History of DNA sequencing technologyinig development

Urmanov Khurshid Nurzhanovich,

Kokand State Pedagogical Institute Teacher of the Department of biology, E-mail: cosmopolit-1975@mail.ru

Annotation: This article discusses the stages of development of DNA sequencing technologies from the first (FGS) to the third generation (TGS).

At present, the introduction of new advanced methods, technologies, innovative ideas into our lives is being carried out at a high pace, using the achievements of Science in the whole Jahon and in our country, effectively applying the achievements of fundamental and Applied Research. The development of new technologies and their improvement, the reduction of their cost in order to satisfy human extirpation and increasing their effectiveness became a necessity of the period. In addition, the creation of advanced methods of biological science will greatly help in solving the problems facing the medical, agricultural and national spheres

The chemical degradation method proposed by Maxam and Gilbert, the chain deoxy-terminology method created by Senger and his team in 1977, and automatic sequencing technologies through celebrated fluorescence developed in the 1990s formed the first generation of sequencing (FGS). Due to its simplicity, the Senger method has become the dominant method in FGS. Sequencing in the Senger method made it possible to read the complete genome of Phix 174 bacteriophage, consisting of 5375 nucleotides. In 2003, within the framework of the international project of the consortium" human genome " (HGP), a map of it was created sequencing the complete human genome, which lasted 13 years in World laboratories.

The second generation of sequencing (SGS), or the next generation of sequencing (NGS), is able to sequencing millions or billions of DNA strands by belonging to high-product technologies for determining DNA nucleotide coherence. In doing so, the sequence detection process allows multiple sequencing of the intended regions and high permeability properties. The third generation of sequencing (TGS) is characterized by the addition of one nucleotides, which provide long and accurate sequencing results, and amplification technologies are not used. Single-cell sequencing belongs to xam TGS technologies.

The development and improvement of methods for determining DNA molecule sequences has been serving in genomics, gene engineering, criminalistics, the creation of new varieties and breeds, economic and environmental innovation. The rise of methods in this direction has its effect on the treatment of hereditary diseases, the correction of genomes, the development of molecular phylogenetic studies, Pharmaceuticals.

In the field of education, teaching topics devoted to sequencing on the basis of Jahan standards takes a place in the light of correct and understandable delivery to the listener. In recent years, we will have to develop a program for the further development of the system of higher educational institutions and introduce it into life.

THE DEVELOPMENT OF TECHNOLOGIES FOR DETERMINING THE SEQUENCE OF NUCLEOTIDES OF A DNA MOLECULE.

It has been several decades since the revolutionary method of reading DNA nucleotide sequences developed by Frederick Senger and his hamkasbs was created. This is due to the fact that research in the field has led to the improvement of new methods and the possibility of rapid implementation of the cheap concentration of DNA.

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After the" Human Genome "Project, the time interval between sequencing technologies decreased, and at the same time scientific knowledge continued to grow in the form of geometric progression. After sequencing on Senger, which was adopted as the first generation, new generations of DNA sequencing began to be introduced into practice one after another.

The development of next generation (NGS) sequencing technologies has served greatly in reducing costs and obtaining tremendous sequencing data.

Currently, three generations of sequencing technologies are allocated.

At present, NGS technologies belonging to the second generation of widely used sequencing are formed from the stages of preparation, amplification and sequencing of bibliotechs, while nucleic acids are directly sequenced in Aloxi in order to create the property of uniformity and high permeability from systemic errors in the third generation sequencing.

The creation of new generations of sequencing has found its own study in a wide range of fields of Molecular Biology, eliminating barriers to traditional methods for determining DNA nucleotide sequences.

On the other hand, along with the development of next-generation technologies, many technical problems arise that arise with the task of their deep evacuation and evaluation.

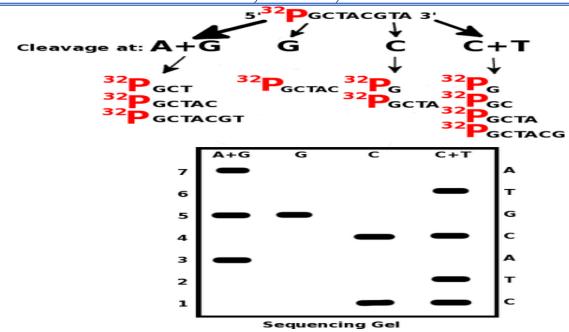
In this article, we will get acquainted from the first generation of DNA nucleotide sequence detection technologies (first generation sequencing (FGS) to the third generation sequencing methods (third generation sequencing (TGS).

THE FIRST GENERATION OF DNA SEQUENCING TECHNOLOGIES

The late 1970s marked the beginning of the 1980s, an extremely critical period for the sciences of genetics and Genomics. The discovery of the polymerase chain reaction (PZR) laid the foundation for the creation of early technologies for sequencing DNA, which could read the entire genome, realizing the possibilities of DNA amplification.

The first-generation sequencing techniques of sequencing according to xisobed Senger and sequencing according to Maxam-Gilbert have been practicing genomics for almost 40 years. They laid the foundation for future technologies of sequencing.

Sequencing according to Maxim – Gilbert (Maxam – Gilbert) is considered one of the earliest platforms for sequencing DNA. This method of sequencing is common in science as a method of chemical decomposition. This technique was developed in 1977 by Harvard University student Allan Maxam Hamda Walterom Gilbertom, based on the nucleotide-specific chemical degradation that occurs when DNA is treated with various chemical agents. Due to the complexity of the technical specification, the method has now lost its actuality.



Picture. 1. Sequencing according to Maxam – Gilbert is based on the specific breakdown of the DNA strand from which DNA fragments are obtained, which are marked differently in size.

Sequencing according to Senger is due to the early methods of DNA sequencing.

Frederick Senger, together with his colleagues, began sequencing technologies first for insulin, then for RNA and finally for DNA. His research led to the creation of the sequencing method of the Senger chain break in 1977.

In 1980, for this discovery, Senger received the second Nobel Prize in chemistry. The technology was commercialized by Applied Biosystems. This method is considered to be the method carried out by Sanger sequencers in many laboratories around the world, sequencing the complete DNA of a person within the framework of the" Human Genome "Project.

Automated DNA Sequencing

The techniques of Senger and Maksama - Gilbert —were complex and difficult. In 1986, Leroy Hood and his hamkash began to use fluorescent badges instead of radioactive tokens, improving the Senger sequencing method. Of the four fluorescent dyes, one is used in the marking of nucleotide primers.

Each dye is used in the flame reaction of sequencing using one of four ddNTP. After reaching the sequencing reaction nihoya

all four reactions are mixed to form polyacrylamide (lane) in a single corridor of gel. The application of four different ddNTP using a celebrated fluorescent target of four different wavelengths allows the sequencing reaction to be conducted in a single test tube rather than in four flames.

This technique was improved in the early 1990s by Harold Sverdlov and hamkasbs as a result of their use of capillaries in sequencing DNA. These capillaries are small in size (inner diameter 50 μm) and work under some high voltage in order to save working time.

1993 year B.L Karger aliased polyacrylamide with a low-thickness separating Matrix, later in 1995 Zyang developed a non-cross-linked polymer with a constant temperature of 60 °C in order to obtain high-quality nucleotide consistency.

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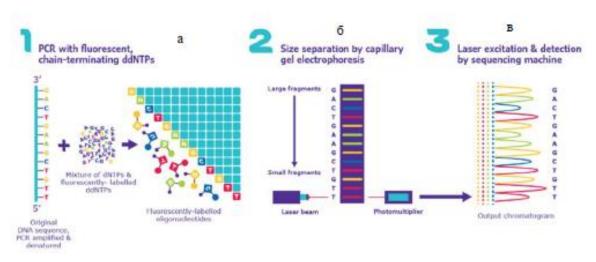


Photo 2. Automatic DNA sequencing.

a-capillary electrophoresis system; laser recording of B —fluorescent characters; V — DNA sequence electrophoregram.

Pirasekvenslash. Pyrosequencing entered into practice starting in 1987 as continuous monitoring of DNA polymerase activity (Nyren, Lundin). In 1988, Edward Hyman continued his DNA sequencing technique.

In 1996, the pyrosequencing platform was created by Ronagi and others. Almost 10 years later, in 2005, Rozberg and hamkasbari presented the first commercial next-generation sequencer based on the pyrosequencing method created in 1996. Later, 454 Life Sciences developed a parallel variant of pyrosequencing purchased by Roche Diagnostics.

SECOND GENERATION OF DNA SEQUENCING TECHNOLOGIES

Sequencing on Senger has been used for almost 30 years. In carrying out this process, the notoriety of cost and time was evident as a major problem. The next wave of sequencing technologies, known as the second generation of sequencing, appeared in the mid-2000s, and it was focused on the goals of reducing outputs, increasing speed and being free from electrophoresis.

Sequencing by synthesis Illumina/Solexa. The Illumina / Solexa platform is the research product of Shankar Subramanyan and David Clenerman, scientists from the University of Cambridge, who have contributed a great deal to the Human Genome Project. They enriched their properties in sequencing through developments known by the name of a new method of synthesizing fluorescent-marked dyes and complement chains using polymerase, sequencing by synthesis. Later they

They founded Solexa Inc (June 1998). In 2004, Solexa acquired molecular clustering technology from Manteia. 2006 Solexa its first sequencer -

Genome introduced Analyzer, which became a powerful machine capable of sequencing 1 gigabyte of data in one burn. In 2007, Solexa was acquired by Illumina, and since then, the Illumina/Solexa platform has been considered the most leading and widespread method of Jaxon in sequencing.

Ligase sequencing: ABI/Solid. Abi binding by sequencing and oligonucleotide detection (Sequencing by Oligonucleotide Ligation and Detection, SOLiD) —such a method of sequencing uses DNA - ligase enzyme rather than DNA - polymerase in the binding process.

In 2008, SOLiD System acknowledged this technology as the only technology of NGS with a precision level of > 99.94%.

ISSN 2277-3630 (online), Published by International journal of Social Sciences &	
Interdisciplinary Research., under Volume: 11 Issue: 12 in December-2022	
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The length of study in ABI/SOLiD technology is from 25 to 35 g. Approximately 40 million readings (rids) are sequenced, and the output data of sequencing is from 2 to 4 gigabytes. Initially, the device was released to the market in 2007, and the output of the devices was discontinued in 2016.

Ion semiconductor Ion Torrent sequencing. Ion semiconductor sequencing technology (Ion semiconductor sequencing) DNA Electronics Ltd. licensed by the company. This technology differs from other technologies in that it does not apply modified nucleotides and optical loops.

Ion semiconductor sequencing is also referred to as Ion torrent sequencing, rn-related sequencing, or semiconductor sequencing.

Ion Torrent offers its systems as fast, compact and economical sequencers.

THIRD GENERATION OF SEQUENCING TECHNIQUES

While second-generation sequencing technologies have allowed sequencing several genomes at a lower price, major structural changes in taxlil and de novo sequencing pose a challenging task for these techniques. The next step in synchrensing DNA is to use DNA amplification to form and aim to provide longer readings in one attempt. However, such technologies Hamon is at the stage of research and research.

Unicamolecular sequencing. Real-time unicamolecular sequencing (Single-mole real-time sequencing (SMRT)) is part of the third generation of DNA sequencing.

This method is used in Real-time reading of relatively long sections of DNA sequences. Technology Pacific Biosciences of California, Inc. developed and patented by 2011. PacBio RS was the first product to be sold commercially.

In April 2013, the company launched a new generation of sequencer called PacBio RS II, which allows for longer readings and has a high bandwidth. In September 2015, the company introduced the seven times more productive, modified and innovation Sequel System sequencer than the PacBio RS II.

Nanoparticles sequencing. The development of nanopore sequencing technologies began before NGS sequencing. In the early 1990s, Dwid Drimer and George Chyorch discovered that single-stranded DNA (ssDNA) independent of one another could be sequenced by passing through nanopores. In 1996, Drimer, Brenton and Kasyanovich published the result of their research, the passage of DNA through the alpha – geiolizin Nanopore.

The big jump in nanopore sequencing technologies occurred in 2001, with the discovery of solid nanopores. In 2005, the Oxford Nanopore Technologies Company was founded. This is the first company to offer commercial sequencers operating on the basis of nanoparticles technology.

Conclusion

After the terminology method of chemical chains, introduced by Maxim and Gilbert in 1977, the Senger method, which was discovered in this year, created a revolution in biology. These techniques resulted in the sequencing of even larger genomes, culminating in the emergence of its high peak, the "human genome" loyix. As a next step, one can cite the example of sequencing projects carried out on a large scale with the aim of studying human variations. However, for such large projects, the Senger method was an extremely expensive and long-lasting method. In 2004, the National Institute for Human Genome Research (NHGRI) launched a program to reduce the cost of studying a full genome to \$ 1,000 in 10 years.

This laid the foundation for the creation of fast and affordable NGS technologies that multiply by many million reactions in one cycle. The main advantage of NGS Technologies was the release from the bacterial cloning of DNA fragments from the electrophoretic separation of forgings and sequens products. Currently, the jaxon market is led by the NGS technologies of the Illumina company. Due to its low cost

	ISSN 2277-3630 (online), Published by International journal of Social Sciences &
	Interdisciplinary Research., under Volume: 11 Issue: 12 in December-2022
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NGS technology has created genome sequencing capabilities for small laboratories. Human genome-a cheap target route from \$ 1000 was carried out several years ago. Currently, NGS technologies are the main consideration in biology and are widely used in clinical and agronomic research.

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278	ISSN 2277-3630 (online), Published by International journal of Social Sciences & Interdisciplinary Research., under Volume: 11 Issue: 12 in December-2022 https://www.gejournal.net/index.php/IJSSIR
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