IJCRT.ORG ISSN : 2320-2882

INTERNATIONAL JOURNAL OF CREATIVE RESEARCH THOUGHTS (IJCRT)

An International Open Access, Peer-reviewed, Refereed Journal

Revolutionizing Genomics: The Future Of Dna Sequencing With Nanopore Technologies

[2]Prajwal Kumar Sinha[1]Ritika Sharma, [3]Anurag
[1]Assistant Professor, [2]Student, [3]Student
[1]University Institute of Pharma Sciences,
[1]Chandigarh University, Mohali, India

Abstract: As sequencing of DNA technologies have evolved across multiple generations, the science of genomics has undergone a major revolution. Starting from earliest first-generation Sanger method sequencing to the emergence of second- and third-generation approaches, this account traces the course that culminated in the innovative development of nanopore sequencing. With each generation, the speed, read length, accuracy, and cost-effectiveness improved. A salient characteristic of nanopore sequencing is its real-time, direct reading of long DNA or RNA strands without needing to tag or amplify them. The portability, simplicity, and flexibility of the technology have made possible applications across a range of fields, such as clinical diagnostics, infectious disease surveillance, agriculture, forensic studies, and personalized medicine. The underlying operation of solid-state and biological nanopores is also explored within this book, with a focus placed on their utilization within modern sequencing platforms. The review also includes advances that aid us in understanding genomic complexity better, such as RNA-seq, single-cell analysis, and long-read and short-read sequencing. Genomics is becoming increasingly accessible, effective, and impactful with the application of nanopore technology, opening the way for revolutionary discoveries in the areas of health, the environment, and more.

Keywords: DNA sequencing, Genomics, Nanopores, RNA sequencing, Cell analysis.

I. INTRODUCTION:-

The technique of determining the four precise nucleotides sequence (A)Adenine, (C)Cytosine, (T)thymine and (G)Guanine in DNA's molecule is called DNA sequencing. It is a core method in genetics and molecular biology that enables researchers to decode the genetic information of an organism. Second Nobel prize was awarded to Fredrick Sanger in Chemistry in 1977 for an invention of the first technique to sequence DNA, called as "Sanger sequencing". This pioneering procedure ushered in contemporary genomics. In attempting to understand better an organism's genetic composition and how genetic differences affect traits, development, and disease, DNA sequencing was created. It was a step that had to be taken to unravel the molecular secrets of life. Big projects like the Project of Human Genome to sequence all genes of the human's genome generated a request for precise DNA sequencing quickly.

Along with chemical techniques, the Sanger technique, an enzymatic technique, was common "(França et al., 2002)". "Nelson et al. (2011)" and "Camargo Mancipe et al. (2020)" suggest that next-generation sequencing techniques such as "Roche 454, SOLID, Illumina, Ion Torrent, PacBio, and Oxford Nanopore" came into being because of the ensuing technological developments. Nelson et al. (2011) suggest that newer techniques provide higher throughput, precision, and cost-effectiveness, opening new fields of application in the biological sciences and making large-scale genomic projects possible.

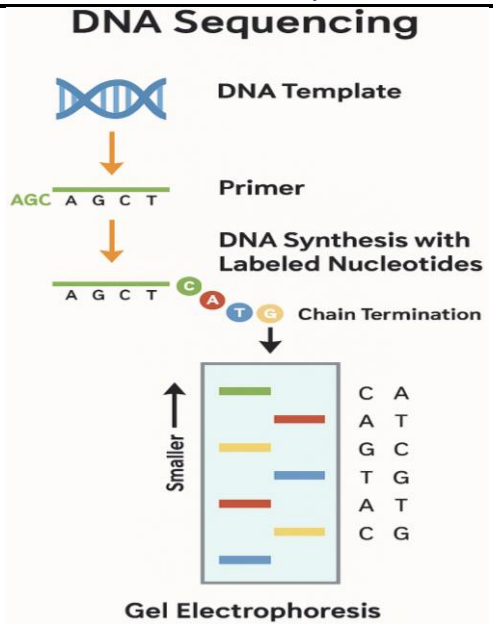

fig. a shows DNA sequencing

Nanopore sequencing is a newer, exciting technology that's transforming how we see DNA. Compared to previous technologies, which are both very chemical- and preparation-heavy, nanopore sequencing directly reads DNA by pumping a single strand through a small opening—a nanopore— & observing a change in electric flow. This way, scientists can read the sequence of DNA in real time, and it is both faster and less complicated. One of the best aspects of this technology is portability. From a laboratory, to a town hundreds of miles away, to space, devices like the Oxford Nanopore MinION are the size of your hand and yet have the capability of DNA sequencing. For use in quick clinic tests, disease outbreak research, or field work, this makes it extremely convenient.

The speed with which it produces an effect is yet another significant benefit. Physicians and medical scientists can draw conclusions earlier as it processes in real time, which is imperative in case of emergencies or diagnosis. It is anticipated that the technology will become an integral part of healthcare, personalized therapies, and home testing kits as well as it continues to develop—faster, more accurate, and simpler to use. I would like to conclude by saying that, nanopore sequencing is paving the way to a future where DNA analysis will be more accessible, less costly, and quicker than ever.

II. GENERATIONS OF SEQUENCING:-

Technology used for "reading" DNA sequences has come a long way in the last two decades. Due to the incredible advancements in DNA sequencing brought about by this speedy evolution, there came into existence the three evolutions or generations of sequencing technology.

1. First- Generation Sequencing:-

During the early DNA and RNA sequencing, the molecules were broken into fragments by chemical or enzymatic techniques so that they could be analysed and separated individually. Through the assistance of an enzyme called ribonuclease purified from Saccharomyces cerevisiae, “Robert Holley” became the first who sequenced a nucleic acid known as alanine tRNA, in 1964. During the same time, “Walter Gilbert and Allan Maxam” evolved a chemical degradation process by which it was possible to sequence the bacteriophage PhiX174 genome. Though all these improvements were made, the greatest milestone was the chain termination method’s discovery by “Fredrick Sanger”—who transformed DNA sequencing and paved the way for contemporary genetic studies. This method resulted in sequence reads of a couple of hundred nucleotides' length with dideoxynucleotides, which terminate DNA strand extensions during replication. Sanger's technique, which allowed the rapid DNA and RNA’s sequencing, was highly utilized and revolutionized molecular- biology. Applied Biosystems' ABI 370, the very first commercially available computerized sequencing machines, was made available in the US in 1987.DNA sequencing was greatly accelerated and improved by this machine, which mechanized the Sanger sequencing technique with fluorescently labelled dideoxynucleotides and capillary electrophoresis. Figure 1 below shows mechanism:-

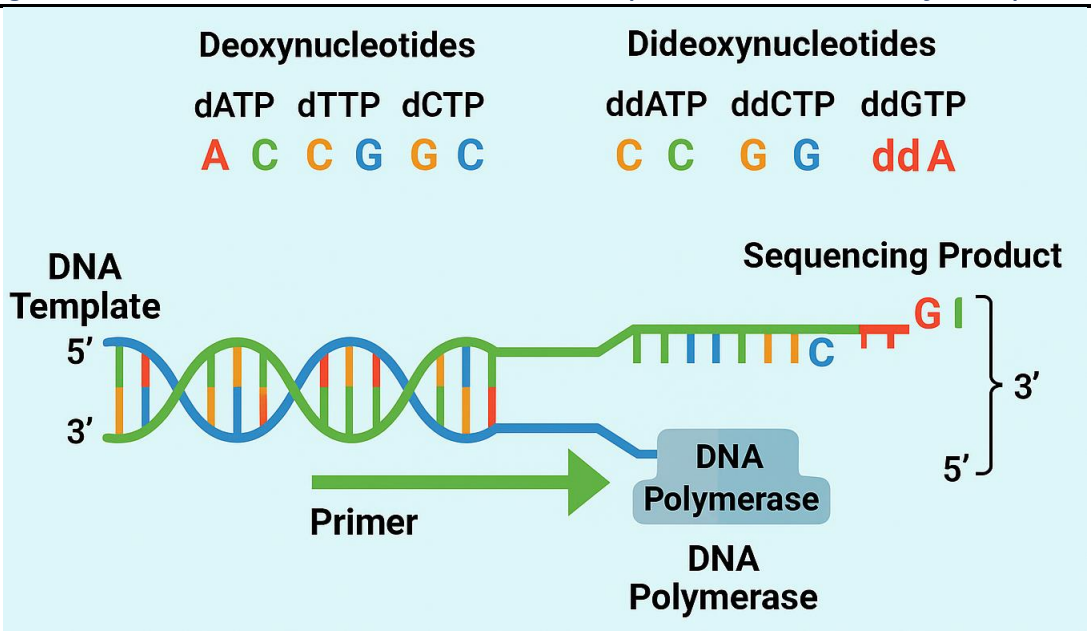

figure 1 shows the mechanism of first-generation sequencing

2. Second- Generation Sequencing: -

By enabling researchers to read hundreds or even millions of fragments of DNA simultaneously, second-generation sequencing has transformed the world of DNA study. These new technologies are parallel sequencing, which speeds the process up dramatically compared to the traditional Sanger approach, which read one fragment at a time. By using a technique called pyrosequencing, one of the most famous is Roche's 454 sequencing. The method employs light signals generated every time, a nucleotide is added with the developing strand of DNA to translate DNA code. Mass analysis of DNA is now quicker, less expensive, and much more useful for research and medical purposes because of this innovation. Ion Torrent sequencing is another technology for sequencing that discovers sequence through the detection of ion of hydrogen which releases during DNA replication. One of the widely used sequencing-by-synthesis technique of the sequencing platform depends on reversible dye terminators. Yet another of the novel technologies, "Solid sequencing (Sequencing by Oligonucleotide Ligation and Detection)" applies a method based on reversible terminators using a ligation method to ascertain the DNA sequence. Throughput and speed of sequencing of DNA have been hugely increased by second-generation sequencing technologies, and now a variety of clinical diagnostics and genomic research applications have opened. Through these technologies, "whole-genome sequencing", "transcriptome profiling, and target sequencing" have led to advancements in genetic variation, different disease studies and personalized medicine. Figure 2 below shows mechanism: -

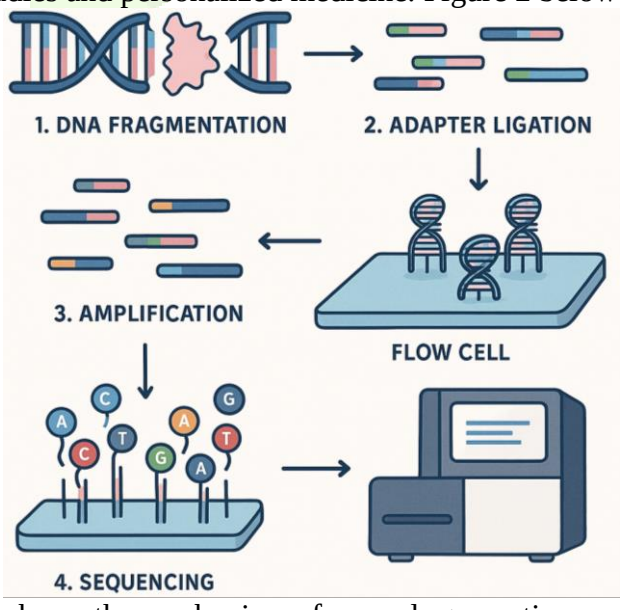

figure 2 shows the mechanism of second- generation sequencing

3. Third- Generation Sequencing:-

In its bid to break the limitations of previous methods, "third-generation sequencing" is the newest DNA sequencing technology. Its capability to read much longer segments of DNA at once makes it unique and enables more understanding of complex genomic regions. PacBio sequencing is one example, with a method called as single-molecule real-time (SMRT) sequencing. Scientists can read DNA strands tens of thousands of bases long with this method by monitoring the addition of fluorescently labelled nucleotides in real time. Oxford Nanopore sequencing is another interesting advance where a single strand of DNA is transferred through an infinitesimal nanopore. Changes in an electric current are monitored to identify the sequence as DNA is passed through. Figure 3 below shows different approaches utilized for analysis of genome and NGS applications, WGS (whole-genome sequencing), WES (whole-exome sequencing), sequencing, ITS (internal transcribed spacer), ChIP (chromatin immunoprecipitation), ATAC (assay for transposase-accessible chromatin), AMR (antimicrobial resistance).

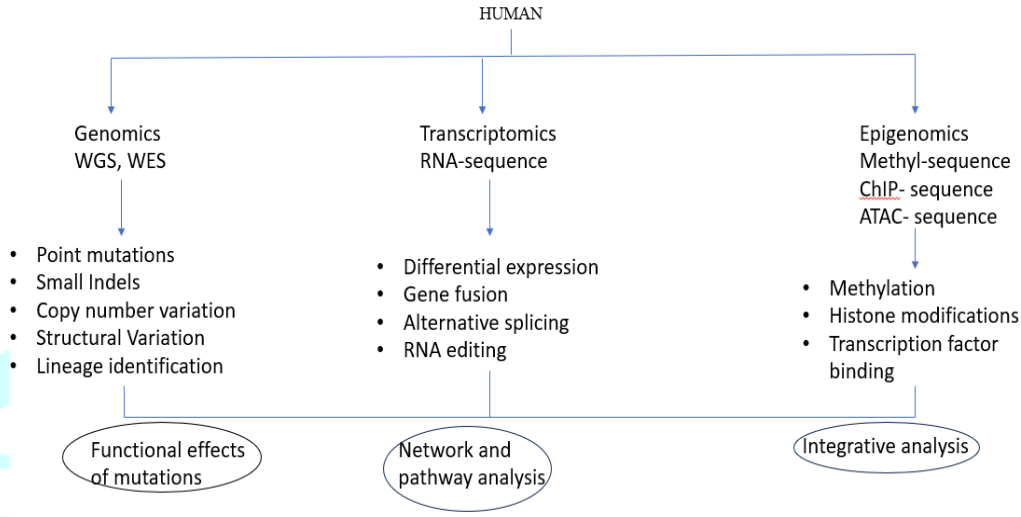

figure 3 shows different approaches for analysis of genomic, transcriptomic and epigenomics

III. NANOPORE SEQUENCING:-

The manner in which we sequence DNA and RNA is being revolutionized by nanopore sequencing, a revolutionary technology. It is unique in that it is able to read extremely long stretches of genetic material, gives real-time results, and even sequences native DNA or RNA without using other means like chemical tagging or amplification. It is thus a more flexible and capable tool than existing and next-generation sequencing technology. Because of these strengths, nanopore sequencing is revealing extremely compelling new opportunities in fields like environmental monitoring, microbial characterization, clinical diagnostics, and personalized medicine. It is one of the most advanced 3rd generation -sequencing technologies, it can quite rightly revolutionize our use and understanding of genetic information itself. Below figure 4 shows the mechanism of nanopore sequencing:-

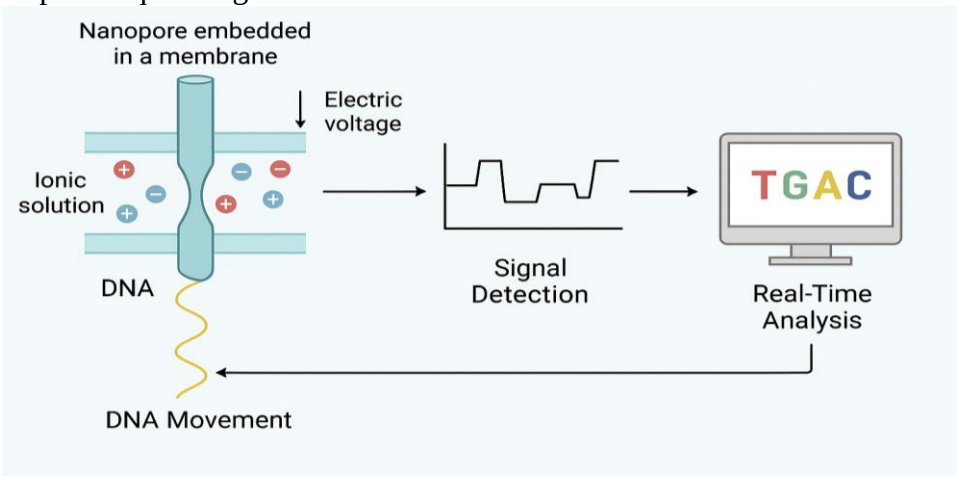

figure 4 shows the mechanism of nanopore sequencing

Nanopore sequencing is of two types:-

1. **Biological nanopore sequencing:-**

Biological nanopores are small pores in lipid membranes, usually created by proteins like porin, MspA, or alpha-haemolysing. A single DNA or RNA strand may move through them due to their ideal size, one to three manometers in diameter. These substances alter the flow of ions, or electricity, through the membrane in various ways as they move through the nanopore. The sequence of nucleotides (the A, T, C and G of Deoxyribonucleic acid or the A, U, C, and G of Ribonucleic acid) is determined by accurately measuring these variations.

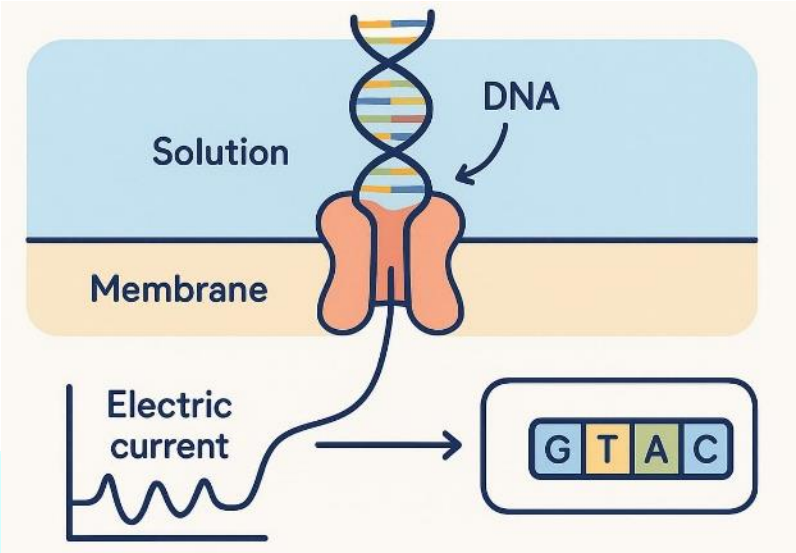

figure 5 shows biological nanopore sequencing

2. **Solid-state Nanopore Sequencing:-**

Graphene, silicon nitride, carbon nanotubes, and other extremely thin films may be used to form solid-state nanopores, which are extremely small pores with diameters a few nanometres in size. The pores themselves range from 1 to 5 nanometres in diameter, and the films themselves are typically a few nanometres thick. They are specifically tailored to allow for efficient and seamless passage through single strands of DNA or RNA. Solid-state nanopores are a great mechanism for genetic material study at the single-molecule level due to their perfection and longevity.

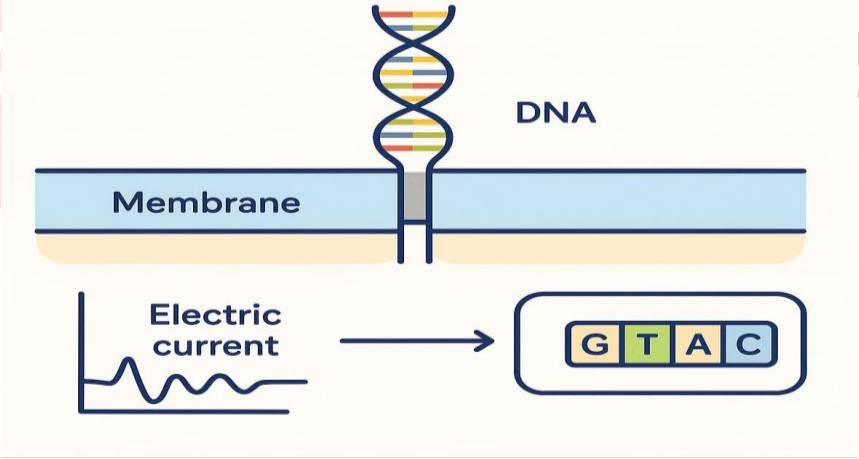

figure 6 shows solid-state nanopore sequencing

IV. EVOLUTION OF TECHNOLOGIES OF SEQUENCING:-

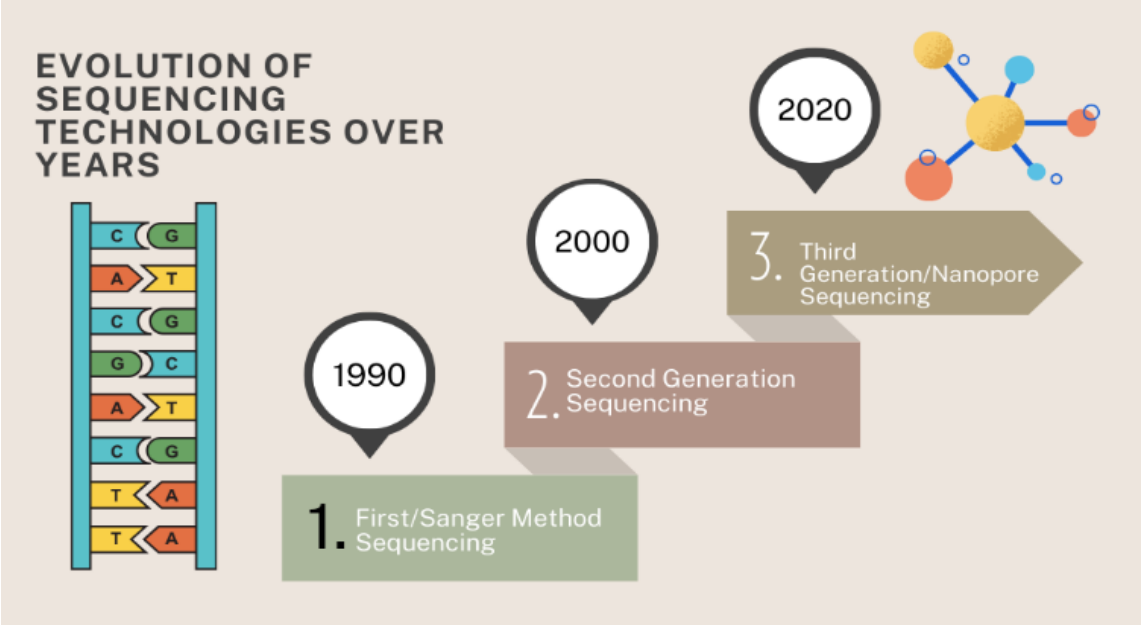

figure 7 shows evolution of sequencing

There has been a tremendous development in sequence technology over the years, with a move from low-throughput manual to efficient, real-time sequencing machines. First-generation sequencing, or Sanger sequencing, invented by Fredrick Sanger, set the ball in motion in the 1970s. This chain termination technique was the industry standard for decades and was instrumental in large-scale projects like the Human Genome Project. Its limitations were low processing rates, low data output, and exorbitant prices.

V. ADVANCES IN SEQUENCING TECHNOLOGIES:-

1. Long- read and short- read sequencing:-

Long-read sequencing is a powerful DNA reading method which can read much longer sequences of DNA than conventional short-read technologies allow. Long- and short-read platforms that are read in smaller 100–300 base pair fragments, these technologies read hundreds or millions of bases in a single read. This enables exploration of content-rich genomic regions that is hard to probe with short reads, including repetitive elements, structural variation, and highly GC-rich regions.

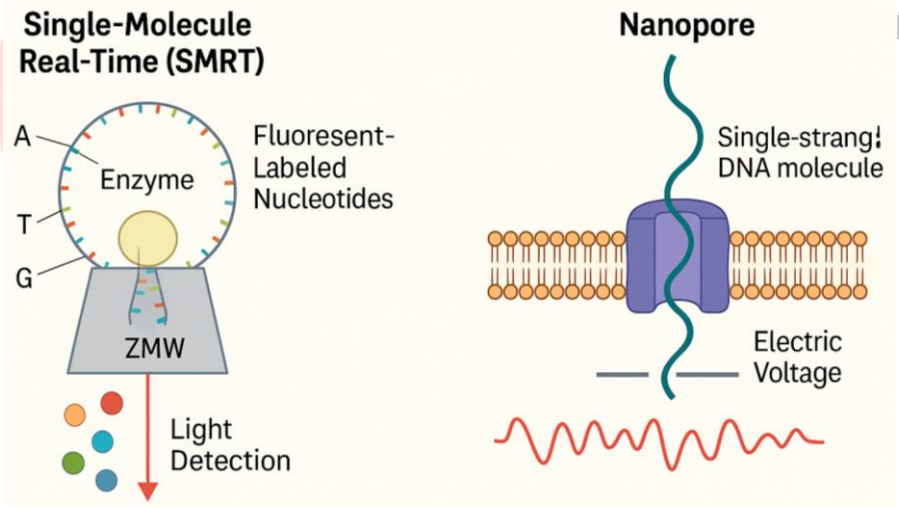

figure 8 shows mechanism of long-read sequencing

A widely used “short-read sequencing” technique commonly applied in next-generation sequencing and it allows quick and thorough examination of DNA. Rather than working with DNA as a whole strand, short fragments (50-300 base pairs) are cut from the long strands. These fragments are joined with pre-made sequences called adapters which assist in the fragments attachment to a solid surface, like a flow cell, while sequencing.

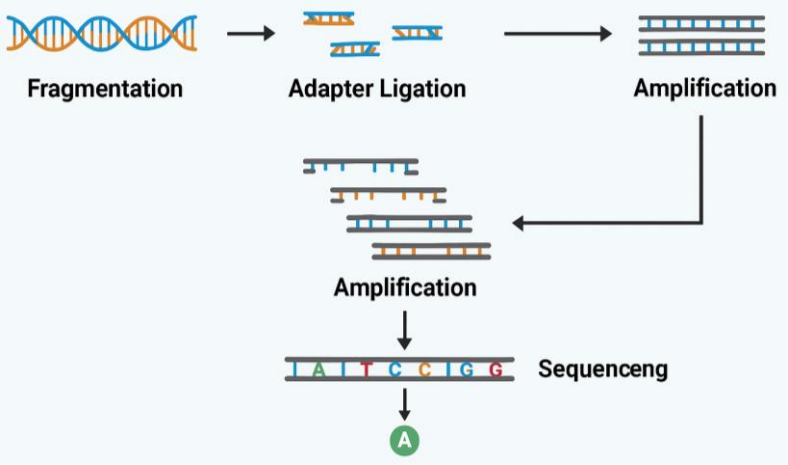

figure 9 shows mechanism of short-read sequencing

2. Single cell sequencing:-

Single-cell fixation unlocks multifaceted biology elements down to individual cells showcasing their vast diversity. The diverse genes in every living being, and how gene expression, DNA methylation, and many other molecular characteristics are controlled at a specific time during a certain time frame, offers new fascinating insights at the single-cell level. It becomes simpler to comprehend developmental, proficient, and even cancer biology functions using single-cell sequencing.

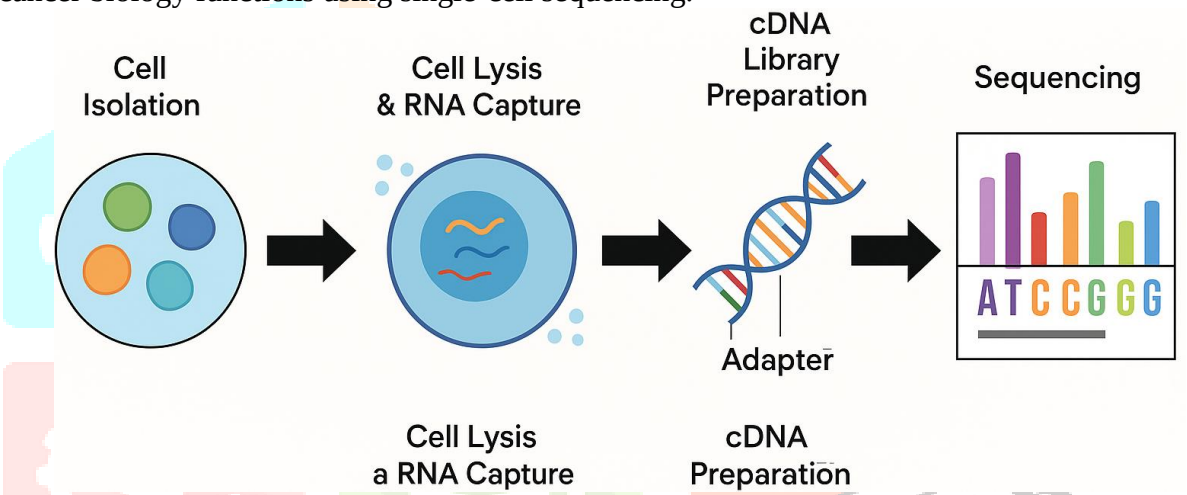

figure 10 shows mechanism of single-cell sequencing

3. RNA sequencing:-

By looking at RNA, a recent technology called RNA-Sequencing, or RNA-Seq, researchers can identify what genes are turned on in a specific cell or tissue. Essentially, the transcriptome gives a snapshot of all the RNA molecules being produced at a given time. This is quite useful for probing the expression of genes, editing or splicing of RNA, and measuring mutations or other changes that could affect the activity of cells.

The step starts with the RNA's extraction from the specific tissue or cells of interest. Reverse transcriptase is an enzyme that first turns R.N.A. into complementary D.N.A., or c.d.n.a., a more stable molecule as R.N.A. is a little brittle. The converted cDNA is then supplied to high-throughput sequencing machines that can read millions of fragments in parallel. The results of sequencing are constructed from nothing or compared of a reference genome that determine which genes are expressed and in what relative quantities.

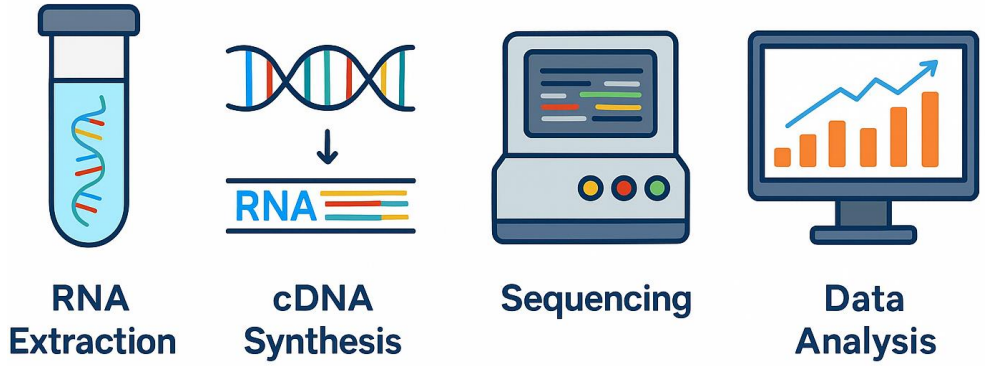

figure 11 shows RNA-seq

VI. APPLICATIONS OF DNA SEQUENCING WITH NANOPORE TECHNOLOGIES:-

1. Real-Time Pathogen Detection:-

Lacking the necessity of culture, nanopore sequencing allows for fast detection of pathogens like bacteria, fungus, and virus from clinical or environmental samples. Researchers and clinicians can quickly detect outbreaks and respond immediately with its real-time output. This is extremely helpful in outbreaks like pandemics or epidemics, where quick diagnosis is required to minimize further disease transmission and implement effective public health intervention.

2. In Cancer Genomics:-

Because nanopore sequencing can identify a broad variety of genetic changes such as mutations, gene fusions, and large structural changes, it has use in the diagnosis and research of cancer. Its capability to better resolve complex genomic areas commonly mutated in cancer is due to its ability to sequence long reads. It can identify epigenetic changes that regulate gene expression in cancers, for example, DNA methylation. These findings contribute to biomarker detection, disease mechanisms, and the development of personalized treatment regimens.

3. Whole Genome Sequencing:-

Nanopore sequencing is currently the most preferred method of whole genome sequencing since it reads much longer DNA fragments than other technologies. This enables scientists to solve complex areas which are hard to assemble using short-read technologies and construct entire genomes with fewer gaps. Nanopore WGS is capable of detecting insertions and deletions, structural variations and other genomic alterations across the entire genome. This is particularly important for studies on microbial genomics, evolution, and genetic diseases. The immediate access of information enables instant access to analysis which is highly important for time sensitive utilizations like clinical diagnostics and epidemic monitoring.

4. Forensic Science: -

Nanopore DNA sequencing is the application of forensic methods in criminal cases that can identify individuals quickly and with high accuracy. This is optimal as it provides the ability to analyze single nucleotide polymorphisms (SNPs), short tandem repeats (STRs), and even degraded DNA samples. DNA is portable; it can be analyzed in situ at crime scenes, improving both response time and data quality. Nanopore technology can also be used to sequence Y-chromosome markers and mitochondrial DNA to determine kinship and ancestry. Its ability to perform real-time sequencing and long-read sequencing enables it to disentangle complex genetic profiles even from contaminated or mixed DNA samples.

5. In agriculture and food safety: -

Nanopore sequencing has various uses like infection identification, food authentication, and health improvement of crops and livestock in food security and agriculture. Genome sequencing of the plant plays a major role in plant breeding programs for improving crop yield and drought resistance. It aids in early disease detection in plants and animals so that they can be stopped from spreading into an epidemic. It prevents adulteration of meat and seafood products by diagnosing microbiological adulterants and authenticating food origin. It is very beneficial for assisting consumer health protection and sustainable agriculture and is portable and real-time. These features make it most ideal for testing in processing plants, farms, and markets.

VII. CONCLUSION:-

At last but not the least I would like to thank my guide Ms. Ritika Sharma for giving me such a interesting topic in which I gained some in-depth knowledge about the Deoxyribonucleic Acid sequencing and the progression of DNA sequencing from Sanger's technique to today's nanopore technology marks a revolutionary period in the science of genomics. Through the capacity to sequence long stretches of DNA or RNA in real time, without the need for amplification, nanopore sequencing is unparalleled in speed, accuracy, cost, and portability. Its adaptability across a range of applications from the laboratory and clinic to far-flung field camps and even for space exploration is unparalleled. Among its various applications, i.e. forensic identification, whole-genome sequencing, cancer genomics, rapid pathogen identification, and agricultural biotechnology. Single-molecule sequencing is enabled by the technical platform of biological and solid-state nanopores. We are also discovering complex genomic architectures and gene expression due to advances like long-read technologies, RNA-seq, and single-cell sequencing. Collectively, nanopore sequencing is not

only enhancing existing techniques, but also broadening the scope of genetic research and its applied applications, opening doors to an affordable, effective, and personalized future genomic science.

REFERENCES:-

[1] "Warburton PE, Sebra RP." Explains about the long- read sequencing DNA and its advances in the recent and remaining challenges. It also shows the periodic review of genomics and mortal genetics. 2023 Aug 25; 24(1) 109- 32. (University of Hong Kong on 2024-12-20)
[2] Dorey, A., & Howorka, S. (2024). In this study, the constituents and mechanisms of nanopore sequencing platforms are described with emphasis on single-molecule proteomics applications. Nature Chemistry, 16(3), 314–334.
[3] "Alphey L." explains about sequencing of DNA? In DNA Sequencing 2023 Jun 14(pp. 1- 9). Garland Science.
[4] Goodwin, S., McPherson, J. D., & McCombie, W. R. (2016). An analysis of ten years of next-generation sequencing developments and their transformative impact on genomics. Nature Reviews Genetics, 17(6), 333–351.
[5] Tax, S. E., & Myers, R. M. (2016). A summary overview of next-generation sequencing technology platforms: past, present, and future. Annual Review of Genomics and Human Genetics, 17, 95–115.
[6] Amarasinghe, S. L., Su, S., Dong, X., Zappia, L., Ritchie, M. E., & Gouil, Q. (2020). This article reports on the possibilities and challenges with long-read data analysis in current genomics. Genome Biology, 21, Article 30.
[7] Kumar, K. R., Cowley, M. J., & Davis, R. L. (2019). Emerging Sequencing Technologies and their Integration in Medical Diagnostics Semin Thromb Hemost. 2019 Oct;45(6):661–673.
[8] Satam, H., Joshi, K., Mangrolia, U., Waghoo, S., Zaidi, G., Rawool, S., et al. (2023). This paper reviews recent trends and developments in next generation sequencing platforms. Biology, 12(7), Article 997.
[9] Searle et al. (2023) analyzes the feasibility of studying epigenetic modifications of DNA through third generation sequencing platforms. Nature communications, 13(1), 1–3
[10] Springer US published a chapter in the book "High Throughput Gene Screening: Methods and Protocols" titled "Next-generation sequencing technologies, methods and applications: The evolution," written by Akintunde O, Tucker T, and Carabetta VJ, which details their advances.
[11] Pugh, J. (2023). This chapter presents the principles and protocols of nanopore sequencing, such as the applications in use today and technological development. In Nanopore Sequencing: Methods and Protocols (pp. 3–14).
[12] Mahajan-Mallakmir S, Mahajan S, Lokur AS, Chaughule RS. Next-generation sequencing and solid-state nanopores. InApplications of Nanotechnology in Microbiology 2024 Feb 6 (pp. 387-405). Cham: Springer Nature Switzerland.
[13] MacKenzie, M., & Argyropoulos, C. (2023). Presents an overview of the evolution, present capabilities, and future potential of nanopore sequencing. Micromachines, 14(2), 459.
[14] Zheng, P., Zhou, C., Ding, Y., Liu, B., Lu, L., Zhu, F., & Duan, S. (2023). Focuses on the practical use cases of nanopore sequencing in the medical and research fields. MedComm, 4(4), e316.
[15] Chen, P., Sun, Z., Wang, J., Liu, X., Bai, Y., Chen, J., et al. (2023). Studies the development and use of portable nanopore sequencing devices. Frontiers in Microbiology, 14, 1043967.
[16] Bracamonte, A. G. (2023). Details how nanotechnology is re-shaping sequencing techniques and developing biosensor technology. Biosensors, 13(2), 260.
[17] Abdi, G., Tarighat, M. A., Jain, M., Tendulkar, R., Tendulkar, M., & Barwant, M. (2024). Evaluates the potential of next-generation sequencing technologies to transform genomic analysis. In Advances in Bioinformatics (pp. 1–33). Springer Nature Singapore.
[18] Zhang, T., Li, H., Jiang, M., Hou, H., Gao, Y., Li, Y., et al. (2024). A review of the recent advances in nanopore sequencing and its coming of age in genomics. DOI: doi.org/10.1016/j.jgg.2023.06.003.
[19] Cuber, P., Chooneea, D., Geeves, C., Salatino, S., Creedy, T. J., Griffin, C., et al. (2023). Assessment of the use of third generation sequencing technologies for DNA barcoding: an ecological genetics analysis. Ecological Genetics and Genomics. 28 (2023) 100181.
[20] Mandlik, J. S., Patil, A. S., & Singh, S. (In press). Next generation sequencing: the opportunities it enables for genomic services and core platforms. 16 (Suppl 1), S41–S45.
[21] Rodriguez R, Krishnan Y. The chemistry of next-generation sequencing. Nature biotechnology. 2023 Dec;41(12):1709-15.
[22] Katsuya Y. Current and future trends in whole genome sequencing in cancer. Cancer Biology & Medicine. 2024 Feb 15;21(1):16.

[23] Wang X. Next-generation sequencing data analysis. CRC Press; 2023 Jul 6.
[24] Lian D, Tang Q, Wu L, Liao X. Using targeted second-generation sequencing technique to guide clinical diagnosis and the effect of medication on the therapeutic effect and prognosis of respiratory tract infection in children: an observational study. Medicine. 2024 May 3;103(18):e37757.
[25] Marudamuthu B, Sharma T, Purru S, Soam SK, Rao CS. Next-generation sequencing technology: a boon to agriculture. Genetic Resources and Crop Evolution. 2023 Feb;70(2):353-72.
[26] Hassan S, Bahar R, Johan MF, Mohamed Hashim EK, Abdullah WZ, Esa E, Abdul Hamid FS, Zulkafli Z. Next-generation sequencing (NGS) and third-generation sequencing (TGS) for the diagnosis of thalassemia. Diagnostics. 2023 Jan 19;13(3):373.
[27] Liao Y, Liu Z, Zhang Y, Lu P, Wen L, Tang F. High-throughput and high-sensitivity full-length single-cell RNA-seq analysis on third-generation sequencing platform. Cell Discovery. 2023 Jan 11;9(1):5.
[28] Hu T, Chitnis N, Monos D, Dinh A. Next-generation sequencing technologies: An overview. Human immunology. 2021 Nov 1;82(11):801-11.
[29] Xiao T, Zhou W. The third generation sequencing: the advanced approach to genetic diseases. Translational pediatrics. 2020 Apr;9(2):163.
[30] Branton D, Deamer DW, Marziali A, Bayley H, Benner SA, Butler T, Di Ventra M, Garaj S, Hibbs A, Huang X, Jovanovich SB. The potential and challenges of nanopore sequencing. Nature biotechnology. 2008 Oct;26(10):1146-53.
[31] Deamer D, Akeson M, Branton D. Three decades of nanopore sequencing. Nature biotechnology. 2016 May;34(5):518-24.
[32] Wang Y, Yang Q, Wang Z. The evolution of nanopore sequencing. Frontiers in genetics. 2015 Jan 7;5:449.
[33] Maitra RD, Kim J, Dunbar WB. Recent advances in nanopore sequencing. Electrophoresis. 2012 Dec;33(23):3418-28.
[34] Rhee M, Burns MA. Nanopore sequencing technology: nanopore preparations. TRENDS in Biotechnology. 2007 Apr 1;25(4):174-81.
[35] Wang Y, Zhao Y, Bollas A, Wang Y, Au KF. Nanopore sequencing technology, bioinformatics, and applications. Nature biotechnology. 2021 Nov;39(11):1348-65.
[36] Ying YL, Hu ZL, Zhang S, Qing Y, Fragasso A, Maglia G, Meller A, Bayley H, Dekker C, Long YT. Nanopore-based technologies beyond DNA sequencing. Nature nanotechnology. 2022 Nov;17(11):1136-46.
[37] Lin B, Hui J, Mao H. Nanopore technology and its applications in gene sequencing. Biosensors. 2021 Jun 30;11(7):214.
[38] Sakamoto, Y.; Sereewattanawoot, S.; Suzuki, A. A new era of long-read sequencing for cancer genomics. J. Hum. Genet. 2020, 65, 3–10. [CrossRef]
[39] Holley, R.W.; Apgar, J.; Everett, G.A.; Madison, J.T.; Marquisee, M.; Merrill, S.H.; Penswick, J.R.; Zamir, A. Structure of a Ribonucleic Acid. Science 1965, 147, 1462–1465. [CrossRef]
[40] Heather, J.M.; Chain, B. The sequence of sequencers: The history of sequencing DNA. Genomics 2016, 107, 1–8. [CrossRef]
[41] Barba, M.; Czosnek, H.; Hadidi, A. Historical Perspective, Development and Applications of Next-Generation Sequencing in Plant Virology. Viruses 2013, 6, 106–136. [CrossRef]
[42] Sanger, F.; Nicklen, S.; Coulson, A.R. DNA sequencing with chain-terminating inhibitors. Proc. Natl. Acad. Sci. USA 1977, 74, 5463–5467. [CrossRef]
[43] Schuster, S.C. Next-generation sequencing transforms today's biology. Nat. Methods 2008, 5, 16–18. [CrossRef]
[44] Pervez, M.T.; Hasnain, M.J.U.; Abbas, S.H.; Moustafa, M.F.; Aslam, N.; Shah, S.S.M. A Comprehensive Review of Performance of Next-Generation Sequencing Platforms. BioMed Res. Int. 2022. [CrossRef]
[45] Slatko, B.E.; Gardner, A.F.; Ausubel, F.M. Overview of Next-Generation Sequencing Technologies. Curr. Protoc. Mol. Biol. 2018, 122, e59. [CrossRef]
[46] Drmanac, R.; Sparks, A.B.; Callow, M.J.; Halpern, A.L.; Burns, N.L.; Kermani, B.G.; Carnevali, P.; Nazarenko, I.; Nilsen, G.B.; Yeung, G.; et al. Human Genome Sequencing Using Unchained Base Reads on Self-Assembling DNA Nanoarrays. Science 2010, 327, 78–81. [CrossRef] [PubMed]
[47] Xu,Y.; Lin, Z.; Tang, C.; Tang, Y.; Cai, Y.; Zhong, H.; Wang, X.; Zhang, W.; Xu, C.; Wang, J.; et al. A new massively parallel nanoball sequencing platform for whole exome research. BMC Bioinform. 2019, 20, 153. [CrossRef] [PubMed]
[48] Jain, M.; Olsen, H.E.; Paten, B.; Akeson, M. The Oxford Nanopore MinION: Delivery of nanopore sequencing to the genomics community. Genome Biol. 2016, 17, 239. [CrossRef]

[49] Costain, G.; Cohn, R.D.; Scherer, S.W.; Marshall, C.R. Genome sequencing as a diagnostic test. Can. Med. Assoc. J. 2021, 193, E1626–E1629. [CrossRef]
[50] Logsdon, G.A.; Vollger, M.R.; Eichler, E.E. Long-read human genome sequencing and its applications. Nat. Rev. Genet. 2020, 21, 597–614. [CrossRef]