

Progress in DNA Sequencing Technology: Recent Breakthroughs and Future Prospects

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Abstract: In the dynamic field of DNA sequencing, continuous advancements in science and technology drive progress. Notably, recent developments have focused on the refinement of techniques and the introduction of innovative tools to enhance sequencing capabilities. For instance, Michael's work in 2005 showcased the integration of microfluidic separation platforms into Sanger sequencing methods, marking a significant milestone in the field. Furthermore, Jay A.'s research in 2008 contributed to the optimization of dideoxy sequencing protocols, further improving the efficiency and accuracy of DNA sequencing processes. Additionally, the pioneering work of Sanger and subsequent reports by Clyde A. Hutchinson in 2007 introduced novel techniques such as plus and minus sequencing, expanding the repertoire of available sequencing methods. Moreover, advancements have been made in the sequencing of methylated DNA and the investigation of DNA and RNA protein interactions, as evidenced by George M. Church's seminal work in 1988. This review endeavors to synthesize and present a comprehensive overview of these cutting-edge techniques and their implications for DNA sequencing methodologies.

Keywords: DNA sequencing, RNA, Application, Techniques, Scope and Sanger

1. INTRODUCTION

DNA sequencing is the process of determining the precise order of nucleotides (A, C, G, T) within a DNA molecule (Loman & Pallen, 2015). It is a fundamental tool for research in genetics and molecular biology and has numerous applications in fields such as medicine, biotechnology, and forensics. The first method of DNA sequencing, known as the Sanger method, was developed in the 1970s and revolutionized the field of molecular biology (Sanger et al., 1977). Since then, many different methods have been developed that allow for faster, cheaper, and more accurate sequencing of DNA.

The basic steps of DNA sequencing involve fragmenting the DNA molecule into smaller pieces, amplifying these fragments through a process called PCR, and then determining the order of nucleotides within each fragment. This information is then assembled to create a complete sequence of the original DNA molecule (Goodwin et al., 2016).

There are two main types of DNA sequencing: whole-genome sequencing and targeted sequencing. Whole-genome sequencing involves sequencing an individual's entire genome, while targeted sequencing focuses on specific regions of interest within the genome. Both approaches have their own advantages and disadvantages depending on the research question and available resources (Mardis, 2017).

The applications of DNA sequencing are vast and include identifying genetic mutations that cause disease, studying the evolutionary history of species, and understanding the genetic basis of complex traits such as intelligence and personality (Burgess et al., 2018). DNA sequencing has also been used in forensics to help solve crimes and identify human remains. In recent years, advances in DNA sequencing technology have led to the development of portable and handheld devices that can sequence DNA in real-time, making it possible to rapidly diagnose infectious diseases and monitor environmental samples in the field (Quick et al., 2015).

More recently, researchers have focused on developing new methods for DNA sequencing, such as microfluidic separation platforms. Michael et al. (2005) reported on the use of microfluidic separation platforms for Sanger sequencing, which allowed for faster, more accurate sequencing of DNA. In addition to developing new methods for DNA sequencing, researchers have also worked on optimizing existing protocols. Jay et al. (2008) developed a best-practice protocol for dideoxy sequencing, which involves using modified nucleotides to terminate DNA synthesis

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