

Whole-Genome Sequencing Approaches in Vegetable Crops

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Article Info	ABSTRACT
<p>Article History Received: 24 December 2025 Revised: 26 December 2025 Accepted: 29 December 2025 Available online: 30 December 2025</p> <p>* Email (Author Corresponding) : deboramarpaung@student.ub.ac.id</p>	<p>Whole-genome sequencing (WGS) technologies have fundamentally transformed vegetable crop research, providing essential genomic information that drives innovation in food biotechnology. This review synthesizes current WGS platforms and analytical approaches, explains their evolution, and evaluates their strengths and limitations for vegetable genomics. We trace progress from short-read technologies that enabled the first reference genomes to recent long-read and telomere-to-telomere assemblies that deliver near-complete genomic landscapes. By linking these technical advances to applied outcomes, such as precise trait discovery, accelerated breeding, improved nutritional quality, and enhanced resilience to biotic and abiotic stresses, this review clarifies how WGS serves as a practical toolbox for developing safer, more sustainable, and higher-value vegetable-based foods.</p> <p>Keywords: Whole Genome Sequencing, Plant Genomics, Pangenome-Based WGS</p>

Introduction

Vegetable crops constitute a critical component of global food systems and human diets. It serves as a primary source of essential vitamins, minerals, dietary fiber, and a diverse array of phytonutrients and functional metabolites (Tripathy et al., 2021). Despite their nutritional significance, many vegetable species face persistent challenges, including genetic erosion, susceptibility to biotic and abiotic stresses, and post-harvest losses, which threaten yield stability and nutritional security (El-Ramady, 2013; Solankey et al., 2021). Recent advances in WGS have driven substantial innovation in our understanding of their genetic architecture, enabling targeted improvement through food biotechnological approaches.

WGS has emerged as an innovative technology in vegetable agriculture, enabling the comprehensive analysis of genetic variations that underpin traits such as yield, disease resistance, and nutritional quality (Liu, 2024; Pandey et al., 2025). By sequencing the entire DNA of a vegetable genome, including coding and non-coding regions, WGS facilitates precision breeding, stress tolerance enhancement, and biodiversity conservation, addressing global challenges like food security and climate change.

Historical Roots of Whole Genome Sequencing

The foundation of WGS relies on pivotal discoveries in molecular biology and sequencing technologies. The discovery of DNA structure in 1953 by James Watson and Francis Crick elucidated DNA's double-helix structure, revealing how genetic information is stored and replicated (Small, 2023). This provided the basis for understanding genomes as sequences of nucleotide bases. In 1977, Frederick Sanger developed the chain-termination method (Eren et al., 2022). This is the first practical DNA sequencing technique, which

sequenced small DNA fragments with high accuracy, becoming the foundation for DNA sequencing, enabling early insights into plant genetics. However, its limitations in speed, cost, and scalability restricted its application to small genomic regions, making WGS of complex vegetable genomes impractical. Sanger sequencing processes one DNA fragment at a time, requiring manual handling and producing only a few hundred base pairs per reaction (Saini et al., 2023).

The advent of next-generation sequencing (NGS) in the mid-2000s overcame these barriers, revolutionizing genomics by enabling high-throughput, cost-effective sequencing of entire genomes. NGS was introduced around 2005 with platforms like 454 and Illumina enabling massively parallel sequencing, producing millions of short reads (50–300 bp) simultaneously generating gigabases of data per run (A. Kumar et al., 2022). However, its short reads struggled with repetitive and polyploid genomes. Therefore, Third-generation sequencing (TGS) emerged around 2009, addressing these issues by producing long reads (10 kb to >2 Mb), improving the assembly of complex vegetable genomes (Oliveira et al., 2024). TGS focuses on sequencing single DNA molecules in real-time, producing ultra-long reads that span thousands to hundreds of thousands of base pairs, resolving structural variants, and handling polyploid genomes common in vegetables. TGS encompasses two primary platforms, which are Pacific Biosciences (PacBio) Single-Molecule Real-Time (SMRT) Sequencing and Oxford Nanopore Technologies (ONT) Nanopore Sequencing.

Whole Genome Sequencing Methods

WGS methods encompass a diverse set of technologies designed to generate comprehensive DNA sequence information across entire genomes. Over the past two decades, these approaches have evolved from labor-intensive, low-throughput platforms to highly automated systems capable of producing massive datasets with increasing accuracy and read length. Understanding the principles, strengths, and limitations of various WGS methods is crucial for selecting suitable strategies in vegetable genomics and food biotechnology research. This subsection outlines the major sequencing platforms and workflows, highlighting how each contributes to the quality of genome assembly, functional annotation, and downstream biological interpretation.

De Novo WGS

De novo WGS is indispensable for the genomic characterization of unexplored or non-model vegetable species lacking prior reference sequences. This approach entails the fragmentation of genomic DNA, followed by high-throughput sequencing technologies to generate long reads that span repetitive or structurally complex regions and subsequent de novo assembly using algorithms such as de Bruijn graph-based or overlap-layout-consensus (OLC) frameworks (De Luca et al., 2025).

Reference-Based WGS (Resequencing)

Reference-based WGS, also known as resequencing, involves sequencing the genome of a target accession and aligning the resulting reads to a pre-existing reference genome to identify genetic variants, such as single-nucleotide polymorphisms (SNPs), insertions, deletions (indels), and structural rearrangements (Kumawat et al., 2022). This comparative approach offers a rapid and cost-efficient alternative to de novo sequencing, as it leverages the genomic framework of well-characterized model species.

Low-Pass WGS

Low-pass WGS represents a cost-effective genotyping strategy that employs low sequencing coverage ranging from $1\times$ to $5\times$, typically across large populations (Sogbe et al., 2025). The approach relies on statistical imputation algorithms to infer unobserved genotypes based on linkage disequilibrium patterns and haplotypes derived from a high-quality reference panel. Predominantly implemented using NGS platforms, low-pass WGS enables the efficient capture of genome-wide variation at substantially reduced costs, making it particularly suitable for genomic selection (GS) and association mapping in plant breeding programs.

Pangenome-Based WGS

Pangenome-based WGS represents an advanced genomic framework that captures the full complement of genetic diversity within a species by sequencing multiple individuals or accessions (Taylor et al., 2024). This approach distinguishes core genes that are conserved across all accessions from dispensable or variable genes, which contribute to phenotypic diversity and environmental adaptation. The construction of a pangenome typically integrates *de novo* assemblies, frequently utilizing third-generation sequencing (TGS) technologies to achieve high contiguity, with reference-based resequencing of broader populations using NGS data. This hybrid strategy allows for comprehensive detection of structural variants, presence-absence variations (PAVs), and novel genomic segments that are often absent in single-reference genomes.

Whole Genome Sequencing (WGS) Prospect for Food Biotechnology

The declining cost and increasing accessibility of high-throughput sequencing technologies have catalyzed an explosion in the number of sequenced vegetable genomes. **Table 1** provides a curated summary of representative vegetable crops that have been sequenced. These foundational genomes are the bedrock upon which modern food biotechnology is built. Whole-genome sequencing, particularly datasets derived from NGS and TGS platforms, has enabled the systematic identification of candidate genes and informative molecular markers, as cataloged in the table, which are being directly leveraged for precision breeding. Thus, the prospect outlined by this growing list of sequenced genomes is one of accelerated, knowledge-driven crop improvement, directly contributing to enhanced food security and nutritional quality.

Table 1. WGS of Vegetable Crops and Their Impacts on Food Biotechnology

Scientific Name	Sequencing Method	Key Advantages	Findings	References
<i>Solanum lycopersicum</i> (tomato)	NGS (Illumina HiSeq 2000), TGS (PacBio)	Integration of short and long reads enabled resolution of repetitive regions and domestication-related loci	Domestication and understanding genome-scale breeding	(Takei et al., 2021)
<i>Solanum tuberosum</i> (potato)	TGS (PacBio),	Improved assembly contiguity and variant detection	Elucidate polyploid genome evolution, differentiation, and implications for potato breeding	(Hosaka et al., 2025)

Scientific Name	Sequencing Method	Key Advantages	Findings	References
		in a polyploid genome		
<i>Capsicum annuum</i> (pepper)	NGS, TGS	Enhanced the detection of structural variants linked to flavor and disease resistance traits	Capsaicin content, bacterial wilt resistance	(Moreno-Contreras et al., 2024)
<i>Solanum melongena</i> (eggplant)	NGS (resequencing)	Cost-effective SNP discovery across diverse accessions for population analyses	Genetic diversity and associated SNPs	(Yu et al., 2024)
<i>Cucumis sativus</i> (cucumber)	TGS (Oxford Nanopore PromethION2 4), NGS (Illumina HiSeq 2000)	Hybrid assemblies improved genome accuracy while enabling population-scale variant analysis	Genome-wide association studies, marker-assisted selection, and genomic prediction models.	(Seiko et al., 2025)
<i>Cucurbita pepo</i> (pumpkin)	NGS (Illumina HiSeq 2000)	Detection of duplication signatures across the genome	Whole-genome duplication event	(Montero-Pau et al., 2018)
<i>Brassica oleracea</i> var. <i>capitata</i> (cabbage)	NGS	Accurate short-read mapping enabled reliable mitochondrial genome reconstruction	Distinct mitochondrial genome	(K. Yang et al., 2018)
<i>Raphanus sativus</i> (radish)	TGS (PacBio, ONT)	Very long reads resolved complex regions underlying flowering-time regulation	Identifies RsMIPS3 as a key regulator of bolting time	(F. Yang et al., 2025)
<i>Allium cepa</i> (onion)	NGS (Illumina NovaSeq 6000), TGS (PacBio)	Improved the assembly of a large, repetitive genome and supported functional annotation	Molecular breeding, evolutionary studies, and functional genomics	(Cho et al., 2025)
<i>Allium sativum</i> (garlic)	NGS (Illumina NovaSeq 6000)	Efficient variant detection across accessions for	Novel loci and candidate genes	(Y. Wang et al., 2025)

Scientific Name	Sequencing Method	Key Advantages	Findings	References
		candidate-gene discovery		
<i>Apium graveolens</i> (celery)	TGS (PacBio)	Long reads enabled identification of resistance-related regions across complex scaffolds	Candidate resistance genes and genomic regions for introgression	(Lee et al., 2025)
<i>Lactuca sativa</i> (lettuce)	NGS, TGS	Combined sequencing resolved structural diversity relevant to species evolution	Evolutionary relationships, potential molecular markers	(Chu et al., 2024)
<i>Spinacia oleracea</i> (spinach)	TGS (PacBio, ONT)	Telomere-to-telomere assemblies captured repeat-rich regions and structural variation	First complete T2T spinach genome	(She et al., 2025)
<i>Beta vulgaris</i> (beet)	NGS	Population-scale sequencing enabled inference of historical gene flow and admixture	Historical gene flow, admixture, and introgression	(Galewski & McGrath, 2020)
<i>Phaseolus vulgaris</i> (green bean)	NGS	Rapid variant discovery facilitated disease-resistance screening and breeding decisions	Virus-free seeds, developing resistant cultivars, and controlling insect vectors	(Astaraki et al., 2025)
<i>Pisum sativum</i> (common pea)	NGS (Resequencing)	Resequencing across lines supported identification of alleles linked to phenology	Early-maturing pea lines	(P. Kumar et al., 2025)
<i>Zea mays subsp. Mays</i> (corn)	NGS (Illumina HiSeq 3000)	Dense variant datasets revealed evolutionary history and adaptive signatures	Revealing evolutionary history, adaptive mechanisms, and functional alleles	(Chen et al., 2022)

Scientific Name	Sequencing Method	Key Advantages	Findings	References
<i>Asparagus officinalis</i> (asparagus)	NGS	Fine-scale variant mapping enabled exploration of sex-chromosome evolution	Early stage of sex chromosome evolution	(Li et al., 2014)
<i>Sechium edule</i> (chayote)	NGS (Illumina NovaSeq 6000), TGS (ONT)	Integration of long and short reads clarified repetitive content and genome expansion	Repetitive-rich genome, polyploidization event, significant gene family expansion	(X. Wang et al., 2025)

Conclusion

WGS has fundamentally transformed vegetable crop science, establishing a foundational pillar for modern food biotechnology. As detailed in this review, the diverse array of WGS methodologies provides a versatile toolkit for research and breeding objectives, enabling the identification of genes and markers underlying agronomically important traits such as disease resistance, stress tolerance, nutritional quality, and yield. Beyond serving as a diagnostic resource, WGS now underpins predictive and precision breeding approaches. Looking forward, integrating WGS with genomic selection, artificial intelligence-driven data analytics, and genome editing technologies promises to accelerate the development of resilient, high-yielding, and nutrient-rich vegetable cultivars. Such synergistic applications will be pivotal in addressing global challenges, including food security, climate adaptation, and human health.

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Conflict of interest

The authors declare there are no conflicts of interest.

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