and Epigenetic Analysis. Future challenges in forensic epigenetic analyses were outlined (Gerra et al., 2024). DNA methylation profiling revealed potential biomarkers for fatal anaphylactic shock induced by β-lactams (Guo et al., 2024). The HumanMethylationEPIC v2.0 BeadChip was evaluated using low-quality and quantity DNA samples (Poggiali et al., 2025). Strategies were developed to handle genetic analyzer-specific differences in DNA methylation measurements (So et al., 2024).

4.3. Lineage markers

Lineage markers consist of Y-chromosome, mitochondrial DNA, and X-chromosome genetic information that may be inherited from just one parent without the regular recombination that occurs with autosomal DNA markers. Research in terms of new markers, assays, and population studies continue to be published for these lineage markers.

Books, Review Articles, and Guidance. Guidance and reviews have solidified the standards for lineage marker analysis. X-chromosome STRs were reviewed for their utility in human identification, highlighting their specific value in complex kinship cases (Alwi et al., 2023). Lineages between individuals were determined using high-density mitochondrial and Y-chromosomal SNPs (Chiao & Ge 2024). Protocols for mitochondrial DNA analysis were detailed in a methods volume (Cooley 2023), and the UK Forensic Science Regulator published updated guidance on Y-STR profiling (Forensic Science Regulator 2025). The application of NGS for analyzing maternal genomes in ancient human remains was discussed (Irfan et al., 2023). An interview with Dr. Lutz Roewer highlighted the history and future of Y-STR analysis (Novroski 2025). SWGDAM released updated interpretation guidelines for mitochondrial DNA analysis (SWGDAM 2024a) alongside supplemental information to support these standards (SWGDAM 2024b).

Y-Chromosome DNA. Research on Y-chromosome DNA has focused heavily on population genetic structure and the validation studies with high-density panels. Genetic insights from the Middle East were reported for Qatar using the PowerPlex Y23 system (Almohammed et al., 2025) and for Yemen (Al-Shoba et al., 2025), while 23 Y-STRs were analyzed in Iraqi populations (Mahdi Al-Zubaidi et al., 2023). Extensive data were published for populations in Kazakhstan, including 27 Y-STR loci in Eastern (Ashirbekov et al., 2023) and Central regions (Ashirbekov et al., 2024), alongside a study of 60 SNP markers in the general Kazakh population (Bukayev et al., 2024). In China, phylogenetic characteristics were detailed for the Qingdao Han population using 41 Y-STRs (Fan et al., 2023b), the Sichuan Bouyei people (Fan et al., 2025), the Hui population in Liaoning (Fu et al., 2023), a Han population in Luzhou (Fu et al., 2023), the Chinese Han population (Miao et al., 2025), the Hunan Han population (Zhao et al., 2023), and the Tibeto-Burman-speaking Lahu population (Xu et al., 2023). Further Chinese population data covered the Va population (Yuan et al., 2023), the Hui population from Yunnan (Zhang et al., 2023), and the Lisu ethnic minority (Zhang et al., 2023).

In the Americas, Y-STR characterization was performed for the Santander department of Colombia (Castillo et al., 2025) and three populations in Northeastern Brazil (do Monte et al., 2025), while paternal heritage was traced in self-declared Ecuadorian indigenous people (Nguidi et al., 2022). Uniparental genetic profiles were used to unravel the complexity of Argentine admixed populations (Mayordomo et al., 2025), and the genetic male component of Afro-descendants from Pará, Brazil, was analyzed (Ribeiro et al., 2025). Studies in Europe and Africa included haplogroup diversity in the British Isles (Iyavoo et al., 2025), Y-STR characteristics in the Balkans (Jankova et al., 2025) and Serbia (Zgonjanin et al., 2025), and haplogroup prediction in the Ghanaian population (Wepeba et al., 2022). Diversity and methylation variation were analyzed among Black and Indian males from KwaZulu-Natal, South Africa (Shabalala et al., 2023).

Statistical methods were refined, with the discrete Laplace method applied to Y-STR matches (Andersen et al., 2023) and extended experimentally for haplotype frequency estimation (Kruijver et al., 2022), alongside calculations for U.S. subpopulations (Letts et al., 2022). Relevant propositions for Y chromosome interpretation were outlined (Bright et al., 2025), and population-specific theta values were estimated for PowerPlex Y23 (Buckleton et al., 2025). The assembly of 43 human Y chromosomes revealed extensive complexity and variation (Hallast et al., 2023). Mutation rates were analyzed in 2548 father-son pairs at 41 loci (Liu et al., 2023), as well as in Korean (Lee et al., 2023) and Nigerian father-son pairs (Knights et al., 2025), and pedigree-based estimation was applied to historical remains (Connell et al., 2025). Analysis of rapidly mutating Y-STRs enabled almost complete discrimination of unrelated and related males from the African continent (Barni et al., 2024).

New tools and kits were tested, including a 41-plex Y-STR panel (Chai et al., 2023), a complementary Y-STR system (Fan et al., 2023a), and the Y-chromosome Ancestry and Region Network (YARN) MPS kit for East Asian lineage analysis (Fan et al., 2024). A novel 8-dye system with 59 Y-STRs and 3 Y-indels was developed (Liu et al., 2024), as well as the AGCU YNFS Y Kit (Sun et al., 2024), a 5-dye multiplex with 30 Y-STRs (Sun et al., 2025), and a 381 Y-SNP panel (Tao et al., 2023). The Investigator Argus Y-28 QS Kit was also evaluated (Vraneš et al., 2022). Machine learning approaches were applied for estimating Eastern Asian origins (You et al., 2025) and for haplogroup prediction using tools like oYSTeR (Claerhout et al., 2025) and YHP (Song et al., 2024). The Universal Y-SNP Database (UYSD) contains data from more than 6600 males across 27 populations to provide insights into human genetic diversity and migration patterns (Ralf et al., 2025). Historical investigations identified George Washington's Y-chromosomal haplotype at Harewood Cemetery (Cavagnino et al., 2024).

A screening approach for sexual assault evidence was investigated using the QIAGEN Investigator Casework GO! kit (Bonsu et al., 2025). Case reports and studies highlighted deletion events in the AZFc region (Flores-Espinoza et al., 2025), Yp11.2 deletions in Turner syndrome (Lai et al., 2023), deletions affecting amelogenin-based sex typing (Marcińska et al., 2025), and multilocus gene deletions (Mo et al., 2025).

Mitochondrial DNA. Advancements in mtDNA analysis have centered on NGS implementation and global population data. Temperature-dependent sequencing was explored for incinerated tooth samples (Aggarwal et al., 2025), and the precision of mitochondrial whole genome systems was enhanced for challenging remains (Canale et al., 2025). Copy number differences were utilized for inferring fingerprints (Chen et al., 2025) and assessing variation relative to nuclear DNA (Naue et al., 2024). Long-fragment amplification strategies were evaluated on DNA nanoball platforms (Chen et al., 2024). NGS pipelines were developed for degraded samples (Cuesta-Aguirre et al., 2024, Vinueza-Espinosa et al., 2023) and for variant analysis (Lee et al., 2023), with specific attention to sequencing quality in decomposed samples (Lee et al., 2025). Nanopore sequencing was applied using Mitopore (Dobner et al., 2024) and automated pipelines for heteroplasmy (Jiang et al., 2023) and variation identification (Liu et al., 2025). The ForenSeq mtDNA Whole Genome Kit was assessed in multiple studies (Hymus et al., 2024, Liu et al., 2023, Pereira et al., 2022, Xuan et al., 2025). Probabilistic assessment tools were created for mtDNA mixtures (McElhoe et al., 2024). A review article from India compared autosomal STRs and mtDNA (Usman et al., 2023).

Complete mitogenomes were analyzed for 334 samples from El Salvador (Aizpurua-Iraola et al., 2023). In India, variation was analyzed in Gujarat (Alqaisi et al., 2024), tribal populations of Chhattisgarh (Dixit et al., 2024), the Jat population of Haryana (Sharma & Verma 2023), and Kavaratti islanders (Tayyeh et al., 2023). Maternal ancestry was characterized in Santander, Colombia (Castillo et al., 2023) and Andean Mestizos from Ecuador (Garzón-Salazar et al., 2025). African maternal origins were traced in Brazilian quilombos (Nguidi et al., 2025), and ancestral KhoeSan patterns were studied in South Africa (D'Amato et al., 2025). Other studies covered the Buyei population in China (Feng et al., 2024), ancient affiliations in Pakistan (Khan et al., 2024), haplogroup expansion in North Macedonia (Jankova et al., 2025), and genome variation in Sweden (Sturk-Andreaggi et al., 2023) and the Han population of Shandong (Zhang et al., 2024).

X-chromosome DNA. X-STRs are increasingly used for complex kinship analysis, with new population data and validation studies. Genetic diversity of X-STRs was reported for Iraqi Sorani Kurds (Albarzinji et al., 2023, Mohammad et al., 2024), the Malaysian Indian population (Alwi et al., 2024), and 12 markers in Namibian populations (Calò et al., 2024). European data included an analysis of 12 markers in Slovakia (Červenák et al., 2023). In China, studies covered the Guizhou Miao and Bouyei groups (Huang et al., 2024), Hubei Han and Guangxi Zhuang populations (Long et al., 2023), the Jining Han population (Wang et al., 2023), and Guangdong Hakka, Teochew, and Cantonese groups (Xiao et al., 2023). Data were also published for Punjabi and Kashmiri populations (Khan et al., 2024), Koreans (Lee et al., 2025), Northeastern Thai populations (Srithawong et al., 2024), and the first X-STR study for

the South African population (Whittaker & Heathfield 2024).

Internal validation studies were performed for reduced PCR reaction volumes of the Argus X-12 QS Kit (Alwi et al., 2023). Issues of mutation assignment between X- and autosomal STRs were investigated (Antão-Sousa et al., 2022). A practical proposal was made for interpreting X-STR profiles from the ForenSeq kit (Cortés-Trujillo et al., 2025, Wepeba & Goodwin 2025). Mathematical frameworks were developed for quantifying X-chromosomal evidence in cases of trisomy X (Faustino et al., 2022, Faustino et al., 2025). New multiplex systems were constructed, including a 13-locus system for the Malay population (Minaguchi et al., 2024) and a 22 X-indel system (Ozyer et al., 2023). Kinship testing using linkage groups was demonstrated on a Tamil pedigree (Pedroza-Matute et al., 2025).

4.4. New markers and approaches

Researchers continue to expand the possible toolbox of techniques to enable effective use of biological evidence. This section reviews efforts with microhaplotype and insertion/deletion markers, proteomics, microbiome, single-cell analysis, environmental DNA, and biomarkers analyzed for molecular autopsies and estimating the post-mortem interval.

Books, Review Articles, and Guidance. A chapter on microbial forensic DNA analysis was included in a recent text (Jadhav et al., 2025). The transition of forensic genetics into the omics era was reviewed to highlight future directions (Kayser 2025). Current challenges facing the field of forensic DNA analysis were outlined (Rao 2025), and the research progress and potential applications of microRNA and other non-coding RNAs were summarized (Song et al., 2024).

Where We Have Come From and Where We Are Going. The culmination of molecular genomic techniques in crime investigation was reviewed (Bhattacherjee et al., 2025), alongside a reflection on the past, present, and future of the *Forensic Science International: Genetics* journal and the field itself (Carracedo 2025). Broader perspectives on the evolution of forensic genetics were published (Gutiérrez-Hurtado et al., 2025), and a bibliometric analysis detailed the knowledge structure within the Asian Forensic Sciences Network from 2008 to 2022 (Halmi et al., 2025). The potential limitations and failures of DNA evidence were discussed to understand the "limits of forensic faith" (Imran & Parmar 2025). A proof-of-concept study demonstrated the potential of human leukocyte antigen alleles to assist in resolving multiple-contributor mixtures (Kuffel et al., 2024). Editorials and special issues addressed current issues (Lee 2023) and the trajectory of the field (Kayser et al., 2023). Integrated detection technologies for DNA and RNA markers were reviewed (Miao et al., 2023), alongside summaries of recent developments in DNA typing (Simayijiang & Yan 2023) and innovations in forensic analysis (Vidaki & McCord 2024).

Microhaplotypes. NGS-based microhaplotype analysis was detailed in a book chapter (Albujja 2023). New panels were developed for kinship testing, including a 188-marker panel for the Hebei Han population (Du et al., 2023) and a 232-marker panel with associated software (Gao et al., 2025). Bioinformatic tools were introduced, such as the MhGeneS pipeline for robust genotyping (Geue et al., 2025) and the MHinNGS Python script (Jønck & Børsting 2022). Mixture deconvolution studies compared microhaplotypes to STRs (Giuffrida et al., 2025) and tested panel performance (González-Bao et al., 2025). A multipurpose panel was proposed for casework (Kidd et al., 2022), and unique molecular identifiers were used to mitigate background noise in amplicon sequencing (Kwon & Shin 2024). Complex mixture interpretation was enhanced using multiple highly polymorphic panels (Li et al., 2025) and continuous models (Wang et al., 2025). Population studies characterized 74 microhaplotypes in Sino-Tibetan groups (Liu et al., 2023), U.S. populations (Oldoni et al., 2022), and utilizing the Ion AmpliSeq MH-74 panel (Qu et al., 2022). Ancestry inference was addressed with a new panel development (Rodrigues et al., 2025). Empirical calling methods were explored (Standage et al., 2022), and systems were optimized for mixture analysis (Tan et al., 2022). Kinship analysis performance was evaluated for a 74-marker assay (Tomas et al., 2024) and a 91-marker panel for pedigree reconstruction (Wei et al., 2024). Novel panels included a 90-marker set (Wang et al., 2023) and a 50-plex assay (Zhang et al., 2023). Pipelines were created for phasing macrohaplotypes in long sequencing reads (Wang et al., 2024). A composite marker combining semen-specific methylation and microhaplotypes was applied to semen-vaginal fluid mixtures (Wen et al., 2025). Databases like MHBase were established to support analysis (Xue et al., 2024). Nanopore sequencing was applied to MiniHap biomarkers for mixture deconvolution (Zhang et al., 2025). Further evaluations focused on the random man not excluded (RMNE) method for complex mixtures (Zhu et al., 2023), single-primer extension systems (Zhu et al., 2024), and unique molecular identifier (UMI)-based panels (Zhu et al., 2025). Panel evaluations for complex kinship were also reported (Xue et al., 2023).

Insertion/Deletion Markers (InDels). A novel five-dye panel for InDel polymorphisms was developed (Avellaneda et al., 2024), and the joint application of autosomal-InDels and miniSTRs was explored for kinship analysis (Cai et al., 2024). Population-specific studies included a 60-plex deletion/insertion polymorphism (DIP) panel for the Dongxiang group (Chen et al., 2023) and an AIM-InDel panel for Guizhou Shui and Dong groups (Dong et al., 2024). For mixture analysis, a SNaPshot-based DIP-TriSNP panel was evaluated (Fan et al., 2024). Panels ranging from 36 to 59 markers were developed for identification in various populations (Fang et al., 2023, Filoglu et al., 2024). The instability of InDels in tumoral tissues was noted for its forensic significance (Gürel et al., 2024). Insertion-Null markers proved effective for analyzing degraded bones and critical skeletal remains (Haarkötter et al., 2024, Haarkötter et al., 2025). Automation was addressed with the Quick TargSeq 1.0 system (Han et al., 2024), while a qPCR panel allowed rapid genotyping of 32 InDels (Han et al., 2023). Several studies validated multi-InDel panels for degraded DNA and challenging samples (Lan et al., 2023a, Lan et al., 2024) and for characterizing populations like the Manchu and Mongolian groups (Lan et al., 2023b). Performance was assessed in admixed Brazilians (Ramos et al., 2025). Compound markers combining InDels and SNPs were used to improve mixture analysis (Tan et al., 2024). A subsequently retracted study investigated the effectiveness of a multi-InDel system in Chinese populations (Wang et al., 2025). Multi-Indel assays were applied to enhance minor component detection in unbalanced mixtures (Wu et al., 2025) and to study diversity in Yunnan Yi and Qinghai Tibetan groups (Wu et al., 2025). Other validations included a 35-indel multiplex (Xie et al., 2023) and a 114-plex NGS panel for genetic admixture analysis (Yang et al., 2023, Yang et al., 2024). Multi-allelic InDel panels were developed, including a 31-marker set (Yao et al., 2023) and a 39-marker assay (Yao et al., 2024). Dual panel approaches explored traits in the Hui group (Yuan et al., 2024), while other studies surveyed populations in southwest China (Zhang et al., 2024) and the Guizhou Han population (Zheng et al., 2023).

Proteomics. Hair proteome profiling was shown to reveal individual demographics (Adav et al., 2023). Methods were developed to detect human contaminant genetically variant peptides in nonhuman samples (Chu & Lin 2025). The persistence of proteomic body fluid signals was observed within DNA workflows (Parker et al., 2025), and mass spectrometry-based proteomics was utilized for source-level attribution following DNA extraction (Zaarour et al., 2025). Multi-omics approaches were reviewed for analyzing biological evidence from flesh to bones (Procopio & Bonicelli 2024). Protein biomarkers were also identified to distinguish human hair from different body parts in intimate contact cases (Xiao et al., 2023).

Microbiome. The Microbiome Forensics Database UZH was introduced (Arora et al., 2022), and systematic reviews highlighted the oral microbiome as a biomarker for identification (Arumugam et al., 2024) and saliva detection (Betser-Cohen et al., 2024). The potential of the human necromicrobiome was explored (Cláudia-Ferreira et al., 2023), alongside pattern finding in urban microbiomes (Contreras-Peruyero

et al., 2024). Annealing temperatures were shown to significantly affect 16S rRNA gene-amplicon sequencing results when analyzing the bacterial community on canine skin (Apostolopoulos et al., 2023). Microbes in fingerprints were investigated for potentially distinguishing fresh versus aged latent fingerprints (De Alcaraz-Fossoul et al., 2023), and the "Sexome" study demonstrated microbial transfer between couples (Dixon et al., 2023). Metagenomics showed promise in predicting job occupations (Dou et al., 2023) and assisting human identification (Franceschetti et al., 2024). Methods for bacterial identification were compared using the ONT MinION sequencer (Graham et al., 2024). Time-dependent changes were observed in semen stains (Gürsoy et al., 2024) and bloodstains (You et al., 2024). Soil microbiomes were used to locate the origin of stains (Hofsvang et al., 2025). Skin microbial patterns were used to infer body locations and identify fluids (Huang et al., 2024), while salivary microbiomes responded to environmental exposures (Huang et al., 2024). Cervical microbiome profiles were distinguished by menopausal status (Kawasaki et al., 2025), and features of vaginal fluids were characterized (Liao et al., 2023).

Oral and skin microbiomes were evaluated as forensic tools (Lovisolo et al., 2022), with specific applications for geographic origin (Ogbanga et al. 2023) and bite mark analysis (Mehar et al., 2024). Differentiation between human and animal salivas was achieved (Mei et al., 2024). Reviews covered geographical location (Moitas et al., 2024), sequencing technologies (Oliveira et al., 2024), and environmental transfer (Ricchezze et al., 2024). High-throughput pathogen detection methods were developed (Pan et al., 2025). The transferability of microbiomes on clothes was assessed (Procopio et al., 2024). Drowning sites were inferred using bacterial composition and machine learning (Su et al., 2023, Su et al., 2025). Diet-related characteristics were revealed in saliva (Sun et al., 2024). Personal genomic information was reconstructed from gut metagenome data (Tomofuji et al., 2023). Reviews and studies addressed habit-specific bacteria (Yadav et al., 2023), machine learning for differentiating samples with 16S rRNA sequencing (Yang et al., 2024), and human papillomavirus (HPV) detection (Yao & Zhang 2023). Skin microbiome signatures aided fingerprint identification (Yılmaz et al., 2024). Sampling methods were optimized for obtaining microbiome results from skin and saliva (Yu et al., 2023), and lifestyle influences like smoking were analyzed (Yu et al., 2024). Full-length 16S rRNA gene sequencing was compared to sub-regions (Zhang et al., 2024), and spatio-temporal stability was studied (Zhang et al., 2025). The effects of drug use on oral microbiota were characterized (Zhang et al., 2023), as were changes in semen microbial communities (Zheng et al., 2024).

Single-Cell Analysis. Cluster analysis was used for grouping partial autosomal haplotypes from single sperm (Anslinger et al., 2024). Phenotype predictions were achieved from two-person mixtures using single-cell analysis (Diepenbroek et al., 2023), and evidentiary evaluation showed high informativeness in associating true contributors across admixtures (Duffy et al., 2023). Single-cell sorting of spermatozoa was compared with differential lysis (Fokias et al., 2025). Studies demonstrated that single-cell data produces genotype distributions concentrated at the true genotype (Grgicak et al., 2024) and examined the independence of data inferences (Grgicak et al., 2025). Targeted recovery of male cells was achieved in same-cell mixtures (Hogg et al., 2024). The current state of single-cell genomics was reviewed (Huffman & Ballantyne 2023a), and probabilistic genotyping software was tested with single-cell STR analysis (Huffman & Ballantyne 2023b) and complex mixture deconvolution (Huffman et al., 2025). Non-targeted single-cell DNA sequencing allowed for the deconvolution of multi-person mixtures (Kulhankova et al., 2024). Weight-of-evidence calculations were developed for combined single-cell and extracellular DNA (Lun & Grgicak 2024). Probabilistic genotyping of clustered single sperm haplotypes reconstituted diploid genotypes (Peters et al., 2025). The DEPArray technology was improved (Schulte et al., 2023) and assessed for forensic applications (Schulte et al., 2024), while other cell-separation techniques were evaluated for sexual assault investigations (Schulte et al., 2025). Flow cytometry was optimized to differentiate epithelial cell origin (Somers et al., 2024), and droplet-based optical trapping was tested (Valle et al., 2024). Stutter characteristics were defined for single cells (Vandepoele et al., 2025), and identification was achieved from mixed-blood spots using just four cells (Yamada et al., 2024).

Using Environmental DNA (eDNA). The detection of human DNA in aquatic environments was explored (Antony Dass et al., 2025), with methods optimized for recovering mitochondrial eDNA (Dass et al., 2024) and isolating DNA from large volumes of water (Chapman et al., 2023). DNA collection methods in air were investigated for human identification (Bibbo et al., 2025), including sampling from within cars (Bibbo et al., 2025) and air conditioner units (Goray et al., 2024). Sewer systems were monitored to detect eDNA of missing persons (Boger & Ozer 2023). Air and dust were characterized as invisible witnesses of human occupancy (Fantinato et al., 2022, Fantinato et al., 2023), with reviews discussing their investigative use (Fantinato et al., 2024, Goray et al., 2024). Dust was analyzed for forensic intelligence (Foster et al., 2023a), and the airborne fraction of soil (dust) was assessed for provenance (Foster et al., 2023b). Robust inferences from soil eDNA were possible even after challenging storage (Frøslev et al., 2023). Sentinel cells were programmed to respond to environmental DNA (Nou & Voigt 2024). Ethical concerns regarding inadvertent human genomic "bycatch" in eDNA studies were raised (Whitmore et al., 2023), and the general forensic utility of eDNA was debated (Novroski 2023). Soil removal methods were also assessed for geological evidence (Tiedge & Meiklejohn 2024).

Biomarkers for Sudden Death, Molecular Autopsy, or Post-Mortem Interval (PMI). A systematic review covered procedures in unnatural death investigations (Almakrami et al., 2024). The effect of CYP2D6, 2C19, and 3A4 phenoconversion was analyzed in drug-related deaths (Aly et al., 2024). DNA degradation estimation using the comet assay was reviewed for PMI estimation (Bhoyar et al., 2025), and dental DNA mutations were proposed as a novel method also for PMI estimation (Bianchi et al., 2024). Massive sequencing in molecular autopsy compared gene panels to whole exome sequencing (Blanco-Verea et al., 2025). Skin bacterial profiles were identified in early deceased bodies (Chong et al., 2024, Iancu et al., 2023), and decomposition in extreme cold was modeled (Iancu et al., 2024). Genetic constraints of sudden unexplained death susceptibility genes were identified (Lin et al., 2025). Cell-death biomarkers were identified for early and late intervals (Medina-Paz & Zapico 2025). Reviews covered microbiology for PMI (Moitas et al., 2024) and skeletal muscle changes (Mostafa et al., 2023). Standardization was called for in formalin-fixed paraffin-embedded molecular analyses (Previderè et al., 2025). Molecular investigations for estimating the time since deposition of bloodstains were reviewed (Sacco et al., 2024), and miRNAs were used for PMI in road traffic accidents (Singh et al., 2023). Attenuated Total Reflectance-Fourier Transform Infrared (ATR-FTIR) spectroscopy was reviewed as a pre-screening technique for PMI assessment and DNA preservation in human skeletal remains (Tamara et al., 2023). The type and growth of microorganisms present were used to infer time since deposition in semen and blood stains (Wang et al., 2025). Soil bacterial communities were characterized after the burial of dismembered bones (Wang et al., 2024). A review addressed biological and molecular methods for PMI in animals and humans (Wenzlow et al., 2023). Plasma exosome-associated piRNA screening was performed for acute myocardial infarction (Zhang et al., 2025).

4.5. Non-human DNA testing and wildlife forensics

Non-human biological evidence may inform criminal investigations when animals or plants are associated with a crime. Non-human DNA testing includes wildlife and domestic animal species as well as forensic botany and has many commonalities and some important differences compared to human DNA testing.

Books, Review Articles, and Guidance. New standards and resources have been published to formalize wildlife forensic practices. A new standard, ANSI/ASB 180, was established for the selection and evaluation of GenBank results to ensure accurate taxonomic assignment in wildlife forensics (ASB Wildlife Forensics Consensus Body 2024). Another standard, ANSI/ASB 216, was also published detailing the requirements for constructing multilocus databases in wildlife forensic science (ASB Wildlife Forensics Consensus Body 2025). The second edition of a text describing principles and applications of forensic botany to criminal casework was updated (Coyle 2024). A review of biological evidence, DNA markers, and analytical approaches highlighted current challenges in wildlife forensic genetics (Kanthaswamy 2024). The Organization of Scientific Area Committees released a detailed process map outlining the workflow for wildlife forensic biology (OSAC Wildlife Biology Subcommittee 2025).

Domesticated Animal DNA (Canine, Feline, Equine, and Bovine). Advances in analyzing domesticated animal DNA have improved individual identification and trait prediction. The impact of the genomic revolution on forensic sciences was explored with a focus on animal models (Cardinali et al., 2023). Findings from the Canine DNA Recovery Project described efforts to optimize recovery methods for canine DNA in forensic contexts (Dawnay et al., 2025), and a qPCR assay was created to quantify canine autosomal DNA recovered from livestock attacks to aid in predator identification (Dawnay et al., 2024). A multidisciplinary forensic approach was detailed for solving a fatal attack by a pack of dogs (Di Nunzio et al., 2024). Developmental validation was reported for a novel multiple genotyping assay comprising 24 canine STR loci (Du et al., 2023). The LASSIE MPS panel was developed to predict externally visible traits in dogs to assist in forensic investigations (Heinrich et al., 2023). A panel of tetranucleotide STR markers was introduced as an alternative approach for distinguishing between wolves and dogs (Hrebianchuk et al., 2024). Population genetics for 18 STR loci were described using the Canine Genotypes Panel 2.1 Kit on purebred dogs in Japan (Kunita et al., 2024). A novel 30-plex STR assay was developed for canine individual identification and parentage testing (Liu et al., 2024). Marker nomenclature and the control of Type I and Type II errors were analyzed for cattle parentage verification using microsatellites (Modorov et al., 2024). Genetic relationships were characterized among semi-feral subpopulations of the Ecuadorian highland creole horse (Navarrete-Mera et al., 2025). Student-led research compared commercial dog breed kits with STR genotyping for identity determinations (Novroski et al., 2023). Cat mitogenome variation was defined using multiplex amplification and nanopore sequencing to account for nuclear mitochondrial DNA segments (Patterson et al., 2023). Finally, a method was reported for sequencing the whole mitochondrial DNA of domestic dogs (Sugasawa et al., 2023).

Plant DNA. Forensic botany has seen progress in timber tracking, barcoding, and extraction methods. DNA barcodes were investigated for plants growing in high-crime areas of Iran to aid in botanical evidence identification (Abdollah et al., 2023). A two-layer machine learning model was developed to classify legal and illegal poppy varieties based on sequence data (An et al., 2024). Methodologies for plant identification by DNA were detailed in a dedicated forensic botany textbook chapter (Bever et al., 2024), and classical and future DNA typing technologies for plants were reviewed (Carita 2024). DNA fingerprinting was applied to track timber of *Jacaranda copaia* from the Amazon forest (Capo et al., 2024). The potential of plant DNA information was explored for determining the potential geographical origin and identity of unknown victims (Chen et al., 2023). DNA extraction from diverse plant taxa was achieved using ionic liquids and magnetic ionic liquids (De Silva et al., 2024). Artificial intelligence was employed alongside a DNA barcode database to enhance timber forensics (Dev et al., 2023). Various markers were analyzed for their efficacy in forensic plant species identification (Dokane 2024). Chloroplast DNA barcoding markers were evaluated for their ability to individualize *Papaver somniferum* (Graham & Houston 2024). The role of plant forensics in solving crimes was reviewed with a focus on botanical evidence (Kunchhal & Kaur 2023). A microsatellite dataset was created for cultivar discrimination in spring orchid (*Cymbidium goeringii*) (Nam et al., 2023). Current state-of-the-art methods and future prospects for using plants in forensics were assessed (Oliveira et al., 2023). Multivariate statistical analysis was performed on Japanese traditional *washi* papers to evaluate DNA presence and quality (Shin & Enomae 2023). Pollen DNA metabarcoding to potentially trace geographical locations and phylogenetics was presented as a breakthrough technique for forensic sciences (Wasti et al., 2024).

Cannabis DNA. Genetic tools for distinguishing cannabis types and linking genetics to chemical profiles were reported. Genetic markers were applied to distinguish between drug-type and fiber-type *Cannabis sativa* L. (Barbarić & Bezbradica 2023). Two fast genotyping assays were developed for the differentiation of hemp from marijuana (Cheng & Houston 2025). Principal component analysis was used to evaluate genetic markers for correlating THC levels in *Cannabis sativa* samples (Cisana et al., 2022), and machine learning was explored to establish associations between these markers and THC levels (Cisana et al., 2024). Nine *Cannabis sativa* chloroplast SNP markers were characterized for crop type determination and biogeographical origin (Di Nunzio et al., 2024). Genetic analysis was leveraged to support forensic toxicology analysis by demonstrating concordance of results among marijuana samples (Di Nunzio et al., 2024). Preliminary studies used STR marker analysis for the genetic identification of cannabis varieties (Marcińska et al., 2022).

Species Classification. New assays and field-portable methods have expanded the capability to characterize diverse species. Multiplex PCR and gas chromatography – tandem mass spectrometry (GC-MS/MS) were used to detect mutton meat fraud involving beef as a genetically related species (Abdelrahman et al., 2023). A short fragment of mitochondrial DNA was identified for the taxonomic assignment of blow flies in northwestern South America (Amat et al., 2023). A review highlighted DNA barcoding as an effective tool for classifying species (Antil et al., 2023). Substrates and deposition time were shown to affect the molecular analysis of fly artifacts (Bini et al., 2022). Multi-locus intron polymorphisms were utilized for species characterization and population genomics (Boscari et al., 2024). A practical guide was published for forensic species assessment using animal and plant DNA analysis (Corradini et al., 2024). A protocol was developed by the Forensic Science Police of Santa Catarina for classifying wildlife species in seized material (de Salles Perecin et al., 2025). A practical workflow was established for forensic species classification using direct sequencing of real-time PCR products (Doi et al., 2024). A nanoplate-based digital PCR assay was developed for species classification with mixture deconvolution capabilities (Ghemrawi & McCord 2022). The IdentiFLY 15-plex SNP assay was validated for the forensic identification of UK blowfly species (Godfrey & Smith 2024).

New markers based on the mitochondrial 16S rRNA gene allowed for rapid and easy classification of animal species (Haider et al., 2023). DNA analysis was performed for species classification of seized helmeted hornbill casques (Hatten et al., 2023). A phosphate-mediated isothermal amplification colorimetric system enabled visual identification of species and sex from bloodstains (Hu et al., 2024). Innovative approaches to food traceability using DNA barcoding were explored beyond traditional labels (Liberty et al., 2025). A multilocus DNA mini-barcode assay was designed to classify twenty vertebrate wildlife species (Liu et al., 2023). Metrological support for nucleic acid sequence analysis was discussed to ensure measurement accuracy (Melkova et al., 2023). Nucleic acid chromatography of hair samples was used for animal species classification (Saito et al., 2023). A highly portable, specific, and sensitive platform using loop-mediated isothermal amplification (LAMP) was presented for fast-track wildlife species classification (Subhashini et al., 2025). Simple field-adapted species classification was achieved by combining multiplex multienzyme isothermal rapid amplification with

lateral flow dipsticks (Sun et al., 2024). A screening assay based on PCR amplification of cytochrome *b* was used for classifying animals in the *Cervus* genus (Suraphak et al., 2024). CO1 analysis identified fly artifacts and fly species at a murder scene with numerous bloodstains (Takayama et al., 2023). A guide was provided for the analysis of DNA-based species identification in forensic casework (Webster et al., 2024). A fluorescence PCR assay was developed and tested for species classification of ten animals (Xia et al., 2025). Forensically important insects recovered from human corpses in Taiwan were studied (Yan et al., 2023). NanoSSID, a bioinformatics pipeline, was introduced for species classification in forensic genetics (Zhao et al., 2025).

Wildlife Forensics. Applications in wildlife forensics have focused on trafficking, conservation, and poaching investigations. The role of forensic DNA experts and artificial intelligence was examined in the context of enhancing wildlife crime investigations in Cyprus (Ali et al., 2025). Molecular analysis detected normal and adulterated meat samples in local markets and restaurants in Kerbala Province (Ali et al., 2024). DNA tools unveiled fifteen years of elasmobranch trade, offering lessons for monitoring and conservation (Alvarenga et al., 2024). A DNA extraction method was developed for preserved hair and skin samples from the Sumatran tiger (Andayani et al., 2023). A DNA profiling system using 16 autosomal STRs was created for the conservation management of the Kamchatka brown bear (Andreassen et al., 2024). An FTIR spectral library was developed for the assessment of Asian elephant ivory (Ann Jose et al., 2024). Molecular analysis techniques were standardized for DNA classification of bird species from eggshells (Araujo et al., 2025). Contemporary eDNA methods were shown to complement conventional microscopy in American lobster post-larvae diet studies (Ascher et al., 2025). Specific differences in *AMELX* and *AMELY* genes were identified for molecular sex identification in Sumatran tigers (Asrori et al., 2024). Lion Localizer software using mitochondrial DNA was introduced to infer the potential geographic origins of tested lions (Au et al., 2024). North Carolina black bear populations were characterized using the UrsaPlex v2.0 panel (Badgett et al., 2023). A reference library for forensic application was constructed through DNA barcoding of southern African mammal species (Baxter et al., 2024). The mitochondrial genome plasticity of mammalian species was explored (Biró et al., 2024). A forensic genetic toolkit was established for species and lineage classification of the trafficked shingleback lizard (Brown et al., 2023). Surface-enhanced Raman spectroscopy swabs using silver nanoparticle biosynthesis were developed for detecting animal blood (Brunauer & Monjardez 2023).

DNA barcoding identified dried seahorses illegally sold in metropolitan Manila as traditional Chinese medicine (Bueno et al., 2024). Species and origin determinations of an ivory chess set were achieved using a specific wildlife forensic workflow (Carrothers et al., 2024). Latent DNA deposited by pangolin scales onto plastic packaging materials was visualized and detected (Chan et al., 2024). Multiple primers were used for eDNA detection of marine vertebrates in an estuarine lagoon subject to anthropogenic influences (Chiquillo et al., 2024). Enzymatic methods were used to remove nuclear mitochondrial DNA segments (Numts) from *Panthera tigris* DNA samples (Creecy et al., 2024). The complete mitochondrial genome of the Indian wild pig was characterized to identify signature sequences (Das et al., 2024). A novel forensic STR multiplex assay was validated for blue, wattled, and grey-crowned cranes (de Bruyn et al., 2024). Techniques and future directions for using scat DNA in low-density carnivore surveys were reviewed (de Oliveira et al., 2025). Practical considerations were outlined for trace DNA recovery and detection of invasive reptiles across different deposition scenarios (Deliveyne et al., 2025). Genetic tracing revealed the illegal trade patterns of the white-bellied pangolin in western Central Africa (Din Dipita et al., 2024). Molecular analysis detected critically endangered European eels in U.S. retail outlets (Ely et al., 2023). TigerBase, a DNA registration system, was launched to enhance enforcement and compliance testing of facilities housing captive tigers (Ewart et al., 2025). Rapid and cost-effective multiplex PCR assays were developed to differentiate catfish of the genus *Brachyplatystoma* sold in Brazil (Freitas et al., 2023). A sensitive qPCR assay detected bear DNA from bile and derived products to support wildlife enforcement (Friedenberger et al., 2023).

Forensic classification of predators was utilized to inform wildlife management and conservation efforts (Ganz et al., 2023). A forensic genetic investigation revealed a captive origin for a wild alien population of raccoons in Italy (Garofalo et al., 2024). Mutations in *Vgsc*-1014 were shown to impact the feeding pattern of *Phlebotomus argentipes* (Gomes et al., 2025). Sequence variation of commercially available kratom products was analyzed at universal DNA barcode regions (Graham et al., 2024). A review discussed the role of animal victim forensics in the courtroom in poaching cases (Harper 2023). Advances in osteology and DNA methods for wildlife forensics were detailed (Hartley & Clark 2023). Perspectives on integrative genomics for human, animal, and plant forensics were discussed in the context of the Pangenome era (He et al., 2025). A robust test system was created for the DNA classification of raccoon dogs (Hrebianchuk et al., 2023). A new set of EST-STR markers was identified for the discrimination of related *Papaver somniferum* L. varieties (Kaňuková et al., 2024). Simplified cytochrome oxidase subunit I (COI) barcoding was applied to blow, flesh, and scuttle flies encountered in medicolegal investigations (Kwiatkowski et al., 2024). Forensic genetics were applied to the conservation of Guiana Dolphins (Laeta et al., 2025). A DNA profile database of *Koompassia malaccensis* was established in Malaysia for application in forensic investigations (Lee et al., 2025).

The forensic potential of environmental DNA in freshwater wildlife crime investigations was reviewed from research to application (Lewis et al., 2024). The informative relevance of 11 microsatellite loci was assessed for forensic classification of wild and farmed American mink (Lukashkova et al., 2023). Forensically important carrion beetles in China were identified based on cytochrome oxidase subunit I and II (COI and COII) markers (Luo & Meng 2023). A 60K SNP chip was developed for caribou (*Rangifer tarandus*) for use in wildlife forensics and management (Mallorie et al., 2024). New DNA collection and genomic methods enabled species classification in suspected shark-related human-shark interactions (Martin et al., 2024). The potential utility and shortcomings of mitochondrial DNA analysis were evaluated for cheetah conservation management (Meißner et al., 2023). The Forensic Genetics for Species Protection (FOGS) SNPSTR marker database and cell culture bank were established to combat wildlife trafficking (Mozer et al., 2025). A SNP panel was used to evaluate genetic variability and relationships in roe deer (Oleński et al., 2023). Forensic genetics was described as a catalyst in the developmental process of Hungarian wildlife forensics (Pádár et al., 2022).

The practical utility of the OSAC proposed standard for using GenBank for taxonomic assignment was assessed in an interlaboratory study (Patel et al., 2023). Domestic cat mitogenome sequences demonstrated lineage expansions and dynamic mutation processes (Patterson et al., 2023). DNA forensic applications were utilized to tackle the illegal trade of sharks and rays in Southeast Asia (Prasetyo et al., 2024). Wildlife DNA forensics facilitated species classification of confiscated Felidae in Indonesia (Priyono et al., 2025). Wildlife forensic genetics was highlighted as a crucial tool for resolving crimes and supporting conservation in the Neotropics (Sandoval-Arias et al., 2023). Molecular analysis techniques were standardized for DNA classification of bird species of the Psittacidae family (Silva et al., 2022). Wildlife DNA forensics revealed an instance of canine cannibalism (Singh et al., 2023). The phylogeography of the Sunda pangolin was analyzed to provide implications for taxonomy and forensic management (Sitam et al., 2023). Focused ultrasound extraction (FUSE) of DNA was utilized to aid in genetic species classification of timber (Stettinius et al., 2024). Environmental DNA captured on fish skin mucus was identified as a potential bias in molecular diet analyses (Števove et al., 2023). A real-time PCR assay allowed for the robust detection of cow and female buffalo DNA (Subramanian et al., 2022). A portable strip test was developed for

discriminating between African and Asian elephant ivory (Thanakiatkrai et al., 2024). A review highlighted the lack of human-focused forensic evidence in the context of wildlife crime investigations (Thomas et al., 2023). Forensic genetics associated with hair analysis served as a tool for jaguar classification (Tremori et al., 2024). DNA-based classification was performed on big cats and traditional Chinese medicine artifacts in the Czech Republic (Vankova & Vanek 2022). The Sunda pangolin was detected for the first time in illegal wildlife seizures from northeast India (Wangmo et al., 2024). Genetic classification of prey was achieved through oral swabs of predators (Young et al., 2023). Finally, a mitochondrial control region database was established for Hungarian fallow deer populations (Zorkóczy et al., 2024).

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Declaration of competing interest

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

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.fsisyn.2026.100705.

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See Supplemental File 1 for a copy of the Zotero database used in this review and Supplement File 2 for the curated full reference list sorted by topics cited in Sections 3 and 4.

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