

The Quantum Leap in Forensic DNA: Using Epigenetics to Reveal New Clues in Old Cases

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Introduction

Forensic science has long been a cornerstone of criminal investigations, with DNA analysis serving as one of its most powerful tools. The advent of DNA profiling in the late 20th century revolutionized the way law enforcement could solve crimes, enabling the identification of perpetrators and the exoneration of the innocent. However, while traditional DNA testing has provided incredible breakthroughs, it often faces limitations when it comes to analyzing degraded or aged samples. This is where a new frontier of forensic science has emerged: epigenetics. The study of epigenetic modifications—changes to gene expression that do not involve alterations to the underlying DNA sequence—has opened up new avenues for solving crimes.

Epigenetics allows forensic scientists to gather information that was previously inaccessible using traditional DNA methods. By exploring how environmental factors, lifestyle choices and even stressors can affect gene expression, epigenetics has the potential to unlock crucial clues in old cases, some of which may have gone cold for years. This new quantum leap in forensic DNA not only strengthens the accuracy of criminal investigations but also promises to uncover information about a suspect or victim that was previously unimaginable [1].

Epigenetics refers to the study of chemical modifications to the DNA molecule and its associated proteins that regulate gene activity without altering the underlying genetic code. These modifications can be influenced by various factors, including environmental exposures, diet and stress. Importantly, these changes can be stable and even passed on to future generations, making them a fascinating area of study for both geneticists and forensic scientists. This process involves adding a methyl group to the DNA molecule, often at cytosine bases. DNA methylation can silence gene expression by preventing the transcription machinery from accessing specific genes. In forensics, DNA methylation patterns can help determine a person's age, ethnicity and even their likely geographic origin. Histones are proteins around which DNA wraps to form chromatin. Chemical modifications to histones, such as acetylation and methylation, can alter how tightly or loosely DNA is packaged, influencing gene expression. In forensics, these modifications can reveal information about how certain genes are expressed, potentially offering insights into an individual's health or behavior. These molecules play a role in regulating gene expression. By studying the expression patterns of non-coding RNA, scientists can learn more about the epigenetic regulation of genes, which could be useful for tracing familial connections or identifying specific traits [2].

Description

Traditional forensic DNA analysis focuses on identifying specific sequences within the genome. These sequences are unique to each individual (except

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for identical twins), allowing forensic scientists to match DNA samples from crime scenes with suspects. However, DNA samples can degrade over time or be contaminated, making it difficult to obtain useful genetic information from old or poorly preserved evidence. Epigenetics, however, provides an exciting avenue for overcoming these challenges. Because epigenetic modifications do not require the DNA sequence to remain intact, scientists can often extract valuable information from degraded or limited samples. For example, studies have shown that even when DNA is too fragmented to be sequenced, the methylation patterns remain largely intact, enabling forensic experts to analyze these markers and gain insight into an individual's identity, lifestyle and even their potential involvement in a crime. Moreover, epigenetic markers can sometimes provide more detailed information than traditional DNA analysis. For example, while DNA profiling can indicate whether a sample is from a male or female, epigenetic testing can provide a much richer context, such as revealing the age, ethnic background and even certain traits like susceptibility to disease [3].

Epigenetic markers, particularly those related to DNA methylation, have been used to develop profiles that can identify the age, gender and geographic origin of an individual. This is particularly useful in cases where only partial or degraded DNA samples are available, such as in cases of unidentified remains or missing persons. For example, scientists can use DNA methylation patterns to estimate the age of skeletal remains, helping to narrow down the search for potential victims or suspects. One of the most significant limitations of traditional DNA analysis is its reliance on intact and high-quality samples. However, epigenetic analysis can often work with much smaller and more degraded samples. This ability is crucial in cold cases where DNA evidence may have been stored for years, possibly undergoing environmental damage such as exposure to heat, moisture, or microbial activity. Epigenetics can also offer a better understanding of the circumstances surrounding a crime. For instance, epigenetic markers can provide clues about a suspect's behavior or psychological state at the time of the crime. Researchers are investigating whether specific stress-induced epigenetic changes could be linked to criminal behavior or whether they might explain certain traits seen in individuals with violent tendencies. In some cases, epigenetics could help to clear individuals who have been wrongfully convicted. By analyzing DNA methylation patterns, scientists may be able to pinpoint discrepancies in a DNA match, providing new evidence that could lead to the exoneration of innocent individuals. Epigenetic analysis can also be used to determine familial relationships, offering a new way to trace ancestry or identify potential relatives. This application has the potential to help solve cases where traditional DNA testing has not been conclusive, such as in cases of disputed paternity or when identifying biological family members from an unknown genetic sample [4].

One of the key technological advancements in epigenetics is next-generation sequencing, which allows scientists to sequence DNA at an unprecedented scale and resolution. NGS enables forensic scientists to detect epigenetic modifications in a sample, such as DNA methylation patterns, with high accuracy. This technology can be applied to trace amounts of DNA, making it invaluable for old cases or degraded evidence. Bisulfite sequencing is a method that converts unmethylated cytosine residues in DNA to uracil, allowing researchers to distinguish between methylated and unmethylated cytosines. This technique is particularly effective for studying DNA methylation, one of the most common forms of epigenetic modification and is frequently used in forensic applications. Microarrays enable the rapid analysis of thousands of DNA methylation sites at once, making them a valuable tool for profiling the epigenome. These arrays can be used to examine the DNA of individuals in a crime scene sample, comparing the methylation patterns to those of potential suspects or identifying other characteristics of interest, such as ancestry [5].

Conclusion

The fusion of epigenetics with forensic DNA analysis represents a quantum leap in the ability of law enforcement and forensic scientists to solve both old and new cases. By exploring how environmental factors and lifestyle choices can influence gene expression, forensic scientists are now able to glean new insights from evidence that was previously deemed unusable. From identifying unknown individuals and analyzing degraded samples to uncovering critical clues about the circumstances of a crime, epigenetics promises to redefine the way crimes are solved and justice is served. However, as with any new technology, the integration of epigenetics into forensic science must be approached carefully, with attention to ethical concerns and challenges related to interpretation and standardization. As research continues to unfold, the hope is that epigenetics will not only help solve cold cases but also become an indispensable tool in the forensic toolbox, providing clarity and closure to cases that have long remained unsolved. In the future, epigenetics may become an integral part of every forensic investigation, enabling investigators to uncover the hidden stories behind the DNA evidence at crime scenes. As this technology matures, it is likely that forensic epigenetics will contribute to a more nuanced understanding of human biology and its role in criminal behavior, ultimately bringing justice to those who have been waiting for it.

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Conflict of Interest

The author declares there is no conflict of interest associated with this manuscript.

References

1. Huang, Lucy, Yun Li Andrew B. Singleton and John A. Hardy, et al. "Genotype-imputation accuracy across worldwide human populations." *Am J Hum Genet* 84 (2009): 235-250.
2. Kling, Daniel, Christopher Phillips, Debbie Kennett and Andreas Tillmar. "Investigative genetic genealogy: Current methods, knowledge and practice." *Forensic Sci Int Genet* 52 (2021): 102474.
3. Antunes, Joana, Paulina Walichiewicz, Elmira Forouzmand and Richelle Barta, et al. "Developmental validation of the forenseq® Kintelligence Kit, miseq Fgx® sequencing system and forenseq universal analysis software." *Forensic Sci Int Genet* 71 (2024): 103055.
4. Gorden, Erin M., Ellen M. Greytak, Kimberly Sturk-Andreaggi and Janet Cady, et al. "Extended kinship analysis of historical remains using SNP capture." *Forensic Sci Int Genet* 57 (2022): 102636.
5. Tillmar andreas, Kimberly Sturk-Andreaggi, Jennifer Daniels-Higginbotham and Jacqueline Tyler Thomas, et al. "The FORCE panel: An all-in-one SNP marker set for confirming investigative genetic genealogy leads and for general forensic applications." *Genes* 12 (2021): 1968.

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