

## **Technical Review**

**Open Access** 

# Portable Nanopore Sequencing Technology: A Revolutionary Progress in Bioinformatics

#### Jim Manson 🔀

The HITAR institute Canada, Vancouver, BC, Canada
Corresponding author email: <u>Jim.mason@hitar.org</u>
Genomics and Applied Biology, 2024, Vol.15, No.1 doi: <u>10.5376/gab.2024.15.0004</u>
Received: 14 Feb., 2024
Accepted: 20 Feb., 2024
Published: 28 Feb., 2024
Copyright © 2024 Manson, This is an open access article published under the terms of the Creative Commons Attribution License, which permits
unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

#### Preferred citation for this article:

Manson J., 2024, Portable nanopore sequencing technology: a revolutionary progress in bioinformatics, Genomics and Applied Biology, 15(1): 22-26 (doi: 10.5376/gab.2024.15.0004)

Abstract With the rapid development of genomic science, portable nanopore sequencing technology has become a revolutionary progress in the field of bioinformatics due to its unique portability, real-time capabilities, and high-throughput sequencing capacity. This paper comprehensively analyzes the principles and characteristics of portable nanopore sequencing technology and its wide applications in environmental monitoring, epidemic prevention and control, and on-site rapid diagnosis. Through practical cases, it demonstrates how this technology provides efficient and real-time new solutions for biological research and public health emergency response. Meanwhile, it discusses the challenges faced by this technology, including data accuracy, sequencing costs, and data processing issues, and looks forward to the future development trends and application prospects. Portable nanopore sequencing technology not only promotes research in the field of bioinformatics but also has a profound impact on the formulation of public health monitoring and disease control strategies.

**Keywords** Portable nanopore sequencing; Bioinformatics; Environmental monitoring; Epidemic prevention and control; Rapid diagnosis; Public health emergency response

#### Introduction

Since the development of the first generation of DNA sequencing technology by Frederick Sanger in 1977, genome sequencing technologies have evolved rapidly. From the initial Sanger sequencing to the second generation of high-throughput sequencing (HTS) technologies (Pareek et al., 2011), and to the recently developed third generation sequencing technologies such as single-molecule real-time sequencing (SMRT) and nanopore sequencing technology (Yanhu et al., 2015), there have been qualitative leaps in the speed, cost, and accuracy of genome sequencing. The advancements in genome sequencing technologies have not only accelerated research in life sciences, facilitated the implementation of precision medicine and personalized treatments, but also shown tremendous potential applications in fields such as agricultural improvement, microbiology, and environmental science (Zheng et al., 2023).

With the advancement of technology and increasing research demands, higher requirements have been placed on genome sequencing technologies, particularly in terms of flexibility, speed, and portability (Chen et al., 2023). The advent of portable nanopore sequencing technology, which allows for direct sequencing of DNA and RNA using miniaturized devices, enables its use outside of the laboratory and provides real-time sequencing data (Samarakoon et al., 2020). The development of this technology marks a new era in genomics research, making it possible to perform genome sequencing in field environments, clinical settings, and even in space (Pomerantz et al., 2018).

Portable nanopore sequencing technology has attracted widespread attention in the field of bioinformatics due to its unique technical advantages. Its innovation lies not only in the portability of the equipment but also in its ability to provide long reads, which are crucial for solving complex genomic regions assembly, identifying repetitive sequences, and detecting epigenetic modifications. Additionally, the capability of this technology to analyze data in real-time offers new solutions for rapid response to public health events, environmental monitoring, and on-site diagnostics, showcasing its broad application prospects across multiple fields.



# 1 Overview of Portable Nanopore Sequencing Technology

# 1.1 Principle of the nanopore technology

Portable nanopore sequencing technology is a revolutionary method of genome sequencing that utilizes tiny channels (nanopores) to detect the DNA or RNA sequences of individual molecules. Its working principle is based on guiding single-stranded DNA or RNA molecules through a nanopore embedded in a membrane made of a resistive material. As the molecule passes through the nanopore, it causes changes in the electrical current. These changes are specifically associated with the nucleotide sequence passing through the pore, thereby allowing real-time sequence identification of the molecules passing through the nanopore (Cummings et al., 2017).

During the sequencing process, a voltage is applied across the membrane containing the nanopore, prompting the charged molecules to pass through the pore. As the molecules pass through the nanopore, the changes in current caused by the nucleotides are detected and recorded. By analyzing the patterns of these electrical signals, the nucleotide sequence of the molecule can be determined (Figure 1).



Figure 1 Schematic of DNA sequencing using a nanopore. DNA passing through a nanopore membrane with electrical signal generation and base identification (Cummings et al., 2017)

# **1.2 Technical features**

The main advantages of portable nanopore sequencing technology include its compact size, portability, independence from biochemical reagents, and the ability to perform readings using physical methods directly. This technology is less complex, cost-effective, and capable of sequencing purified genomic DNA, PCR amplicons, cDNA samples, or RNA in real-time and rapidly (Cummings et al., 2017). Additionally, this technology also enables single-molecule sequencing without PCR (Chen et al., 2023).

## 1.3 Technology development

Since the first observation of nucleic acids translocating through nanopores in the 1990s, nanopore sequencing technology has evolved from laboratory experiments to commercial tools. Although the current technology has not yet achieved single-nucleotide resolution sequencing of deoxyribonucleic acid, there have been multiple reports using  $\alpha$ -hemolysin protein nanopores for basic DNA analysis, as well as the manufacture of various synthetic nanopores. The commercialization of these technologies has begun, turning nanopore sequencing devices into an inexpensive, fast genomic tool that not only allows for reading lengths exceeding 100 kb but also features portability, low cost, and speed (Rhee and Burns, 2006; Bayley, 2015).

Portable nanopore sequencing technology has shown its potential in multiple fields, including microbial diversity research, disease diagnostics, drug target discovery, species conservation, SARS-CoV-2 detection, and applications in microgravity environments (Benítez-Páez et al., 2015; McIntyre et al., 2015; Chen et al., 2023). Furthermore, this technology has also demonstrated potential in forensic analysis, potentially becoming a viable solution for small to medium-sized forensic laboratories (Hall et al., 2020). As nanopore sequencing technology continues to improve and application tools are integrated, its incorporation into laboratory or remote field workflows will further simplify the sequencing process (Pomerantz et al., 2018; Hall et al., 2020).



# 2 Applications of Portable Nanopore Sequencing Technology

The development of portable nanopore sequencing technology has brought revolutionary advances to the field of bioinformatics, especially showing its unique value and broad application prospects in environmental monitoring, epidemic prevention and control, and onsite rapid diagnosis. In environmental monitoring, portable nanopore sequencing technology has been used to study microbial diversity. For example, studies have shown that the MinION<sup>™</sup> system can analyze microbial communities through 16S rRNA gene sequencing, allowing for classification and measurement of relative abundance at the species level (Benítez-Páez et al., 2015; Benítez-Páez and Sanz, 2017). This is very valuable for understanding the composition and dynamics of microbes in complex ecosystems.

In the area of epidemic prevention and control, the technology has proven to be able to quickly and accurately identify and monitor pathogens. For instance, MinION<sup>TM</sup> has been used for the detection and surveillance of pathogen outbreaks, as well as the study of human genome variations (Benítez-Páez and Sanz, 2017; Magi et al., 2017). This rapid sequencing capability is crucial for responding to public health emergencies.

In onsite rapid diagnostics, portable nanopore sequencing technology provides a method for species identification under field conditions. Research indicates that using the MinION device and portable laboratory equipment, researchers can generate high-accuracy consensus sequences less than 24 hours after collecting samples, thereby achieving species resolution (Pomerantz et al., 2018). This is significant for conservation efforts and speeding up species identification in research facilities in developing countries.

Overall, portable nanopore sequencing technology demonstrates great application potential in environmental monitoring, epidemic prevention and control, and onsite rapid diagnostics. It not only accelerates scientific research but also plays a crucial role in biodiversity conservation, public health emergency response, and enhancing research capabilities in developing countries.

# **3** Challenges and Prospects of Technology

Portable nanopore sequencing technology is a cutting-edge genomics technology based on single-molecule detection, which identifies nucleotide sequences by monitoring the changes in electrical current as DNA molecules pass through a nanopore. Despite this technology's significant potential in genetic testing, it still faces a range of technical challenges.

# 3.1 Technical challenges

The challenges of nanopore sequencing include effectively detecting signals from specific bases, controlling the size and surface characteristics of the nanopore, and regulating the speed and behavior of DNA molecules as they shuttle through. A key challenge is achieving high-quality nanopore fabrication, which requires the assistance of modern micro and nano-fabrication technologies (Liu et al., 2016). Additionally, even though Oxford Nanopore Technologies (ONT) has made notable advancements in the past two years, using nanopore data to detect small variations remains challenging. Currently, it requires combining with complementary short-read sequencing to reduce the inherent biases of nanopore sequencing technology (Magi et al., 2017).

## **3.2 Solutions**

To overcome these challenges, researchers have developed a multitude of algorithms and tools for base calling, data processing, read mapping, de novo assembly, and variant detection. The development of these tools and algorithms helps to enhance the efficiency of nanopore data utilization, especially in genome de novo assembly and structural variation discovery, achieving unprecedented accuracy and resolution (Magi et al., 2017). The research field of solid-state nanopore sequencing is also continuously expanding in terms of materials, device assembly, manufacturing methods, the shuttling process, and specific challenges (Yang et al., 2013).



#### **3.3 Prospects**

As a fourth-generation sequencing technology, nanopore sequencing offers advantages such as low cost, long reads, and ease of integration onto chips. With the rapid development of semiconductor technology, it is now possible to manufacture high-speed, high-throughput nanopore gene sequencing microchips (Chen et al., 2014). Furthermore, the latest technological innovations of Oxford Nanopore Technologies (ONT) hold promise for addressing the implementation challenges in clinical laboratories, such as high costs, lengthy result times, and the demand for specialized technical and bioinformatics expertise. The ONT sequencing platform has become an attractive option for clinical laboratories due to its low cost, fast turnaround time, and user-friendly bioinformatics workflow (Petersen et al., 2019).

In summary, despite facing a series of challenges, portable nanopore sequencing technology still has a very broad prospect in genomic research and clinical diagnostics. As the technology continues to advance and optimize, these challenges will be gradually overcome, and nanopore sequencing is expected to become an important tool for future genetic sequencing.

#### References

Bayley H., 2015, Nanopore sequencing: from imagination to reality, Clinical chemistry, 61(1): 25-31.

https://doi.org/10.1373/clinchem.2014.223016

Benítez-Páez A., and Sanz Y., 2017, Multi-locus and long amplicon sequencing approach to study microbial diversity at species level using the MinION™ portable nanopore sequencer, GigaScience, 6: 1-12.

https://doi.org/10.1101/117143.

Benítez-Páez A., Portune K., and Sanz Y., 2015, Species-level resolution of 16S rRNA gene amplicons sequenced through the MinION™ portable nanopore sequencer, GigaScience, 5.

https://doi.org/10.1186/s13742-016-0111-z

- Chen P., Sun Z., Wang J., Liu X., Bai Y., Chen J., Liu A., Qiao F., Chen Y., Yuan C., Sha J., Zhang J., Xu L., and Li, J., 2023, Portable nanopore-sequencing technology: Trends in development and applications, Frontiers in Microbiology, 14. <u>https://doi.org/10.3389/fmicb.2023.1043967</u>
- Chen W., Luo J., and Zhao C., 2014, Solid-State Nanopore: The Next-Generation Sequencing Technology——Principles, Fabrication and Challenges, 44: 649-662

https://doi.org/10.1360/N052014-00091

- Cummings P., Olszewicz J., and Obom K., 2017, Nanopore DNA Sequencing for Metagenomic Soil Analysis, Journal of Visualized Experiments: JoVE <a href="https://doi.org/10.3791/55979">https://doi.org/10.3791/55979</a>
- Hall C., Zascavage R., Sedlazeck F., and Planz J., 2020, Potential applications of nanopore sequencing for forensic analysis, Forensic Science Review, 32(1): 23-54.
- Liu Z., Wang Y., Deng T., and Chen Q., 2016, Solid-State Nanopore-Based DNA Sequencing Technology, Journal of Nanomaterials, 5284786. https://doi.org/10.1155/2016/5284786
- Magi A., Semeraro R., Mingrino A., Giusti B., and D'Aurizio R., 2017, Nanopore sequencing data analysis: state of the art, applications and challenges, Briefings in Bioinformatics, 19(6): 1256-1272. <u>https://doi.org/10.1093/bib/bbx062</u>
- McIntyre A., Rizzardi L., Yu A., Rosen G., Alexander N., Botkin D., John K., Castro-Wallace S., Burton A., Feinberg A., and Mason C., 2015, Nanopore Sequencing in Microgravity, bioRxiv. <u>https://doi.org/10.1101/032342</u>
- Pareek C., Smoczyński R., and Tretyn A., 2011, Sequencing technologies and genome sequencing, Journal of Applied Genetics, 52: 413-435. https://doi.org/10.1007/s13353-011-0057-x
- Petersen L., Martin I., Moschetti W., Kershaw C., and Tsongalis G., 2019, Third-generation sequencing in the clinical laboratory: exploring the advantages and challenges of nanopore sequencing, Journal of Clinical Microbiology, 58. https://doi.org/10.1128/JCM.01315-19

```
Pomerantz A., Peñafiel N., Arteaga A., Bustamante L., Pichardo F., Coloma L., Barrio-Amorós C., Salazar-Valenzuela D., and Prost S., 2018, Real-time DNA barcoding in a rainforest using nanopore sequencing: opportunities for rapid biodiversity assessments and local capacity building, GigaScience, 7. 
https://doi.org/10.1093/gigascience/giy033
```

- Rhee M., and Burns M., 2006, Nanopore sequencing technology: research trends and applications, Trends in biotechnology, 24(12): 580-586. https://doi.org/10.1016/J.TIBTECH.2006.10.005
- Samarakoon H., Punchihewa S., Senanayake A., Hammond J., Stevanovski I., Ferguson J., Ragel R., Gamaarachchi H., and Deveson I., 2020, Genopo: a nanopore sequencing analysis toolkit for portable Android devices, Communications Biology, 3. <u>https://doi.org/10.1038/s42003-020-01270-z</u>



Yang Y., Liu R., Xie H., Hui Y., Jiao R., Gong Y., and Zhang Y., 2013, Advances in nanopore sequencing technology, Journal of nanoscience and nanotechnology, 13(7): 4521-4538.

https://doi.org/10.1166/JNN.2013.7756

- Yanhu L., Lu W., and Li Y., 2015, The principle and application of the single-molecule real-time sequencing technology, Yi chuan = Hereditas, 37(3): 259-268. https://doi.org/10.16288/j.yczz.14-323
- Zheng P., Zhou C., Ding Y., Liu B., Lu L., Zhu F., and Duan S., 2023, Nanopore sequencing technology and its applications, MedComm, 4. https://doi.org/10.1002/mco2.316