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Review Article

Environmental and Post-Mortem Factors Influencing DNA Degradation: Mechanisms, Patterns, and Analytical Implications

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ABSTRACT:
DNA degradation is a major determinant of the quality, interpretability, and evidentiary value of biological material in forensic genetics, particularly when samples are exposed to adverse environmental or post-mortem conditions. Following death and loss of cellular homeostasis, DNA becomes increasingly susceptible to enzymatic, hydrolytic, oxidative, photochemical, and microbial damage, resulting in progressive strand fragmentation, base modification, and loss of amplifiable genetic targets. This review examines the principal environmental and post-mortem factors governing DNA degradation, with emphasis on temperature, humidity and moisture, ultraviolet radiation, microbial activity, substrate characteristics, post-mortem interval, autolysis, putrefaction, and tissue type. The molecular consequences of these processes are considered in relation to low-template and touch DNA, including allelic dropout, heterozygote imbalance, preferential loss of longer targets, and reduced amplification efficiency. The review further evaluates conventional and contemporary approaches for assessing degraded DNA, including restriction fragment length polymorphism, flow cytometry, comet assay, polymerase chain reaction-based approaches, quantitative PCR, capillary electrophoresis, and next-generation sequencing. Particular attention is given to mini STRs, single nucleotide polymorphisms, and microhaplotypes as strategies for obtaining genetic information from highly fragmented templates. Emerging approaches involving targeted enrichment, artificial intelligence, and advanced sequencing technologies are also discussed in the context of improving the analysis and interpretation of compromised forensic samples. Overall, understanding the mechanisms and patterns of DNA degradation is essential for informed evidence selection, optimized DNA recovery and analysis, appropriate interpretation of partial genetic profiles, and development of robust forensic genetic workflows. Continued advances in sequencing, bioinformatics, and standardized analytical frameworks are expected to enhance the recovery and interpretation of genetic information from environmentally and post-mortem compromised biological evidence.

Keywords: Post-Mortem, DNA Degradation, Microbial Activity, Quantitative PCR

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1. INTRODUCTION

Deoxyribonucleic acid (DNA) integrity and preservation are essential to molecular taphonomy, bioarchaeology, and forensic genetics. DNA's structural stability is essentially a temporary state within the biological protection of a living cell, despite the fact that it is frequently described as a remarkably stable molecule in comparison to RNA or proteins—capable of enduring for millennia under extraordinary circumstances (Lindahl, 1993) doi:10.1038/362709a0. The complex enzymatic repair mechanisms that preserve genomic integrity malfunction when life ends, transforming the genome from a controlled information carrier into a deteriorating substrate vulnerable to a variety of damaging factors (Bhoyar et al., 2024; Pokines et al., 2021).

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Significance of Genomic degradation

Maintaining the scientific validity and evidentiary usefulness of forensic genetic analysis requires an understanding of DNA degradation. Hydrolytic, oxidative, and enzymatic activities that break apart DNA molecules and decrease the number of intact amplifiable targets lead to degradation. Particularly for longer STR markers, fragmented DNA causes locus-specific dropout, peak imbalance, and decreased amplification efficiency, as noted by Pajnič (2025) in Genes. If these molecular changes are not appropriately treated, they may lower discriminatory power and directly jeopardize profile stability. (https://doi.org/10.3390/genes16111375).

Thus, methodological developments like short-amplicon STR systems, optimized extraction chemistries, and degradation-sensitive quantification assays have been spurred by the study of degradation. Patterns of tissue-specific preservation, including the improved DNA protection in dental structures described (https://doi.org/10.3390/genes16040364), further illustrate how evidence selection and recovery techniques are influenced by knowledge of ambient and post-mortem factors.

The ramifications for interpretation are equally significant. According to the standards set out by the Scientific Working Group on DNA Analysis Methods (SWGDAM, 2020), in order to preserve reproducibility and reduce error, degraded DNA brings stochastic effects that call for validated analytical thresholds and interpretation frameworks. In order to ensure legal admissibility in court proceedings and interoperability with established forensic workflows, such standardization is crucial. (https://www.swgdam.org/publications.)

When taken as a whole, research on DNA degradation improves laboratory procedures, maintains discriminatory ability, boosts molecular stability evaluation, and supports the legal defensibility of forensic DNA evidence. Therefore, its study is essential to contemporary forensic genetics rather than incidental.

Table 1: Differences Between DNA Degradation in Living and Dead Organisms

Aspects	DNA Degradation in Living Organisms	DNA Degradation in Dead Organisms
Mechanisms	1) Nucleases involved in DNA replication, repair, and apoptosis 2) Autophagy 3) Oxidative stress 4) DNA repair pathways	1) Autolysis and post-mortem processes 2) Nucleases released from the lysed cells 3) Microbial enzymes 4) Environmental factors (temperature, humidity, ultraviolet radiation)
DNA Fragmentation	Possible DNA fragmentation due to enzymatic cleavage	DNA fragmentation often accompanies DNA degradation
Cellular Regulation	Tightly regulated and controlled to maintain genomic integrity	No active cellular regulation or control
Importance	Ensures proper DNA replication, repair, and programmed cell death	Implications for forensic science and paleogenomics

Butler, John M. *Advanced topics in forensic DNA typing: methodology*. Academic press, 2011.

Biochemical Mechanisms of DNA decay

Environmental exposure and intrinsic molecular instability control the time-dependent biochemical process of DNA breakdown. Spontaneous hydrolysis results in abasic sites and strand breaking at the molecular level through depurination and depyrimidination. Base lesions such 8-oxo-guanine

are introduced by oxidative stress, while pyrimidine dimers that obstruct polymerase progression are induced by UV light. These accumulating lesions lead to decreased amplifiable template length and increasing fragmentation over time. A mechanistic overview of post-mortem biochemical processes is provided by forensic science research, which emphasizes autolysis and microbial growth as key factors in early DNA destruction. (https://doi.org/10.1080/20961790.2020.1733724). Similarly, it has been shown that exposure to the environment, especially heat and humidity, greatly speeds up the kinetics of skeletal remains' fragmentation, resulting in predictable size-dependent disintegration patterns. (https://doi.org/10.1016/j.fsigen.2021.102567).

Both the rate and the pattern of degradation are influenced by environmental factors. Moisture promotes hydrolytic cleavage, whereas temperature increases reaction kinetics exponentially (Arrhenius principle). UV light, microbial nucleases, and soil chemistry all influence breakdown processes. Crucially, not all tissues experience degeneration in the same way. According to recent preservation research published in the International Journal of Legal Medicine (2022), dense cortical bone and dental tissues show delayed fragmentation because of structural protection. Together, these results demonstrate that DNA degradation over time follows quantifiable biochemical and environmental trajectories, resulting in template loss and fragment size variations that have a direct bearing on the success of forensic amplification.

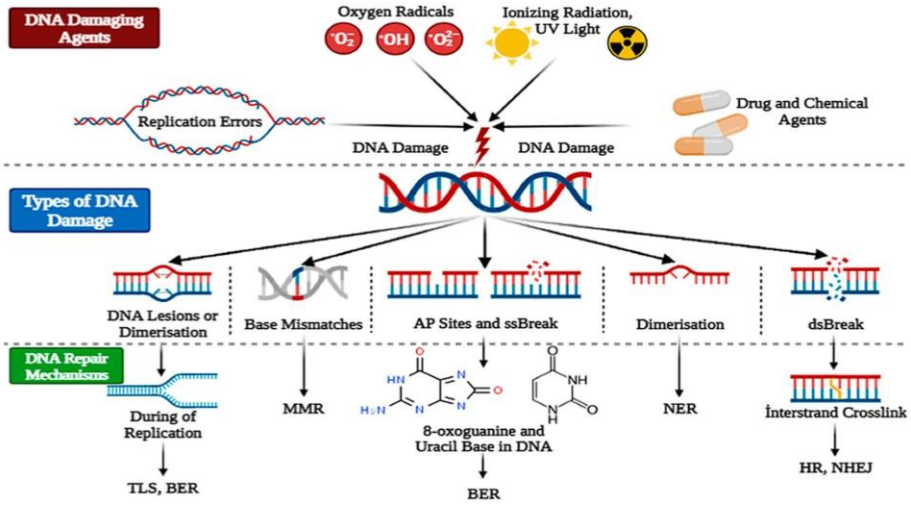


Fig 1: DNA Degradation and Repair Mechanism

DNA Degradation in Low-Template and Touch DNA Samples

Because low beginning material increases the impact of deterioration, low-template DNA (LT-DNA) and touch DNA samples pose additional difficulties. (https://doi.org/10.1016/j.fsigen.2019.102223), Describe how stochastic effects—allelic dropout, heterozygote imbalance, and increased peak height variability—become statistically significant when template copies fall below ideal thresholds in Forensic Science International: Genetics. Larger STR loci are disproportionately impacted by amplification bias when degradation and low quantity coincide, leading to incomplete or distorted profiles. Touch DNA samples are especially susceptible to environmental damage because of surface exposure, transfer kinetics, and low cellular integrity, according to van Oorschot et al. (2021) in Genes. DNA fragmentation is accelerated even prior to collection by friction, UV radiation, and varying humidity. Touch samples, in contrast to high-template biological stains, frequently contain extracellular or partly lysed DNA, making them more vulnerable to microbial and oxidative degradation. (https://doi.org/10.3390/genes12020148). These restrictions have been somewhat lessened by developments in massively parallel sequencing (MPS) and miniSTR technologies. Studies have demonstrated how SNP panels and short amplicon systems improve success rates in degraded LT-DNA situations. Interpretive frameworks are still crucial, though. (https://doi.org/10.1016/j.fsigen.2019.102186).

According to the Scientific Working Group on DNA Analysis Methods (2020), in order to guarantee statistical robustness, probabilistic genotyping models need to take into consideration stochastic variation brought about by both degradation and low template amount. Therefore, degradation in low-template and touch DNA samples is not just a quantitative problem but a combined molecular and interpretive difficulty that calls for sophisticated statistical modeling and integrated biochemical understanding.

Environmental Factors that Influence DNA Degradation (Mechanisms and Patterns)

The pace and pattern of DNA degradation in forensic samples are significantly influenced by environmental factors. The chemical stability of DNA molecules and the integrity of amplifiable genetic fragments are both impacted by environmental elements such temperature, humidity, UV radiation, microbial activity, and substrate type once biological material is deposited in the environment. Temperature

One of the most important environmental elements influencing DNA stability is temperature. High temperatures speed up chemical processes including hydrolysis and depurination, which lead to phosphodiester backbone cleavage and progressive DNA fragmentation. Additionally, higher temperatures increase nucleases' enzymatic activity, which aids in the breakdown of molecules. Because of this, heat-exposed DNA samples frequently exhibit decreased template amount, increased fragmentation, and preferential loss of longer STR loci. Conversely, lower temperatures help maintain DNA integrity for longer periods of time by slowing down chemical breakdown processes (Al-Sheikhly et al., 2021).

Ultraviolet (UV) Radiation

Long-term UV exposure causes strand breaks and fragmentation, which frequently results in partial DNA profiles due to preferential degradation of larger genetic fragments. UV light also causes the formation of cyclobutane pyrimidine dimers and other photoproducts that distort the DNA double helix and interfere with polymerase activity during amplification. (Sharma et al., 2020).

Humidity and Moisture

Hydrolytic processes are the main way that humidity speeds up DNA breakdown. DNA molecules become less stable when water molecules encourage depurination and strand break formation. Additionally, microbial development is encouraged by moist circumstances, which leads to increased enzymatic breakdown through nuclease activity. As a result, forensic samples stored in dry settings usually exhibit higher molecular fragmentation and poorer DNA yields than samples subjected to high humidity. (Khorwal et al., 2024).

Microbial Activity

DNA breakdown is greatly aided by microorganisms found in soil, water, and decomposing tissues. Nucleases and other enzymes that can split DNA molecules into smaller pieces are produced by bacteria and fungi. In biological materials that are decomposing, microbial colonization becomes especially noticeable, resulting in quick disintegration and a lower chance of getting entire DNA profiles from evidence exposed to the environment.

Substrate Type

DNA preservation is also influenced by the type of surface that biological material is placed on. Fabrics and paper are examples of porous substrates that can absorb biological fluids and offer some protection from exposure to the environment. On the other hand, DNA is directly exposed to environmental stressors like UV light and temperature changes on non-porous surfaces like glass or metal, which causes faster disintegration and less recovery of intact DNA molecules. (Khorwal et al., 2024).

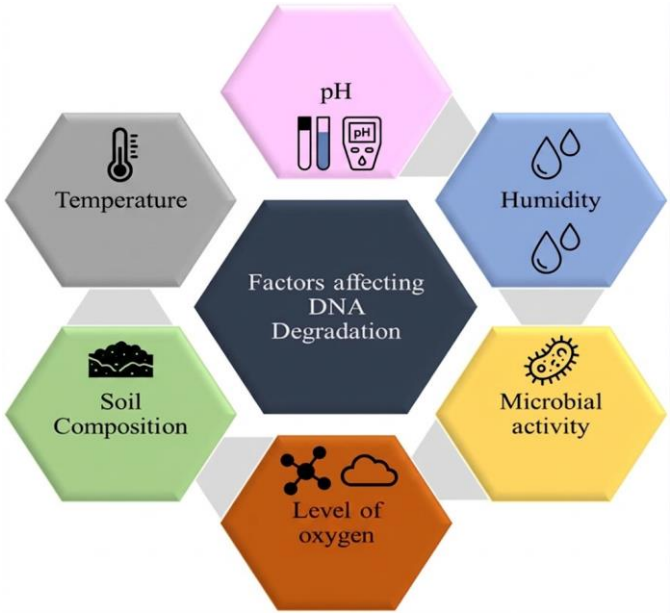


Fig 2: Factors Affecting DNA Degradation *(Krista E. Latham, et al. 2019)*

Post-Mortem Factors Influencing DNA Degradation (Mechanisms and Patterns):

The integrity of DNA in tissues is impacted by a number of biological and biochemical activities after death. DNA repair mechanisms are eliminated when cellular metabolism stops, leaving genetic material more susceptible to environmental, microbial, and enzymatic damage. During forensic analysis, these post-mortem procedures result in progressive DNA fragmentation, a decrease in template quantity, and a lower success rate for amplification. Autolysis, microbial activity, post-mortem interval (PMI), and the kind of biological tissue are important variables that affect DNA destruction after death.

Autolysis occurs shortly after death when intracellular enzymes, particularly nucleases, are released due to cellular membrane breakdown. These enzymes initiate degradation of nucleic acids, causing strand breaks and fragmentation of DNA molecules, which reduces the amount of intact DNA available for analysis (Pajnič, 2025).

Microbial Activity

Microorganisms from the body and surroundings multiply during decomposition, releasing nucleases that further break down DNA. https://doi.org/10.1080/20961790.2020.1733724.

DNA fragmentation is accelerated by this microbial enzymatic activity, which frequently produces severely damaged genetic material. (Dinis-Oliveira, 2020).

Post-Mortem Interval (PMI)

DNA preservation is significantly influenced by the amount of time that has passed since death. DNA experiences cumulative enzymatic and chemical damage as PMI rises, resulting in progressive degradation and decreased recovery of amplifiable genetic content. (Loreille et al., 2021).

Tissue Type

This kind of tissue also affects DNA storage. While mineralized tissues, like bone and teeth, offer structural protection that helps store DNA for longer periods of time, soft tissues break down quickly due to enzymatic breakdown and microbial colonization. (Salazar et al., 2025).

Mechanisms of DNA Degradation

Due to the termination of cellular repair processes, DNA degradation is a multifactorial process that begins right after cell death. Enzymatic repair processes preserve DNA integrity in living cells, but after death, DNA is more vulnerable to environmental, chemical, and enzymatic damage. (Lindahl, 1993; https://doi.org/10.1038/362709a0).

Enzymatic Degradation (Autolysis and Putrefaction)

Autolysis is the first stage of degradation, when intracellular nucleases are released after membrane disruption and start breaking DNA into smaller pieces. Putrefaction follows, during which more nucleases are introduced by microbial growth, hastening DNA fragmentation and lowering DNA quality. (Bär et al., 1988) Dinis-Oliveira, 2020).

Hydrolytic Damage

One important chemical mechanism of DNA destruction is hydrolysis. It causes depurination and depyrimidination, which produce abasic sites that cause strand breaks and disrupt the DNA helix. Environmental factors, especially temperature and moisture, have a significant impact on these responses. (Lindahl, 1993; https://doi.org/10.1038/362709a0).

Oxidative Damage

DNA is oxidatively damaged by reactive oxygen species (ROS), which results in base alterations, strand breakage, and decreased amplification efficiency. 8-hydroxy-2′-deoxyguanosine (8-OHdG), a biomarker of oxidative stress, is a well-known oxidative lesion. (Valavanidis et al., 2009; https://doi.org/10.1080/10934520902737328).

UV-Induced Damage

The DNA helix is distorted and polymerase activity is inhibited when ultraviolet (UV) exposure causes pyrimidine dimers to form. Long-term exposure can cause considerable DNA fragmentation and strand breaks, especially in samples exposed to the environment. (Cadet et al., 2005; https://doi.org/10.1016/j.mrfmmm.2005.03.012).

Cross-Linking and Fragmentation

Because it prevents strand separation during amplification, chemical cross-linking within DNA or between DNA and proteins makes analysis much more difficult. All degradation routes ultimately result in DNA fragmentation, which usually reduces fragment size to 100–500 base pairs. This has a substantial impact on STR profiling and raises the possibility of allelic dropout. (Butler, 2012).

1.2 Environmental and Post-Mortem Influences

The interaction between intrinsic biological elements and extrinsic environmental stimuli greatly influences the non-uniform rate and pattern of this deterioration. The most important factor is temperature; high temperatures greatly speed up hydrolytic and oxidative reactions, whereas freezing or cold storage can dramatically slow down, though not completely stop, the deterioration process. (Bär et al., 1988; Perry et al., 1988). Additionally, there are humidity and moisture levels. While dry settings may result in spontaneous mummification and better DNA retention, high-moisture environments encourage hydrolytic cleavage and create a suitable niche for microbial proliferation. (Bhoyar et al., 2024).

Additionally, the success of DNA recovery depends on the Post-Mortem Interval (PMI) and the particular substrate (such as bone, teeth, blood, or soft tissue). In situations of severe degradation, tissues like the tooth pulp and cortical bone serve as the main suppliers of genetic material because they provide a mineral matrix that protects DNA from environmental stresses. (Williams et al., 2015; Bhoyar et al., 2024).

Forensic and ancient DNA analysis face serious difficulties due to the effects of DNA deterioration. Allelic dropout, stochastic effects during PCR amplification, and the presence of PCR inhibitors (such as humic acids from soil or heme from blood) are frequently caused by fragmentation and chemical changes. Advances in Next-Generation Sequencing (NGS) and Single Nucleotide Polymorphism (SNP) analysis have emerged as reliable approaches to retrieve genetic profiles from highly fragmented DNA, while traditional Short Tandem Repeat (STR) typing frequently fails with severely degraded data. (Bhoyar et al., 2024). Therefore, enhancing sample recovery procedures and guaranteeing the correctness of genetic results in legal and historical contexts require an understanding of the particular mechanisms and environmental causes of DNA degradation.

Assessment of DNA Degradation Using Different Molecular Techniques

The accuracy and dependability of genetic analysis are significantly impacted by DNA degradation, especially in forensic and postmortem investigations. It results in fragmentation, base alteration, and loss of genomic integrity and is caused by a variety of environmental, chemical, and biological causes. The success of downstream

applications including profiling, identification, and result interpretation is directly impacted by the degree of DNA degradation.

Assessment of DNA Degradation using RFLP

One of the first methods in forensic DNA analysis was restriction fragment length polymorphism (RFLP). It depends on identifying differences in the lengths of DNA fragments following digestion by restriction enzymes. However, this approach is extremely vulnerable to degradation since it requires high molecular weight, and undamaged DNA.

Research by Budowle et al. (1991) and Jeffreys et al. (1985) showed that damaged DNA causes smearing and fragmentation, which leads in low band resolution and untrustworthy interpretation. The likelihood of acquiring full restriction fragments sharply declines with increasing DNA degradation.

As a result, RFLP is deemed inappropriate for forensic materials that have been contaminated or deteriorated, and PCR-based methods have generally taken its place.

Assessment of DNA Degradation by Flow Cytometry Analysis

Cellular DNA concentration and fluorescence intensity are measured using flow cytometry, a quick and quantitative technique for assessing DNA degradation. Fluorescent dyes are used to stain DNA, and variations in signal strength that correlate to DNA fragmentation are analyzed.

Research by Cina (1994) and Di Nunno et al. (1998) https://doi.org/10.3390/ijms21103540 Flow cytometry makes it possible to identify:

fragmentation of DNA

Apoptotic alterations

interruption of the cell cycle

Its dependability declines in advanced decomposition due to substantial cellular disintegration, notwithstanding its effectiveness for early postmortem intervals.

Assessment of DNA Degradation by Single Cell Gel Electrophoresis (Comet Assay)

A highly sensitive method for identifying DNA strand breaks at the single-cell level is Single Cell Gel Electrophoresis (SCGE), also referred to as the comet assay. During electrophoresis, damaged DNA migrates and forms a distinctive "comet tail," where the degree of damage is correlated with the extent of migration. https://doi.org/10.1016/s0379-0738(02)00027-0. Key parameters include:

- Tail length
- Tail DNA percentage
- Tail moment

The comet assay is particularly useful because it:

- Detects early-stage degradation
- Requires small sample quantities
- Provides quantitative measurement of DNA damage

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Recent reviews highlight its potential as a **molecular tool for estimating postmortem interval (PMI https://doi.org/10.1080/20961790.2017.1379893)**.

Assessment of DNA Degradation by DNA Amplification Analysis (PCR-Based Methods)

- The most popular techniques for evaluating DNA deterioration in forensic research are PCR-based techniques. These methods use the effectiveness of DNA amplification to assess deterioration. Research by Butler (2012) and Gill et al. (2006) showed that damaged DNA causes:
- Allelic dropout
- Short DNA fragment preferential amplification (miniSTRs)
- Long fragment amplification failure
- A degradation index that contrasts the amplification of long and short targets can also be calculated using quantitative PCR (qPCR). PCR-based techniques are very beneficial because they

Work with **low quantity and degraded DNA**

- Provide **high sensitivity and specificity**
- Are compatible with modern forensic workflows

Assessment of DNA Degradation by Other DNA Techniques

In addition to conventional methods, several advanced techniques are used to assess DNA degradation

Capillary Electrophoresis (CE): Identifies patterns of degradation and fragment size dispersion

Butler, J.M. (2012) is cited. Methodology is an advanced topic in forensic DNA typing. Scholarly Press.

Quantitative PCR (qPCR): Provides degradation index values by comparing amplification of different fragment lengths *Reference:* Kline, M.C. et al. (2009). *Developmental validation of qPCR assay for human DNA quantification*. Analytical and Bioanalytical Chemistry.

Useful for highly degraded samples due to higher copy number per cell *Reference:* Holland, M.M. & Parsons, T.J. (1999). *Mitochondrial DNA sequence analysis – validation and use in forensic casework*. Forensic Science Review.

Next-Generation Sequencing (NGS): Enables high-resolution analysis of fragmented and degraded DNA *Reference:* van Dijk, E.L. et al. (2014). *Ten years of next-generation sequencing technology*. Trends in Genetics.

ELISA-based assays: Detect oxidative DNA damage such as 8-OHdG *Reference:* Valavanidis, A. et al. (2009). *8-hydroxy-2'-deoxyguanosine as a biomarker of oxidative stress*. Journal of Environmental Science and Health.

In general, the sensitivity and application of DNA degradation evaluation methods differ. Modern techniques like PCR, comet assay, and NGS offer reliable analysis even in degraded materials, making them indispensable tools in forensic and postmortem investigations, while conventional techniques like RFLP are restricted to intact DNA.

Emerging Technologies and Future Directions in DNA Degradation Analysis

The analysis of damaged DNA has been greatly improved by recent developments in molecular biology and forensics. While traditional techniques like quantitative PCR (qPCR) and capillary electrophoresis (CE) are still crucial, new technologies are progressively enhancing the sensitivity, accuracy, and interpretive capability of degraded DNA analysis.

Quantitative PCR (qPCR) One essential method for evaluating DNA degradation is still quantitative PCR (qPCR). By comparing the amplification of short and long DNA targets, it makes it possible to calculate degradation indices and provide an estimate of DNA integrity (Correa et al., 2020). Despite its dependability, qPCR's capacity to extract precise genetic information from severely fragmented samples is restricted, requiring the use of more sophisticated methods.

Next-generation sequencing (NGS), sometimes referred to as massively parallel sequencing (MPS), has transformed the analysis of damaged DNA by enabling the sequencing of millions of DNA fragments at once. Because it uses shorter amplicons and allows the recovery of genetic information from highly fragmented DNA, this method is especially beneficial for degraded materials (Alketbi, 2024; MDPI, 2024). Additionally, NGS makes it easier to find single nucleotide polymorphisms (SNPs) and enhances the analysis of complex DNA mixes, which are frequently difficult to do with conventional STR-based techniques. (Parson et al., 2017).

The use of alternative genetic markers, such as SNPs and microhaplotypes, has drawn a lot of interest in addition to advances in sequencing. Because of their short amplicon size and less sensitivity to artifacts, microhaplotypes—which are made up of closely related SNPs inside brief genomic regions—offer excellent discrimination power and are ideal for damaged DNA (Kidd et al., 2018). These markers are being investigated more and more as trustworthy substitutes for traditional STR markers in forensic applications.

In the investigation of DNA degradation, new molecular methods like CRISPR-Cas systems are also demonstrating promise. Targeted DNA identification and enrichment are made possible by CRISPR-based techniques, which are especially helpful for low-template and degraded materials

(Kumari et al., 2026). By increasing sensitivity and specificity, these technologies raise the success rate of DNA profiling in difficult circumstances.

Additionally, machine learning and artificial intelligence (AI) are changing how degraded DNA data is interpreted. Compared to conventional statistical techniques, AI-based models can more accurately assess complicated sequencing data, forecast degradation patterns, and aid in mixture interpretation (Bright et al., 2019; Alketbi, 2024). Workflows for forensic DNA analysis are anticipated to be greatly enhanced by the integration of AI with high-throughput sequencing technology.

Forensic DNA phenotyping, which makes it possible to predict externally evident traits like eye color, hair color, and ancestry from DNA samples, is another significant advancement. Advanced sequencing technologies can extract enough genetic information to enable phenotypic predictions even in circumstances of partial degradation, offering useful research leads (Kayser, 2015).

Despite these developments, a number of issues still exist, such as exorbitant expenses, intricate technology, a lack of standards, and moral dilemmas around the use of DNA data. In order to improve degraded DNA analysis, future research is probably going to concentrate on creating quick, portable DNA analysis equipment, enhancing bioinformatics tools, and integrating multidisciplinary techniques (Ndayizeye et al., 2024; Alketbi, 2024).

Challenges and Future Perspectives

Despite these advancements, several challenges remain:

- High cost and technical complexity of NGS technologies
- Standardization issues across laboratories
- Ethical concerns related to DNA data usage
- Limitations in interpreting highly degraded or contaminated samples

Future research is expected to focus on:

- Development of portable and rapid DNA analysis systems
- Integration of multi-omics approaches
- Improved bioinformatics tools for degraded DNA interpretation
- Wider adoption of AI-driven forensic platforms

REFERENCE:

1. Lindahl T. Instability and decay of the primary structure of DNA. Nature. 1993;362(6422):709-715. doi:10.1038/362709a0.

2. Bhoyar L, Mehar P, Chavali K. An overview of DNA degradation and its implications in forensic caseworks. Egypt J Forensic Sci. 2024;14:15. doi:10.1186/s41935-024-00389-y.

3. Pajnič IZ. Analysis of human degraded DNA in forensic genetics. Genes (Basel). 2025;16(11):1375. doi:10.3390/genes16111375.

4. Salazar AM, Huerta PA, Coliboro-Dannich V, Castro AF, Barbaro A. Evaluation of DNA in human teeth—ante-mortem and post-mortem factors affecting degradation and preservation: a literature review. Genes (Basel). 2025;16(4):364. doi:10.3390/genes16040364.

5. Latham KE, Miller JJ. DNA recovery and analysis from skeletal material in modern forensic contexts. Forensic Sci Res. 2019;4(1):51-59. doi:10.1080/20961790.2018.1515594.

6. Khorwal D, Mathur GK, Ahmed U, Daga SS. Environmental factors affecting the concentration of DNA in blood and saliva stains: a review. J Forensic Sci Res. 2024;8(1):9-15. doi:10.29328/journal.jfsr.1001057.

7. Tozzo P, Scrivano S, Sanavio M, et al. The role of DNA degradation in the estimation of post-mortem interval: a systematic review of the current literature. Int J Mol Sci. 2020;21(10):3540. doi:10.3390/ijms21103540.

8. Johnson LA, Ferris JA. Analysis of postmortem DNA degradation by single-cell gel electrophoresis. Forensic Sci Int. 2002;126(1):43-47. doi:10.1016/S0379-0738(02)00027-0.

9. Shukla RK. Forensic application of comet assay: an emerging technique. Forensic Sci Res. 2017;2(4):180-184. doi:10.1080/20961790.2017.1379893.

10. Huffman JL, Sundheim O, Tainer JA. DNA base damage recognition and removal: new twists and

grooves. Mutat Res. 2005;577(1-2):55-76. doi:10.1016/j.mrfmmm.2005.03.012

11. Gill P, Hicks T, Butler JM, Connolly E, Gusmão L, Kokshoorn B, et al. DNA commission of the International Society for Forensic Genetics: assessing the value of forensic biological evidence—guidelines highlighting the importance of propositions. Part II: evaluation of biological traces considering activity level propositions. Forensic Sci Int Genet. 2020;44:102186. doi:10.1016/j.fsigen.2019.102186.

12. Macfarlane D, Roca G, Stadler C, Zapico SC. The Mystery of the Hidden Trace: Emerging Genetic Approaches to Improve Body Fluid Identification. Genes. 2026;17(2):146. doi:10.3390/genes17020146

13. Liao YH, Er LK, Wu S, Ko YL, Teng MS. Functional Haplotype of LIPC Induces Triglyceride-Mediated Suppression of HDL-C Levels According to Genome-Wide Association Studies. Genes. 2021;12(2):148. doi:10.3390/genes12020148

14. Chaudhary B, Shukla PK, Bastia BK. Role of clinical forensic medicine unit in quality and standardization of medico-legal reports. J Forensic Leg Med. 2020;74:102007. doi:10.1016/j.jflm.2020.102007

15. Li Z, Chen D, Wang Q, Tian H, Tan M, Peng D, Tan Y, Zhu J, Liang W, Zhang L. mRNA and microRNA stability validation of blood samples under different environmental conditions. Forensic Sci Int Genet. 2021;55:102567. doi:10.1016/j.fsigen.2021.102567