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Human DNA Quantification as a Tool for Enhancing DNA Profiling in Ancient Skeletal Remains

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Introduction

The study of ancient skeletal remains is an invaluable resource for understanding human history, migration patterns, and evolutionary biology. The analysis of DNA extracted from these remains, known as ancient DNA (aDNA), provides insight into the genetic makeup of past populations, offering a glimpse into the genetic diversity of our ancestors. Over the years, advancements in DNA extraction and sequencing technologies have allowed researchers to recover genetic material from even the most degraded skeletal remains. However, despite these technological improvements, ancient DNA often exists in minuscule quantities, and its degradation poses a significant challenge in obtaining comprehensive genetic profiles [1].

DNA quantification has emerged as an essential tool for overcoming these obstacles. The accurate measurement of DNA in ancient skeletal remains not only enhances the efficiency of DNA extraction but also informs the choice of appropriate techniques for downstream analysis. By determining the quantity of recoverable DNA, scientists can tailor their approach to maximize the chances of obtaining usable genetic data. This article explores the role of DNA quantification in enhancing DNA profiling from ancient skeletal remains, highlighting its importance, techniques, challenges, and potential implications for the field of bioarchaeology and forensic science [2].

Description

DNA quantification is the process of measuring the amount of DNA present in a sample. In the context of ancient skeletal remains, the DNA found is often highly fragmented, degraded, and present in low concentrations. As a result, obtaining a high-quality, intact genetic profile from these remains is challenging. DNA quantification plays a pivotal role in determining whether a sample contains sufficient DNA for further analysis and informs decisions on the best methods for DNA recovery and profiling. Quantifying DNA in ancient remains is crucial for several reasons. First, it provides a gauge of the DNA's preservation quality, allowing researchers to assess the feasibility of obtaining reliable genetic information. Second, DNA quantification helps in the selection of appropriate techniques for DNA extraction and amplification. For instance, if a sample has very low DNA content, highly sensitive techniques such as polymerase chain reaction (PCR) may be necessary to amplify the DNA. Conversely, if a sample contains sufficient DNA, traditional extraction methods may suffice. Furthermore, knowing the DNA concentration helps optimize the sequencing process, ensuring that valuable resources are not wasted on samples that are unlikely to yield meaningful results [3].

Ancient DNA is often present in skeletal remains in very small amounts, making it challenging to extract and amplify. The DNA found in ancient remains is typically degraded due to environmental factors such as temperature fluctuations, humidity, microbial activity, and exposure to UV light over time. As a result, ancient DNA is often fragmented into small pieces, and its integrity is compromised. In addition to degradation, the presence of contaminants, such as modern human DNA from handling, as well as microbial DNA, can further complicate the extraction process. The challenges associated with ancient DNA extraction are compounded by the fact that skeletal remains are often buried in soils that contain various substances, including organic matter, minerals, and chemicals, which can interfere with the recovery of DNA. Overcoming these challenges requires the development of specialized extraction protocols that account for the unique nature of ancient DNA and its degradation patterns. DNA quantification is essential in this context, as it helps guide researchers in their choice of extraction techniques and the amount of starting material required. Several methods are used to quantify DNA in ancient skeletal remains. The choice of technique depends on the level of DNA degradation, the sensitivity required, and the available equipment. Below are some of the most commonly used DNA quantification methods in ancient DNA research [4].

Fluorometric quantification is one of the most commonly used methods for measuring DNA concentration in ancient samples. This technique uses fluorescent dyes that bind specifically to DNA molecules, emitting fluorescence when exposed to Ultraviolet (UV) light. The fluorescence intensity is directly proportional to the amount of DNA in the sample. Fluorometric quantification provides high sensitivity and can accurately measure low DNA concentrations, making it ideal for ancient DNA samples that may be degraded or fragmented. One popular fluorometric assay is the PicoGreen assay, which specifically binds to double-stranded DNA and is often used in combination with a spectrophotometer or fluorometer to determine the DNA concentration. Fluorometric methods are particularly useful for determining DNA quantity before proceeding with further steps in ancient DNA analysis, such as amplification or sequencing. Quantitative polymerase chain reaction (qPCR) is a more specific method for DNA quantification that can measure both the quantity and quality of DNA in ancient skeletal remains. Unlike traditional PCR, which only provides a qualitative result, qPCR provides quantitative data by measuring the amount of DNA amplified during the PCR process. The amount of DNA present is determined by monitoring the fluorescence emitted during each amplification cycle. The number of amplification cycles required to reach a certain fluorescence threshold is inversely proportional to the DNA concentration in the sample [5].

Conclusion

The quantification of DNA in ancient skeletal remains is a powerful tool that enhances DNA profiling efforts and provides valuable insights into the genetic history of past populations. As ancient DNA research continues to evolve, DNA quantification methods have become indispensable for optimizing DNA extraction, amplification, and sequencing techniques. By measuring DNA concentration and quality, researchers can make informed decisions about which methods to employ and ensure that valuable genetic material is not wasted. DNA quantification also plays a critical role in advancing our understanding of human evolution, migration, and the genetic diversity of ancient populations.Despite the challenges of working with degraded and low-concentration DNA, advances in quantification techniques and sequencing technologies have significantly improved the reliability and accuracy of ancient DNA research. As these technologies continue to evolve, the potential for further breakthroughs in understanding our genetic past will only expand, allowing us to learn more about the lives of our ancient ancestors and their contributions to the genetic makeup of modern populations. Ultimately, DNA quantification represents an essential tool in the ongoing quest to unlock the

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genetic secrets of ancient skeletal remains and reconstruct the complex history of humanity.

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Conflict of Interest

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

References

1. Sturk-Andreaggi, Kimberly, Michelle A. Peck, Cecilie Boysen and Patrick Dekker, et al. "AQME: A forensic mitochondrial DNA analysis tool for next-generation sequencing data." *Forensic Sci Int Genet* 31 (2017): 189-197.
2. Andrews, Richard M., Iwona Kubacka, Patrick F. Chinnery and Robert N. Lightowlers, et al. "Reanalysis and revision of the Cambridge reference sequence for human mitochondrial DNA." *Nat Genet* 23 (1999): 147-147.
3. Anderson, Sharon, Alan T. Bankier, Bart G. Barrell and Maarten HL de Bruijn, et al. "Sequence and organization of the human mitochondrial genome." *Nature* 290 (1981): 457-465.
4. Hofreiter, Michael, Jiri Sneberger, Martin Pospisek and Daniel Vanek. "Progress in forensic bone DNA analysis: Lessons learned from ancient DNA." *Forensic Sci Int Genet* 54 (2021): 102538.
5. Xavier, Catarina, Mayra Eduardoff, Barbara Bertoglio and Christina Amory, et al. "Evaluation of DNA extraction methods developed for forensic and ancient DNA applications using bone samples of different age." *Genes* 12 (2021): 146.

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