

## Unravelling the Mysteries of Plant Pathogens: Cutting-Edge Whole Genome Sequencing Techniques and their Recent Advances

Biradar Pratiksha Dnyanoba<sup>1</sup> and Patil Lalit Pandurang<sup>2</sup>

<sup>1</sup>Ph.D. Scholar, Department of Plant Pathology, Mahatma Phule Krishi Vidyapeeth, Rahuri (M.S.)

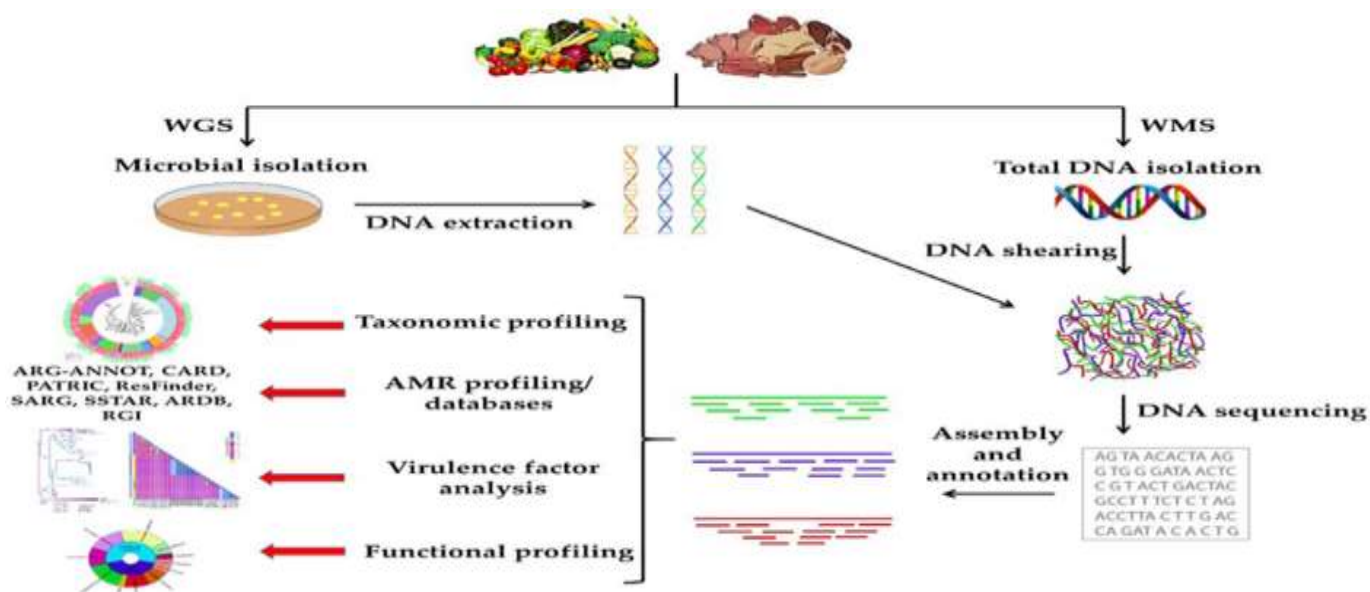
<sup>2</sup>Ph.D. Scholar, Department of Plant Pathology, Indian Agricultural Research Institute, Pusa, New Delhi

### SUMMARY

Plant pathogens are microorganisms that cause diseases in plants, leading to severe economic losses and food insecurity worldwide. Whole genome sequencing (WGS) of plant pathogens has become an essential tool in understanding their biology, evolution, and developing control strategies. In this article, we will explore various methods and new techniques used for whole genome sequencing of plant pathogens.

### INTRODUCTION

Plant pathogens pose significant threats to global agriculture, inciting diseases that devastate crops and trigger substantial economic losses, ultimately impacting food security. In recent years, whole genome sequencing (WGS) has emerged as a pivotal tool in comprehending the biology, evolution, and devising effective control strategies against these elusive adversaries. By delving deep into the genetic makeup of plant pathogens, researchers have unlocked invaluable insights into their molecular intricacies, virulence mechanisms, and host interactions. In this article, we embark on a journey through various cutting-edge methods and novel techniques employed in whole genome sequencing of plant pathogens, shedding light on the groundbreaking discoveries that hold the promise of transforming plant pathology and safeguarding global agriculture.



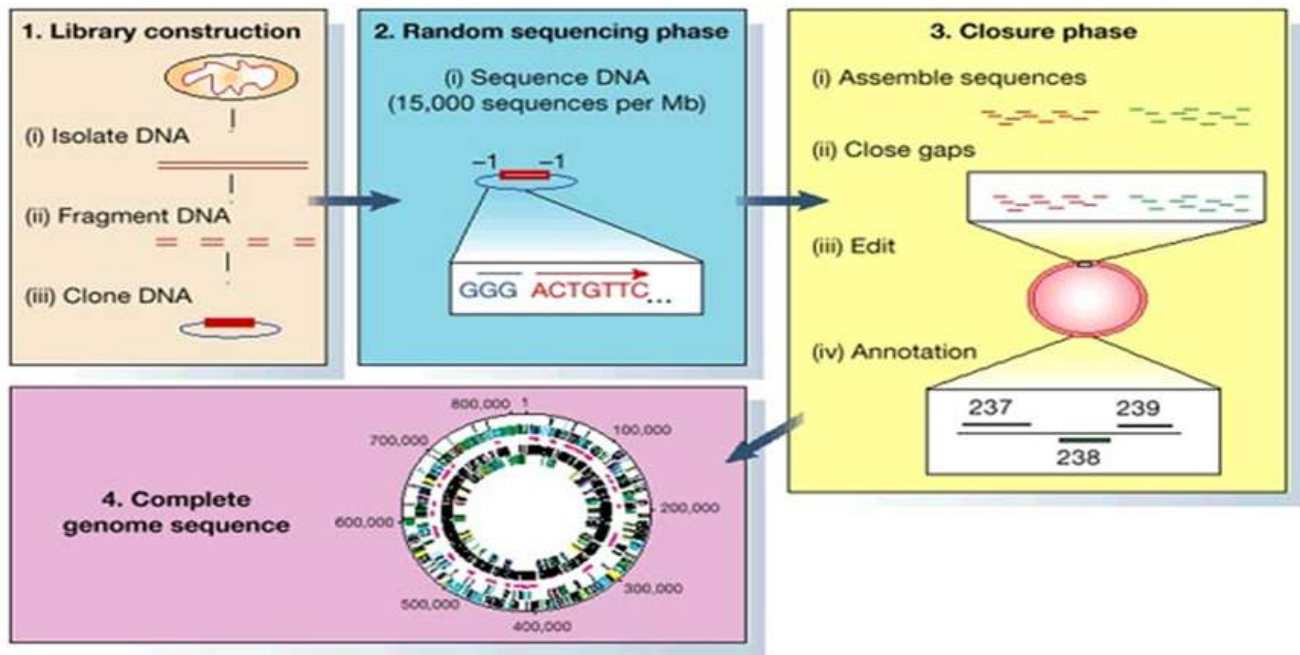
### A. Methods for Whole Genome Sequencing of Plant Pathogens:

**1. Shotgun sequencing:** In shotgun sequencing, the DNA is randomly fragmented, and the resulting fragments are sequenced. The sequencing reads are then assembled into contiguous sequences (contigs), and the contigs are further assembled into complete genome sequences. This method is widely used for sequencing bacterial genomes.

**2. Linked-read sequencing:** Linked-read sequencing is a method that uses barcoded beads to link long fragments of DNA from individual cells or tissue samples. The barcodes allow the identification of which reads belong to the same molecule, enabling the reconstruction of phased haplotypes. This method is useful for sequencing complex plant genomes.

**3. Chromosome conformation capture sequencing:** Chromosome conformation capture sequencing (Hi-C) is a method that uses cross-linking and ligation to capture the spatial proximity of DNA fragments within the

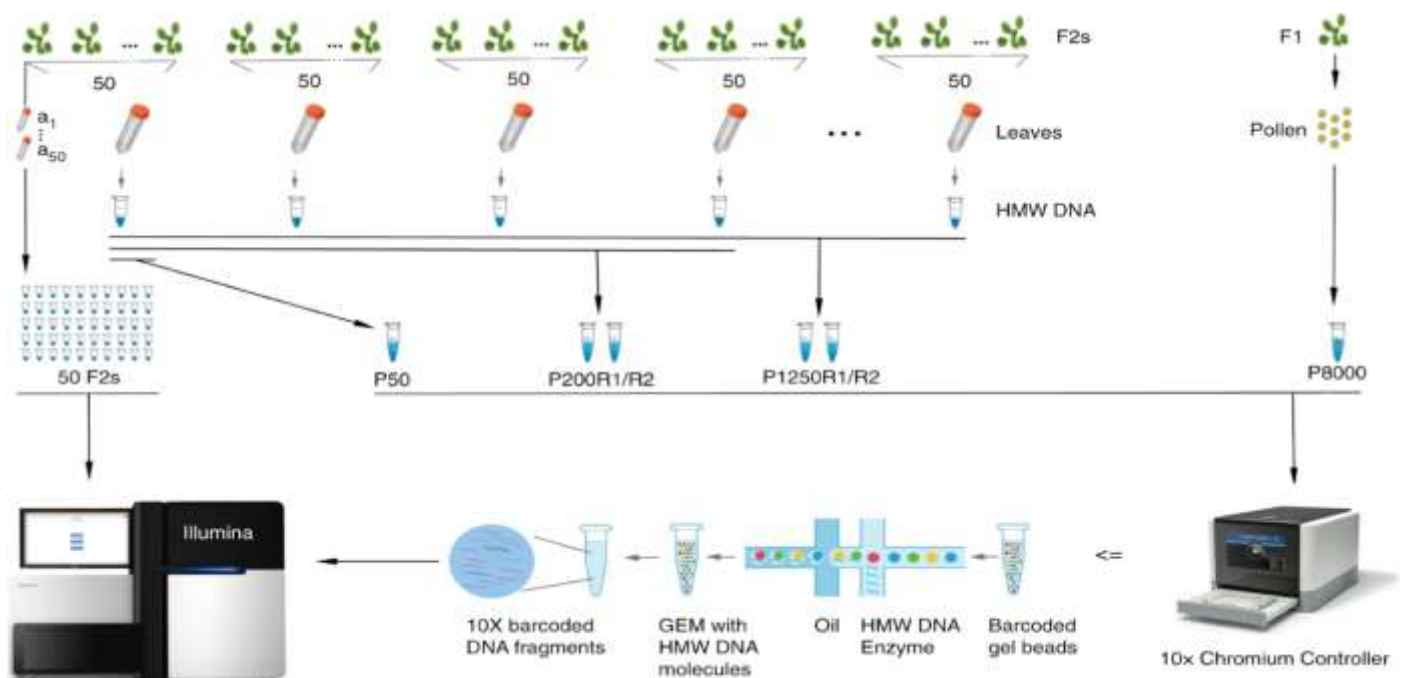
nucleus. Hi-C can be used to assemble the genome sequence of complex plant pathogens by generating scaffolds that span long-range interactions between genomic regions.



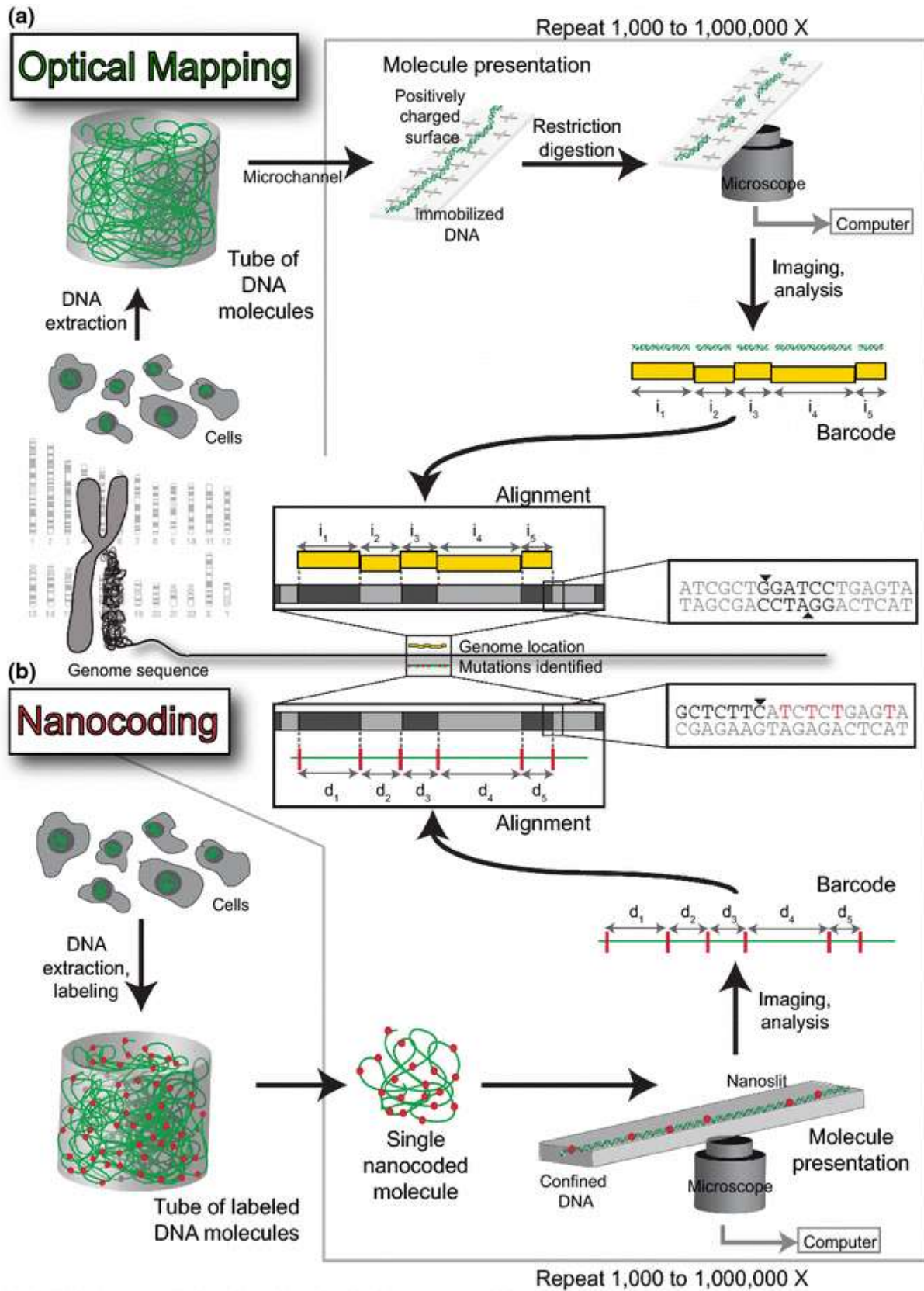
**B. New Techniques for Whole Genome Sequencing of Plant Pathogens:**

**1. Nanopore sequencing:** Nanopore sequencing is a third-generation sequencing technology that uses protein nanopores to directly sequence single-stranded DNA or RNA molecules. Nanopore sequencing can produce long reads that can span entire genomes and can detect base modifications, which are important for understanding the virulence and pathogenicity of plant pathogens.

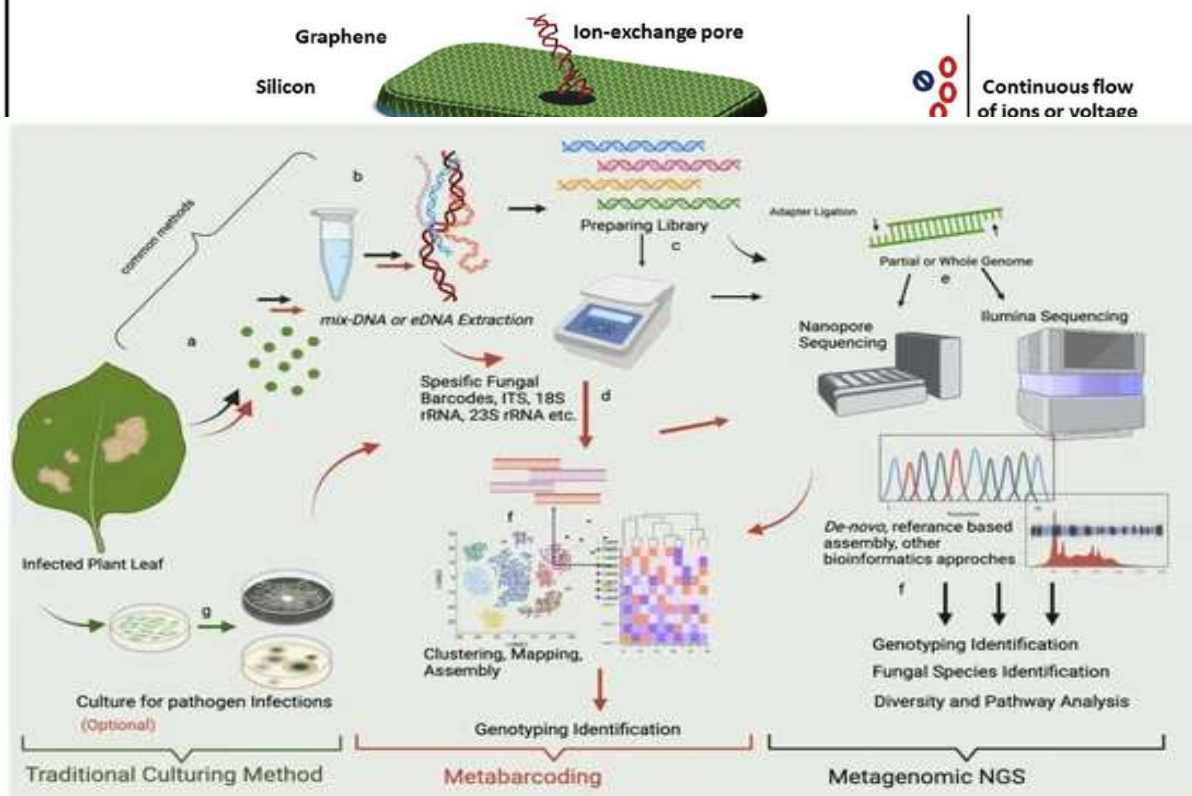
**2. PacBio sequencing:** PacBio sequencing is another third-generation sequencing technology that uses single-molecule real-time sequencing. PacBio sequencing can generate long reads that can span complex genomic regions and can detect base modifications. PacBio sequencing is useful for resolving complex plant genomes and for detecting structural variations and haplotypes.



**3. Optical mapping:** Optical mapping is a method that uses high-resolution imaging to map the positions of restriction enzyme recognition sites on genomic DNA. Optical mapping can be used to construct physical maps of plant pathogen genomes and to validate genome assemblies.



## Nano-pore Sequencing



**4. Metagenomic sequencing:** Metagenomic sequencing is a method that involves sequencing DNA from complex microbial communities. Metagenomic sequencing can be used to identify plant pathogen species and to understand their interactions with other microorganisms in the environment.

## CONCLUSION

In conclusion, whole genome sequencing of plant pathogens has revolutionized our understanding of their biology, evolution, and virulence. Various methods and new techniques have been developed for sequencing plant pathogen genomes, and each has its advantages and limitations. Choosing the appropriate method or technique depends on the research question, the complexity of the genome, and the available resources. Whole genome sequencing of plant pathogens will continue to be an essential tool for developing sustainable control strategies against plant diseases.

## REFERENCES

- Kozik, A. (2019). Whole Genome Sequencing of Plant Pathogens: Current Status and Applications. *Plant Disease*, 103(12), 2989-2997.
- Xiong, Q., & Zhang, J. (2020). Recent Advances in Plant Pathogen Genome Sequencing. *Current Issues in Molecular Biology*, 38, 33-50.
- Kono, T. J., Fu, F., Mohammadi, S., Hoffman, P. J., Liu, C., Stupar, R. M., ... & Michelmore, R. W. (2018). The PacBio and Hi-C technologies combine for comprehensive genome and transcriptome studies of the common reed (*Phragmites australis*). *BMC Genomics*, 19(1), 1-17.
- Payne, A., Holmes, N., Rakyan, V., & Loose, M. (2019). BulkVis: a graphical viewer for Oxford nanopore bulk FAST5 files. *Bioinformatics*, 35(13), 2193-2198.
- Zhao, S., Zheng, P., Dong, S., Zhan, X., Wu, Z., Shao, Y., & Chen, X. (2019). The genome of a pathogenic *Rhodococcus* isolate reveals clues to its biotoxicity and pathogenicity mechanisms on plants. *Microorganisms*, 7(12), 667.