

From PCR to NGS: The Technological Leap in Forensic DNA Profiling

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Introduction

DNA analysis in forensic medicine has seen significant advancements, reshaping the field of criminal investigations. While traditional methods like Polymerase Chain Reaction (PCR) and Short Tandem Repeat (STR) profiling have long been foundational, recent innovations have expanded the scope and reliability of DNA testing in forensic cases. PCR, a key technique in DNA analysis, enables the amplification of specific genetic sequences. Recent improvements in PCR technology have enhanced its sensitivity, shortened reaction times, and reduced contamination risks. The adoption of Multiplex PCR, which allows for the simultaneous amplification of multiple DNA targets, has become standard practice, making it easier to analyze complex samples efficiently. Next-Generation Sequencing (NGS) has revolutionized forensic genomics, offering high-throughput sequencing that enables the simultaneous analysis of multiple samples and in-depth genomic profiling. This technology provides a higher resolution of DNA analysis, allowing for more precise identification of individuals. NGS is particularly useful for cases involving degraded or mixed DNA samples, offering capabilities that surpass traditional methods [1].

Advancements in Y-chromosomal DNA profiling have enhanced the forensic analysis of paternal lineage. The identification of Y-chromosomal markers enables investigators to trace male relatives and determine the potential source of male DNA in crime scenes. This advancement has proven crucial in cases with limited DNA evidence, providing valuable information for criminal investigations. Mitochondrial DNA (mtDNA) analysis has been a significant tool in forensic medicine, especially in cases where nuclear DNA is degraded or scarce. Recent advancements in mtDNA analysis techniques have improved sensitivity and resolution, enabling the identification of individuals with maternal lineage specificity. This has been instrumental in cases involving hair, bones, or other degraded biological samples. The incorporation of Single Nucleotide Polymorphism (SNP) typing has added another layer of precision to forensic DNA analysis. SNP markers offer increased discrimination power, allowing for more accurate identification in cases involving closely related individuals. The integration of SNP typing enhances the forensic community's ability to differentiate between individuals with similar genetic profiles [2].

Description

The utilization of bioinformatics tools has become indispensable in handling the vast amount of data generated by advanced DNA analysis techniques. Bioinformatics assists in data interpretation, comparison and database management, streamlining the investigative process. The integration of bioinformatics has also contributed to the establishment of comprehensive DNA databases, aiding in the identification of potential suspects and solving

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cold cases. Despite these advancements, challenges persist in the forensic DNA analysis domain. Issues such as sample contamination, privacy concerns and legal admissibility of DNA evidence continue to be areas of focus. Ongoing research aims to address these challenges and further improve the efficiency and reliability of forensic DNA analysis. The continuous evolution of DNA analysis techniques has propelled forensic medicine into a new era of investigative precision and efficiency. From the foundational PCR to the transformative power of NGS, each advancement contributes to the enhancement of forensic capabilities. As technology continues to progress, forensic DNA analysis will undoubtedly play an increasingly pivotal role in ensuring justice is served and the innocent are protected [3].

Beyond the fundamental advancements discussed earlier, recent developments have also expanded the scope of forensic DNA analysis. These include the exploration of novel genetic markers, epigenetic modifications and the integration of other omics technologies. Researchers are continually exploring novel genetic markers to enhance the discrimination power of DNA analysis. In addition to traditional markers, such as STRs and SNPs, new markers are being investigated, providing additional layers of specificity. Microhaplotypes, for example, have gained attention for their potential in improving the discrimination power, especially in cases involving degraded or mixed DNA samples. The field of forensic epigenetics has emerged as a promising avenue for enhancing DNA analysis. Epigenetic modifications, such as DNA methylation patterns, can offer insights into the tissue origin of DNA samples. This information can be particularly valuable in distinguishing between different cell types, aiding in the interpretation of complex forensic samples [4].

The integration of omics technologies, such as proteomics and metabolomics, is expanding the analytical capabilities of forensic investigations. Combining DNA analysis with these approaches allows for a more comprehensive understanding of the biological evidence at crime scenes. This integrative approach can provide valuable information about the individual's physiological state, lifestyle and potential exposure to environmental factors. Advancements in DNA analysis techniques are also addressing challenges related to sample processing. Technologies designed to handle challenging sample types, such as touch DNA, low-copy-number DNA and mixtures, are continually being refined. Improved sensitivity and robustness in sample processing contribute to a higher success rate in obtaining DNA profiles from trace amounts of biological material.

As forensic DNA analysis becomes more sophisticated, concerns regarding privacy and ethical considerations come to the forefront. The increased sensitivity of DNA analysis techniques raises questions about the potential misuse of genetic information. Striking a balance between the pursuit of justice and protecting individual privacy remains a crucial aspect of the ongoing dialogue within the forensic community. The admissibility of DNA evidence in legal proceedings is an ongoing challenge. As forensic techniques advance, the need for establishing reliability, accuracy and validity becomes paramount. Ensuring that forensic DNA analysis meets the legal standards of admissibility is an area of active research and collaboration between the scientific and legal communities. In an era of globalized crime and interconnected populations, international collaboration and standardization of forensic DNA analysis protocols are essential. Harmonizing methodologies, sharing databases and establishing common standards contribute to the effectiveness and efficiency of cross-border investigations [5].

Conclusion

The establishment and interconnection of global DNA databases can

enhance international cooperation in solving crimes. Sharing DNA profiles and information across borders allows for the identification of individuals involved in transnational criminal activities. However, this also raises concerns about privacy, data security and the need for standardized ethical and legal frameworks. In the ever-evolving field of forensic DNA analysis, continuous research and collaboration between scientists, forensic practitioners, legal experts and policymakers are paramount. Addressing emerging challenges, staying ahead of technological advancements and ensuring ethical practices are critical components of the ongoing efforts to enhance the reliability and effectiveness of forensic DNA analysis in the pursuit of justice.

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Conflict of Interest

There is no conflict of interest associated with this manuscript.

References

1. Grisedale, Kelly S. and Angela van Daal. "Comparison of STR profiling from low template DNA extracts with and without the consensus profiling method." *Investig Genet* 3 (2012): 1-9.
2. Peakall, R. O. D. and Peter E. Smouse. "GENALEX 6: Genetic analysis in excel. Population genetic software for teaching and research." *Mol Ecol Notes* 6 (2006): 288-295.
3. Barash, Mark, Dennis McNevin, Vladimir Fedorenko and Pavel Giverts. "Machine learning applications in forensic DNA profiling: A critical review." *Forensic Sci Int Genet* (2023): 102994.
4. Gill, Peter, Jonathan Whitaker, Christine Flaxman and Nick Brown, et al. "An investigation of the rigor of interpretation rules for STRs derived from less than 100 pg of DNA." *Forensic Sci Int* 112 (2000): 17-40.
5. Budowle, Bruce, Arthur J. Eisenberg and Angela van Daal. "Validity of low copy number typing and applications to forensic science." *Croat Med J* 50 (2009): 207-217.

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