


REVIEW

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High-throughput sequencing in plant disease management: a comprehensive review of benefits, challenges, and future perspectives

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Abstract

High-throughput sequencing (HTS) has instigated a paradigm shift in plant pathology, showcasing its transformative role in the management of plant diseases. As a powerful tool, HTS aids in identifying pathogens and enhances disease management strategies by detecting novel and emerging pathogens, tracking disease outbreaks, and contributing to developing disease-resistant cultivars. Despite these benefits, the implementation of HTS faces obstacles due to the complexity of data interpretation and economic factors that affect its widespread adoption. This comprehensive review summarizes the strengths, limitations, and opportunities associated with using HTS in managing plant diseases. The article also delves into the prospects of HTS, incorporating technological advancements, synergy with complementary methodologies, capacity-building initiatives, and the development of best practices and guidelines. By acknowledging and addressing these obstacles while harnessing the full capabilities of HTS, we advocate for a refined approach to managing plant diseases. This approach is critical for ensuring global food security, especially in the context of a growing global population and climate change.

Keywords Pathogen detection, Disease outbreaks, Emerging pathogens, Global food security, Novel pathogens

Background

Plant diseases, caused by an array of pathogenic microbes such as bacteria, fungi, viruses, and nematodes, significantly jeopardize global food security, particularly in developing nations (Strange and Scott 2005). These diseases result in substantial crop losses (Vurro et al. 2010), necessitating the urgent development of effective plant disease management strategies in light of a burgeoning global population and the exacerbation of climate change (Chakraborty and Newton 2011). While High-throughput Sequencing (HTS) has shown promise as an

advanced tool for these purposes, comprehensive reviews elucidating its merits, limitations, and future prospects are notably scarce in existing literature. Although current studies often focus on discrete applications of HTS—ranging from pathogen identification to the development of disease-resistant cultivars—a more encompassing, integrative review is needed. Such a review would articulate the expansive influence of HTS on plant disease management and delve into its potential future applications.

HTS technologies have fundamentally altered the landscape of genomics and molecular biology by allowing the rapid and precise sequencing of millions to billions of DNA or RNA molecules (Ghosh et al. 2018). This capability offers unprecedented insights into an organism's genetic makeup (Graveley 2008). When compared to traditional methods of pathogen identification and diagnosis, HTS offers numerous advantages, including heightened sensitivity and specificity, the

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ability to detect multiple pathogens simultaneously, and the potential for identifying novel pathogenic agents (Van Dijk et al. 2014; Loman and Pallen 2015). Moreover, HTS is instrumental in large-scale monitoring of disease outbreaks and tracking pathogen evolution, both of which are crucial for devising effective disease management approaches (Van der Heyden et al. 2021; Kawasaki et al. 2023). HTS also facilitates a deeper understanding of plant-pathogen interactions and aids in pinpointing genetic markers for disease resistance, thereby expediting the breeding of disease-resistant cultivars (Shafi et al. 2019).

This review aims to offer a comprehensive synthesis of the role of HTS in the management of plant diseases. It outlines its varied applications, including pathogen detection and identification, disease outbreak surveillance, and the breeding of disease-resistant plants. We also address the challenges that constrain the effective implementation of HTS, while looking ahead at its promising future, which includes technological advancements,

integration with other methods, and the establishment of best practices and guidelines.

Benefits of HTS in plant disease management

HTS offers several advantages in plant disease management, including rapid and precise pathogen identification and the facilitation of plant breeding and genetic engineering (Fig. 1).

Traditional methods for pathogen detection, such as repetitive extragenic palindromic polymerase chain reaction (Rep-PCR) and polymerase chain reaction (PCR), have been staples in molecular diagnostics (Zupunski et al. 2011). Both techniques utilize DNA amplification for pathogen identification and quantification but have limitations in terms of sensitivity, specificity, and the detection of novel pathogens. Rep-PCR, commonly employed to distinguish between bacterial species and subspecies, targets repetitive sequences in noncoding genomic regions to generate a unique genetic fingerprint for each pathogen (Versalovic et al. 1991). Despite its

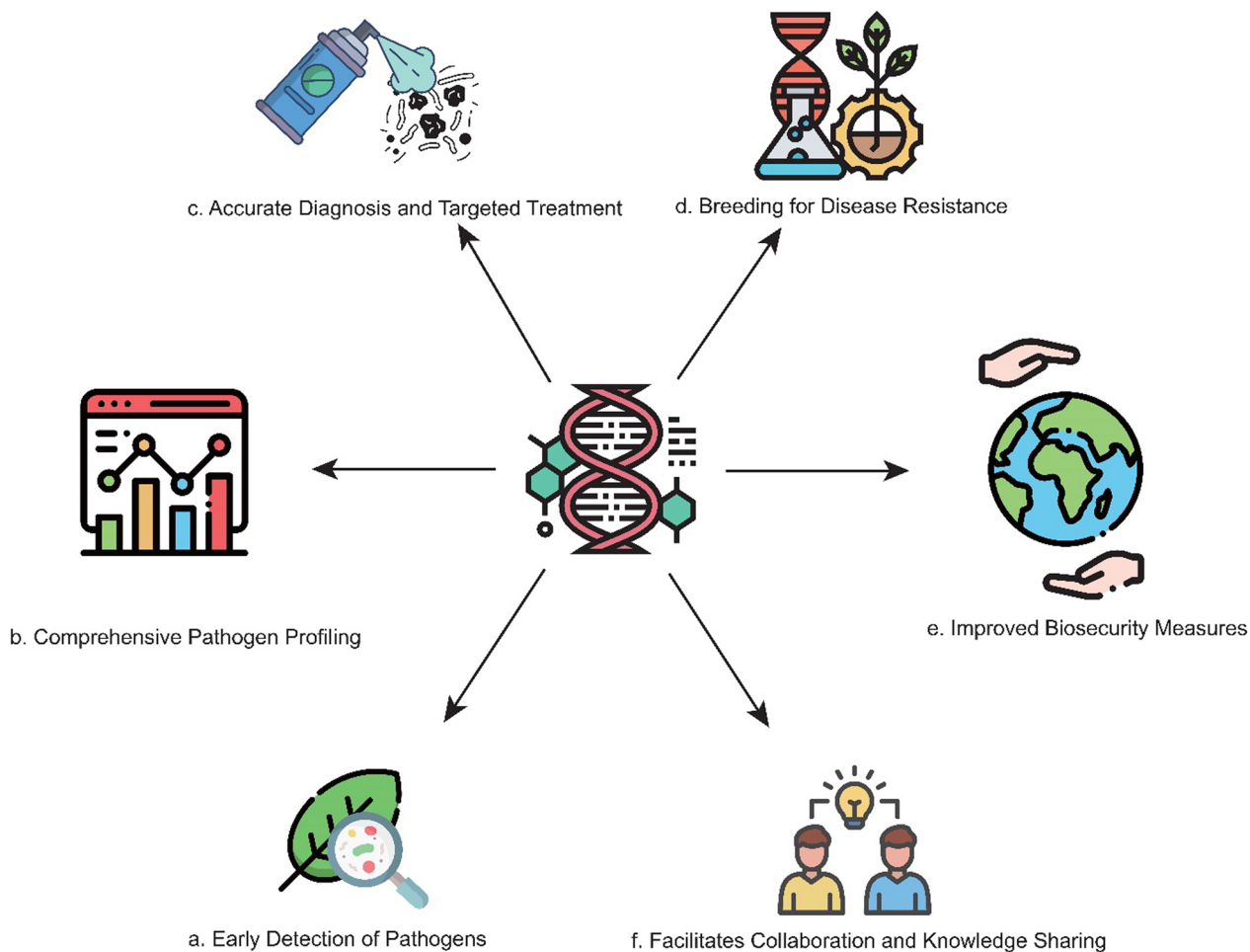


Fig. 1 Benefits of HTS in plant disease management

ability to reveal genetic diversity among closely related strains, Rep-PCR struggles with the differentiation of genetically similar strains and demands stringent laboratory conditions for reliable results (Dombek et al. 2000). PCR, conversely, employs custom-designed primers to amplify targeted DNA segments, thus allowing pathogen detection and quantification even in mixed samples (Mackay 2004). However, the efficacy of PCR can be compromised by primer performance and specific sample components, potentially leading to false negatives (Wilson 1997). Additionally, while PCR offers certain advantages, it lacks the capability to provide insights into pathogen viability and requires specialized instrumentation and trained personnel (Bustin et al. 2009).

Recent technological advances have ushered in more accurate and rapid techniques for pathogen detection. For instance, primer-mediated asymmetric-PCR (RM-PCR) in conjunction with SYBR Green I and TaqMan real-time PCR can detect pathogen concentrations as minuscule as 0.1 femtograms (fg) and 1.0 fg, respectively (Yuan et al. 2009). Other methods like loop-mediated isothermal DNA amplification (LAMP) and multiplex PCR have shown high sensitivity toward extremely low DNA concentrations (Pieczul et al. 2018). However, the successful implementation of these advanced techniques necessitates a high level of technical expertise and precision. Real-time PCR, recognized for its exceptional specificity, sensitivity, and reliability, is often restricted in its widespread application due to its cost-prohibitive nature (Fang and Ramasamy 2015). Droplet digital polymerase chain reaction (ddPCR), although precise in absolute DNA quantification, may not be suitable for the detection of emerging or novel pathogens due to its high specificity (Hindson et al. 2011; Pinheiro et al. 2012).

In this context, HTS presents itself as a formidable tool for the identification of plant pathogens. Owing to its extensive sequencing depth, HTS has the capability to detect both known and previously unidentified pathogens, even those present in trace amounts. By sequencing genetic material directly from infected samples, HTS functions as either an alternative or a supplementary approach to both traditional and cutting-edge pathogen detection methods. The ensuing section explores the myriad advantages that HTS offers in the realm of plant disease management.

Rapid and accurate pathogen identification

Plant pathogen identification has undergone a significant transformation with the advent of HTS technology. This innovative approach has proven to be more precise and efficient compared to traditional methods like microscopy, culturing, and serological tests (Adams et al. 2018). Traditional techniques, while valuable, often

require extensive labour and time, and their accuracy can be compromised by limitations in sensitivity and specificity (Collins et al. 2017). In contrast, HTS offers a host of advantages that overcome these constraints, making it an indispensable tool for diagnosing and characterizing plant pathogens (Table 1).

Table 1 elucidates the transformative effects of HTS on the rate, precision, and comprehensiveness of plant pathogen detection. Utilizing HTS for rapid sequencing directly from infected plant samples bypasses the need for more time-consuming conventional assays. Such speediness is instrumental in allowing prompt responses to emerging disease outbreaks, thereby curbing economic losses and enhancing the overall effectiveness of disease management strategies (Tedersoo et al. 2021). Additionally, the high accuracy afforded by HTS ensures reliable pathogen identification, which in turn informs the development of robust strategies for disease control, management, and prevention (Piombo et al. 2021).

Moreover, HTS furnishes exhaustive genetic data on pathogens, facilitating a nuanced understanding of evolutionary patterns, virulence factors, and host specificity. This information proves invaluable in crafting targeted and more effective control measures (Quijada et al. 2020). Remarkably, the multiplexing capability of HTS enables the simultaneous identification of multiple pathogens from a single sample, including previously unidentified species, thus enhancing surveillance capabilities and deepening our understanding of pathogen-host dynamics (Al Rwahnih et al. 2018). The scalability and amenability to automation of HTS protocols permit the concurrent analysis of numerous samples. This not only enables large-scale monitoring but also potentially lowers costs through automated processes (Martinez et al. 2020).

HTS has ushered in a new era in identifying and understanding plant pathogens, outclassing traditional diagnostic methods in speed, accuracy, and depth of information. The rich genetic data gleaned from HTS significantly contributes to a more holistic comprehension of pathogenic behavior, thereby aiding in formulating effective and targeted disease control and management strategies.

Uncovering novel and emerging pathogens

The advent of HTS has revolutionized our capacity to detect and examine novel and emerging pathogens. This power technology bypasses the constraints of traditional diagnostic methods, rendering it feasible to identify previously undetectable pathogens (Pérez-Losada et al. 2020). HTS offers several advantages, including direct detection and genetic analysis of pathogens in infected samples, which streamlines the discovery of new

Table 1 Advantages and implications of HTS in plant pathogen detection and management

Advantages	Description	Implications	Reference
Speed	Nanopore-based Third-Generation Sequencing accelerates the sequencing process up to 10 times faster	Enables faster responses when rapid platforms are used, reducing economic losses and improving disease management by up to 50%	Goodwin et al. (2016); Jain et al. (2016); Lu et al. (2016); Tedersoo et al. (2021)
Accuracy	Next-generation sequencing technologies enhance the accuracy of pathogen identification by approximately 20%	Ensures more reliable pathogen identification, leading to effective disease management/control strategies	Prombo et al. (2021)
Comprehensive genetic information	Next-generation sequencing technologies provide a comprehensive view of a pathogen's genetic makeup	Enhances understanding of pathogen biology, enabling targeted/effective control measures	Köser et al. (2014); Kwong et al. (2015); Quijada et al. (2020)
Detection of mixed infections & novel pathogens	Identify multiple and novel pathogens in a single sample	Allows enhanced surveillance, improved understanding of interactions, early detection of novel pathogens	Al Rwahnih et al. (2018)
Automation & scalability	Modern sequencing technologies significantly enhance efficiency by enabling automation and scalability	Enables efficient large-scale monitoring, faster outbreak responses, and significant cost savings due to automation	Chen et al. (2017); Slatko et al. (2018); Martinez et al. (2020)

pathogens and assists in the design of targeted disease management strategies (Table 2).

For instance, HTS has played a crucial role in detecting novel strains of existing pathogens, such as *Fusarium oxysporum* (Zhao et al. 2018), *Alternaria solani* (Sarkar et al. 2017), and *Phytophthora parasitica* (Naveed and Ali 2018). It has also facilitated the identification of previously unknown pathogens such as *Stemphylium lycopersici* (Yang et al. 2017) and *Cladosporium fulvum* (Zhang et al. 2020). In each case, HTS not only enabled the detection of these pathogens but also provided a comprehensive analysis of their genetic makeup, yielding invaluable insights into their biology, ecology, and potential impact on the host.

Furthermore, HTS has transformed our understanding of plant resistance by allowing for genome-wide identification of plant resistance genes, such as the NLR gene family (Hamim et al. 2022). This development has significantly advanced plant disease resistance breeding, leading to the development of disease-resistant crop varieties. These examples illustrate the substantial contribution of HTS to advancements in plant disease resistance breeding. Moreover, HTS can be used to effectively study pathogens such as *tomato spotted wilt tospovirus* (TSWV) (Padmanabhan et al. 2019), *tomato yellow leaf curl virus* (TYLCV) (Chen et al. 2013), *potato spindle tuber viroid* (PSTVd) (Góra-Sochacka et al. 2019), *Verticillium dahliae* (Tan et al. 2015), *Xanthomonas perforans* (Du et al. 2015), and *Meloidogyne incognita* (Shukla et al. 2018), which are among the many pathogens that can be effectively studied using HTS.

Recent breakthroughs in plant disease management owe much to advances in HTS technology. This state-of-the-art approach enables an in-depth investigation of both new and emerging pathogens, delivering crucial insights for the formulation of effective control measures. Furthermore, HTS has considerably deepened our grasp

of pathogen biology and the nuanced interplay between pathogens and their host plants (Singh et al. 2023).

Plants deploy a complex defense system that activates upon pathogen exposure. This defense architecture involves intricate signaling pathways culminating in a robust response against a wide variety of pathogens. Honed through evolutionary processes, this defense system is a byproduct of intricate host–pathogen interactions. Defense responses include signaling cascade activation, gene expression modulation, the synthesis of specialized defensive metabolites, and hormonal balance adjustment. Collectively, these mechanisms work to thwart or impede pathogen colonization, thereby sustaining plant health and viability (Zhang et al. 2019).

HTS has been pivotal in dissecting the molecular basis of pathogen resistance. Specifically, it has facilitated the identification of numerous cellular receptors that play a direct role in recognizing pathogenic molecules. This has expanded our understanding of plant–pathogen interaction intricacies. The plant's first line of defense is typically activated by pattern recognition receptors (PRRs), specialized proteins that detect pathogen-associated molecular patterns (PAMPs). This recognition triggers a cellular response cascade known as PAMP-triggered immunity (PTI), serving as a critical frontline defense against various pathogens. HTS has proven invaluable in elucidating the mechanisms underpinning PTI, enabling genome-wide monitoring of cellular responses, thereby illuminating the pathogen colonization and dissemination processes within plant hosts (Dodds et al. 2010; Peng et al. 2018; Zipfel et al. 2014).

Moreover, HTS has proven instrumental in studying the evolution and diversity of PRRs and PAMPs. This has yielded significant insights into the co-evolutionary dynamics between plants and pathogens, thereby guiding the development of enhanced plant disease resistance strategies. HTS remains a cornerstone in our concerted

Table 2 Role of HTS in uncovering novel and emerging pathogens

Advantages	Description	Implications	Reference
Uncovering novel pathogens	HTS uncovers unknown pathogens by detecting and analyzing genetic material directly from infected samples	Facilitates the discovery of new pathogens, providing valuable insights into their biology, ecology, and potential impact	Suminda et al. (2022)
Identifying new strains/variants	HTS can detect genetic mutations/variants within pathogen populations	Allows for monitoring pathogen evolution, informing disease management strategies to ensure effectiveness	Pandey and Szpara (2019)
Understanding host–pathogen interactions	HTS enables the analysis of the genetic material of both the host and pathogen, providing a comprehensive view of their interactions	Assists in identifying factors influencing infection, transmission, and host resistance	Karamitros et al. (2021)

efforts to bolster global food security and environmental protection (Singh et al. 2023).

Through the employment of HTS, we can now achieve a holistic understanding of the complex molecular interplay between plant hosts and pathogens. This knowledge not only illuminates the dynamic nature of plant-pathogen interactions but also provides a solid foundation for formulating strategies aimed at bolstering plant disease resistance (Michelmore et al. 2017). The sustained use of HTS in plant disease management will be indispensable for ensuring global food security and environmental conservation (Olmos et al. 2018).

Disease surveillance and tracking

HTS has unquestionably become an essential tool in disease surveillance and tracing (Nunes et al. 2017). By generating comprehensive genetic data on pathogens, HTS significantly augments our ability to oversee disease spread, detect new strains or variants, and understand pathogen evolution (Suminda et al. 2022). HTS applications span an array of bacteria, such as *Pseudomonas*, *Azospirillum*, *Azotobacter*, *Klebsiella*, *Enterobacter*, *Alcaligenes*, *Arthrobacter*, *Burkholderia*, *Bacillus*, and *Serratia* (Singh et al. 2017). The following discussion (Table 3) explores several ways in which HTS-empowered surveillance systems enhance disease control and management strategies.

HTS significantly contributes to disease surveillance and tracing by offering extensive genetic insights into pathogens. These data are instrumental in the early detection of disease outbreaks, overseeing disease spread, tracking the emergence of new strains or variants, and understanding the evolutionary patterns of pathogens. Incorporating HTS into surveillance systems dramatically bolsters our capacity to react promptly to disease threats and facilitates the development of efficient management strategies. This, in turn, safeguards global food

security and preserves the environment. This unprecedented resolution and scale make HTS an invaluable asset in contemporary disease control and management.

Facilitating plant breeding and genetic engineering

HTS offers tremendous potential for advancing plant breeding and genetic engineering, particularly enhancing disease resistance. By pinpointing disease-resistant genes and other advantageous traits across a range of crops, HTS facilitates the development of robust new crop varieties endowed with fortified defenses against various pathogens. Such advances are indispensable for achieving food security and promoting sustainable agriculture.

Over time, pathogens have evolved intricate mechanisms to outmaneuver plant defenses. One such tactic involves the production of effector molecules designed to weaken plant pattern-triggered immunity (PTI). To counteract this, plants have developed resistance (R) proteins, a unique class of intracellular receptors capable of recognizing these effector molecules. This identification triggers a second, more potent layer of defense known as effector-triggered immunity (ETI), which tends to be more specific and robust than PTI (Gassmann et al. 2012; Rosli et al. 2015).

Among the various families of plant resistance genes, those encoding nucleotide-binding site leucine-rich repeat (NBS-LRR) proteins—or NLR immune receptors—stand out for their prevalence. These receptors play a pivotal role in detecting the effector molecules that pathogens release to enable infection (Dangl et al. 2013). Upon recognizing a pathogen or pest effector molecule, these NLRs initiate substantial transcriptional reprogramming, often culminating in localized cell death to prevent the pathogen from spreading further. This process is known as the hypersensitive response (Eulgem et al. 2005).

Table 3 HTS and its influence on disease surveillance and management strategies

Advantages	Description	Implications	Reference
Early detection of disease outbreaks	HTS detects pathogens directly from infected samples, even at low concentrations	Timely interventions, preventing the spread of diseases	Vidyadharani et al. (2022)
Monitoring disease spread	HTS helps track the movement of diseases across regions and populations	Understanding transmission dynamics, implementing appropriate control measures to curb infections	Doyle et al. (2017)
Understanding pathogen evolution	HTS offers genetic information for studying pathogen evolutionary history and population dynamics	Identifying factors driving pathogen evolution, informing strategies to mitigate the emergence of new diseases or drug resistance	Tedersoo et al. (2019)
Global collaboration & data sharing	HTS generates massive amounts of data that can be shared among researchers and institutions worldwide	Rapid identification/response to emerging diseases, improved understanding of pathogen biology and epidemiology	The GAIN Collaborative Research Group (2007)

Table 4 Advantages of HTS in plant breeding and disease resistance

Advantages	Description	Implications	Applications	Reference
Identifying disease-resistant genes	HTS helps identify specific genes/molecular markers associated with resistance in plants	Understanding the genetic basis of disease resistance, guiding breeding efforts	Disease resistance research, plant breeding	Parihar et al. (2022)
Accelerating plant breeding	HTS provides molecular markers linked to desirable traits for faster plant breeding	Reduced time/resources for developing new crop varieties	Plant breeding, crop improvement	Kaiser et al. (2020)
Enhancing genetic engineering	HTS informs GM crop development with improved disease resistance	Introduction of resistance genes into susceptible plants, improved crops	GM crops, gene editing, crop improvement	Gbashi et al. (2021)
Precision breeding	HTS enables targeted plant breeding with detailed information on genes/functions	Development of crop varieties with better resistance profiles, reduced unintended consequences	Precision breeding, crop improvement	Maclot et al. (2020)
Expanding genetic diversity	HTS reveals genetic variations within/between plant species for novel resistance genes	Creation of more resilient/diverse crop varieties, better equipped to withstand disease pressures	Breeding for genetic diversity, crop improvement	Rasheed and Xia (2019)

Table 4 highlights several of the transformative benefits of HTS in plant disease management and breeding. This table elucidates how HTS is instrumental in identifying disease-resistant genes, deciphering the mechanics of host–pathogen interactions, expediting the plant breeding process, and fostering the development of genetically engineered crops with enhanced disease resistance. These collective advancements contribute significantly to global food security and sustainable agricultural practices.

The application of HTS presents a myriad of benefits in the realm of plant disease management. Its contributions span from swift and precise pathogen identification to the detection of new and emerging pathogens. Additionally, it assists in disease monitoring and tracing while bolstering plant breeding and genetic engineering endeavors. As a whole, these merits cement HTS as a potent instrument in the battle against plant diseases, ensuring food security and fostering the sustainability of agriculture.

HTS for post-harvest disease management

HTS has brought a transformative shift in plant pathology and post-harvest disease management, with various applications and advantages. Its critical uses in managing post-harvest diseases are outlined in Table 5.

While HTS offers many applications and benefits, it also presents challenges, such as handling vast amounts of data, significant costs, and complex sample preparation. Nonetheless, with the steady progression of HTS technologies and the amalgamation of multiomics strategies, it is anticipated that HTS will assume an ever-growing role in managing plant diseases post-harvest in the years to come.

Challenges in Implementing HTS for plant disease management

While HTS provides many advantages for managing plant diseases, several obstacles must be addressed to maximize its potential. In this section, we delve into the primary challenges inherent in the deployment of HTS for plant disease management.

Technical and logistical challenges

HTS technologies have undeniably revolutionized plant pathogen research and disease management. However, like all powerful tools, HTS introduces its unique set of challenges and limitations that must be thoroughly addressed for its successful implementation:

Platform-specific limitations

HTS platforms differ significantly in terms of their read length, accuracy, throughput, and cost (Tedersoo et al. 2021). As a result, the selection of technology for various applications requires a thorough evaluation of each

platform's strengths and weaknesses. Such assessments call for a balance between research objectives and the capabilities and constraints of accessible HTS platforms, accounting for both financial and technical factors.

Sample preparation and processing

These crucial steps significantly influence the quality of subsequent analyses and can be labor intensive, requiring specialized equipment and expertise (Yu et al. 2021). The complexity involved and the need for rigorous quality control measures may present significant hurdles, particularly for smaller research groups or those with limited resources.

Data storage and management

HTS generates vast amounts of data, which can pose significant challenges in terms of storage capacity, data handling, maintenance, transfer, and archiving (Hashem et al. 2015). These requirements can impose substantial financial and logistical burdens, especially for institutions with restricted resources. Additionally, the management of such large datasets necessitates sophisticated data analysis tools and expertise, adding another level of complexity.

Data analysis and interpretation

Although recent advancements have streamlined the process, interpreting HTS data can still present challenges for researchers unfamiliar with bioinformatics (Kutnjak et al. 2021). Therefore, it is imperative to nurture bioinformatics capacity and expertise to ensure the processing and accurate interpretation and application of HTS data.

Legal and social implications

The application of HTS, especially in genetic engineering and gene editing, brings forth legal and social considerations. It is, therefore, crucial to carefully address and manage concerns regarding potential environmental effects, impact on biodiversity, patenting, and intellectual property rights (Jiang 2020).

Accessibility

The costs and expertise required for HTS can limit access to these potent tools, particularly for researchers in developing countries or those with limited resources (Nick et al. 2012; Lightbody et al. 2019). Hence, global collaborations, capacity building, and efforts to democratize access to HTS technologies are vital for the worldwide realization of their benefits.

Despite these challenges, HTS technologies harbor immense potential in reshaping plant disease management and breeding endeavors. Through continuous advancements in sequencing technologies,

Table 5 HTS applications, benefits, and challenges in post-harvest plant disease management

Application	Benefit	Challenges	Reference
Post-harvest pathogen identification	Rapid and accurate identification of pathogens; implementation of appropriate management strategies	Data handling, cost, sample preparation	Adams et al. (2018)
Post-harvest pathogen diversity	Insights into genetic diversity; development of targeted control measures	Data handling, limited availability of reference genomes	Chen et al. (2020)
Detection of novel post-harvest pathogens	Early detection and prevention of potential outbreaks	Data handling, cost, sample preparation	Guo et al. (2020)
Post-harvest host–pathogen interactions	Understanding of molecular mechanisms behind diseases; development of novel control strategies	Data handling, integration of multi-omics approaches	Jayaprakash et al. (2019)
Post-harvest resistance breeding	Identification of disease resistance genes; development of resistant cultivars	Data handling, limited availability of reference genomes	Campos et al. (2021)
Post-harvest microbiome analysis	Insights into microbial communities; promotion of beneficial microorganisms and suppression of pathogens	Data handling, bioinformatics expertise, cost, sample preparation	Zhang et al. (2021)

bioinformatics tools, data management solutions, and heightened global collaborations, these challenges are expected to be surmounted, assuring wider and more equitable use of HTS across the globe.

Data analysis and interpretation

HTS undeniably generates substantial amounts of data. This vast data can create hurdles in bioinformatics analysis and the interpretation of results, especially for researchers or diagnostic settings with limited familiarity in this field. The primary challenges accompanying the analysis and interpretation of HTS data are outlined in Table 6.

To tackle these challenges, there is a vital need for capacity building in bioinformatics and the creation of

user-friendly tools and pipelines for HTS data analysis. Collective endeavors among researchers, institutions, and the industry can facilitate overcoming these obstacles by pooling expertise, resources, and best practices. Moreover, incorporating bioinformatics training into pertinent educational programs can help cultivate a proficient workforce capable of fully exploiting the potential of HTS technologies in plant disease management and wider applications.

Legal considerations

The exchange of genetic resources and data brings legal concerns to the fore, making it essential to establish clear guidelines and agreements to address these issues. Some

Table 6 Challenges and solutions in HTS data analysis for plant disease research

Challenges	Description	Implications	Solutions	Reference
Bioinformatics expertise	HTS data analysis requires specialized bioinformatics expertise	The barrier to fully leveraging HTS is the potential difficulty in data analysis	Training collaboration with bioinformatics experts	Brinkmann et al. (2019)
Computational tools & pipelines	Development and optimization of HTS data analysis tools can be time-consuming and resource-intensive	Challenge in selecting and adapting tools for specific research questions	Utilize open-source tools and seek guidance from experts	Krewski et al. (2020)
Data interpretation	Difficulty distinguishing between true pathogen sequences and contaminants or host-derived sequences	False positives/negatives, additional validation required	Validation with traditional methods, complementary omics approaches	Khan et al. (2018)
Standardization of analysis methods	Lack of standardized methods and protocols for HTS data analysis	Inconsistencies in interpretation, challenging comparisons between studies	Develop standardized methods and best practices for HTS data analysis	Malo et al. (2006)
Integration of multi-omics data	Complex integration of HTS data with other omics approaches	Requires advanced bioinformatics tools and expertise	Collaboration with experts and development of user-friendly integration tools	Zhou et al. (2021)

of the key considerations and potential solutions include the following:

Access and benefit sharing

The Convention on Biological Diversity (CBD) and the Nagoya Protocol form a legal framework for the fair and equitable sharing of benefits derived from the utilization of genetic resources (Silvestri and Mason 2023). Such international agreements aim to maintain a balance between the users and providers of these resources. Adhering to these principles fosters transparency and respect while contributing to biodiversity conservation and the sustainable use of genetic resources.

Intellectual property rights (IPR)

Intellectual property rights, including patents and plant variety protections, have become crucial in HTS research involving genetic resources (Dhingra 2020). Transparent IPR ownership, licensing, and sharing agreements can stimulate innovation while ensuring equitable benefit distribution. The International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) provides a model system for managing these concerns (Shukor 2011).

Data sharing and public databases

In the HTS context, it is critical to establish clear guidelines and best practices for data sharing. These guidelines should encompass standardized formats, metadata, and data access, privacy, and security agreements. Sequencing data are typically deposited in public databases such as NCBI SRA and MG-RAST. These repositories enable the storage and retrieval of colossal volumes of sequencing data and encourage data sharing within the scientific community. The existence of these databases and their data-sharing guidelines make HTS research more accessible and collaborative. Initiatives such as the Global Biodiversity Information Facility (GBIF) and the Genomic Standards Consortium (GSC) play a crucial role in promoting the sharing of genetic data while tackling legal considerations (Lane and Edwards 2007; Field et al. 2011).

Capacity building and technology transfer

A focus on capacity building and technology transfer is needed to ensure equitable access and benefit sharing. Providing training and resources to developing countries enhances participation in genetic resource research and utilization. Furthermore, supporting local research

infrastructure can foster self-sustainability and strengthen scientific capabilities within these countries.

Informed consent and community engagement

We must emphasize informed consent and community engagement when employing genetic resources in HTS research. By involving communities in the decision-making process, we respect their rights and interests and ensure that the use of their resources or traditional knowledge is performed ethically.

Therefore, while HTS technologies offer potent tools for understanding and exploiting genetic resources, navigating these waters with legal and ethical considerations at the forefront is critical. Clear guidelines and agreements can help guarantee that innovation, collaboration, and responsible use of these resources are carried out for the mutual benefit of all stakeholders.

Economic factors

The cost of implementing HTS remains a substantial hurdle, particularly for settings with limited resources or for developing countries. Despite the dramatic decrease in sequencing costs, the associated expenses for sample preparation, data storage, and bioinformatics analysis can still be prohibitively high for some institutions. To enhance accessibility to HTS and overcome these challenges, several strategies can be employed:

Collaboration and resource sharing

One effective way to make HTS more accessible is through partnerships. Collaborative projects allow for the pooling of resources and the distribution of costs, and they also amplify capacity, facilitate knowledge exchange, foster the standardization of protocols, and encourage innovation (Rehm et al. 2021).

Capacity building

Implementing comprehensive training programs for researchers and technicians can empower individuals and cultivate a broader culture of HTS expertise. Such initiatives can promote the adoption of HTS technologies and ensure that researchers stay updated with the latest advancements (Aragona et al. 2022).

Development of cost-effective technologies and methods

Advancements in technology and streamlined sample preparation methods can diminish the cost and complexity of HTS. Portable sequencing platforms and simplified HTS workflows can extend sequencing capabilities to a broader user base and reduce the resources required for sample processing (Reuter et al. 2015; Plešivkova et al. 2019).

Data management solutions

Effective data management solutions, including cloud-based storage, data compression techniques, and open-source data management platforms, can help overcome challenges related to data storage, sharing, and accessibility. Such solutions can enable more efficient and cost-effective utilization of HTS data (Sahal et al. 2020).

Funding and grant opportunities

Financial support from governmental, nongovernmental, or private organizations can help cover the costs associated with HTS implementation. International collaborations and capacity-building initiatives can provide financial backing and resources, promoting equitable access to HTS technologies (Jjingo et al. 2022).

Addressing these aspects makes it feasible to surmount the cost barriers associated with HTS and ensure its benefits are accessible globally. It is critical to consider all these factors, along with technical and logistical obstacles, data analysis and interpretation challenges, and legal considerations, for the successful application of HTS in plant disease management.

Future perspectives and potential of HTS in plant disease management

As HTS technologies continue to evolve and improve, we anticipate expanding and amplifying their applications in plant disease management. This section presents a forwards-looking perspective on the potential of HTS in plant disease management.

Technological advancements

The relentless march of advancements in sequencing technologies and bioinformatics tools offers a promising future, making HTS more accessible, affordable, and efficient. These improvements will significantly impact plant disease management and research, manifested in several ways:

Enhanced sequencing capabilities

Read length, precision, and throughput improvements will empower researchers to conduct more intricate analyses of pathogen genomes and transcriptomes. Such advancements will facilitate more reliable identification and characterization of pathogens, enhance studies of pathogen evolution and virulence mechanisms, and provide deeper insights into host–pathogen interactions (Yu et al. 2018).

Single-cell sequencing

Developments in single-cell sequencing technologies will enable researchers to scrutinize individual cells

within a given sample. This granularity of examination can better understand pathogen diversity and infection dynamics and reveal crucial differences in pathogen behaviour and resistance. This will inform the development of more precise disease management strategies (Wang et al. 2018).

Enhanced bioinformatics tools

The continual evolution of bioinformatics tools, including more streamlined data analysis pipelines, improved data visualization techniques, and the integration of machine learning applications, will make the processing and interpretation of HTS data more user-friendly and efficient (Davis-Turak et al. 2017).

Integration of multiomics approaches

The emergence of tools that allow for the integration of HTS data with other omics approaches (such as proteomics, metabolomics, and epigenomics) will provide a more holistic understanding of host–pathogen interactions and disease mechanisms. This could lead to the discovery of novel targets for disease management and the creation of more effective intervention strategies (Zhou et al. 2021).

Reduction in costs

As sequencing technologies continue to advance, the cost of HTS is expected to decrease, making it more financially accessible to a broader range of research and diagnostic settings. This will facilitate more comprehensive studies and increased data generation, fostering a more inclusive and equitable scientific community (Krewski et al. 2020).

These ongoing advancements hold immense promise and are expected to contribute to the development of more effective strategies to combat plant diseases and ensure global food security.

Integration with other technologies and techniques

Integrating HTS with other omics approaches and advanced imaging techniques provides a more comprehensive understanding of plant–pathogen interactions, paving the way for revolutionary strides in plant disease management. These complementary techniques offer numerous advantages, as detailed in Table 7.

The amalgamation of HTS with other omics methodologies and advanced imaging techniques holds significant potential to redefine plant disease management. These integrated approaches can foster the design of more precise, productive, and sustainable strategies by offering an in-depth, holistic view of plant–pathogen interactions.

Table 7 Benefits of integrating omics data and advanced imaging in plant pathogen detection and management

Benefit	Description	Applications	Challenges	Reference
Novel Insights	Integration of omics data provides a comprehensive view of plant-pathogen interactions, uncovering novel insights	Pathogen research, disease-resistant crop development, understanding plant defense mechanisms	Data integration, computational complexity, and understanding of biological systems	Großkinsky et al. (2018)
New Intervention Targets	Understanding plant-pathogen interactions helps identify new intervention targets, such as genes, proteins, or metabolites	Targeted gene editing, new crop protection chemicals, and natural resistance mechanisms for breeding	Target validation, off-target effects, regulatory hurdles	Rato et al. (2021)
Effective Management Strategies	A comprehensive understanding of plant-pathogen interactions facilitates targeted and effective disease management strategies	Disease-resistant plant breeding, innovative control agents, optimizing existing management practices	Balancing resistance and agronomic performance, resistance-breaking pathogens, economic considerations	Nelson (2020)
Early Detection and Monitoring	The synergy between HTS and advanced imaging enables early detection and monitoring of plant diseases at the field level	Remote sensing for monitoring, early warning systems, and improved decision-making for disease management	Sensing and imaging limitations, data storage and processing, and translating data to actionable information	Oerke (2020)
Precision Agriculture	Integrating omics data and advanced imaging contributes to precision agriculture, tailoring management decisions to individual plants or fields	Site-specific management, crop input optimization, sustainable practices, improved crop productivity, and resource efficiency	Initial investment costs, farmer adoption and education, data privacy concerns, and infrastructure requirements	Holzinger et al. (2023)

These strategies can not only combat plant diseases more effectively but also contribute to securing global food supplies.

Capacity building and global collaboration

Capacity building and promoting global collaboration are paramount to fully harnessing the potential of HTS in plant disease management, especially within resource-limited settings and developing countries (Nelson 2020). By nurturing capacity development and encouraging collaborative endeavors, we can expand the accessibility of HTS benefits to a wider community of researchers and institutions, fostering a more equitable dissemination of resources and knowledge. To accomplish this, several strategies can be implemented:

Training programs and workshops

These initiatives could concentrate on HTS technologies, bioinformatics, and their applications in plant disease management. They could be tailored for researchers, technicians, and extension agents, enabling them to effectively incorporate HTS methods into their research or field operations (Cardwell and Bailey 2022).

Online courses and resources

Offering access to comprehensive knowledge about HTS technologies, data analysis procedures, and their applications in managing plant diseases can democratize learning. These globally accessible resources support self-paced learning and widespread knowledge dissemination (Nagy et al. 2021).

Research partnerships

Encouraging collaborations between institutions from developed and developing nations can facilitate the exchange of expertise, resources, and technology. This would allow for the wider application of HTS tools in battling plant diseases and create a more inclusive scientific community (Watkins et al. 2015).

Capacity-building initiatives

The active involvement of international organizations, governments, and nongovernmental organizations is crucial in promoting the use of HTS in resource-limited settings. This could involve financial assistance to institutions for acquiring HTS equipment, offering technical aid and training programs to researchers, and fostering knowledge exchange and collaboration through international partnerships.

Promotion of open access and data sharing

Championing open access to research results and data greatly enhances knowledge dissemination and supports

the integration of HTS technologies in plant disease management. Data-sharing platforms can accelerate scientific discoveries and foster collaborative efforts (Adenle et al. 2012; Schaduangrat et al. 2020).

Implementing these strategies can democratize access to HTS and its benefits, culminating in more effective plant disease management approaches and contributing to global food security.

Developing policies and guidelines

Establishing best practices and regulatory frameworks for utilizing HTS in plant disease management is paramount to ensure its responsible and effective use. Developing and implementing these policies and guidelines will help safeguard data integrity and protect intellectual property rights. The following are key aspects that require careful consideration:

Sample preparation

Guidelines for sample collection, storage, and processing must be established to ensure consistent and high-quality results. Standard operating procedures (SOPs) must be developed and strictly adhered to to minimize variability and contamination during sample preparation.

Data analysis

To ensure accurate and reliable results when analyzing data, it is important to establish best practices for quality control, filtering, and normalization. This may involve developing and validating standardized bioinformatics pipelines and using appropriate statistical methods for data interpretation.

Quality control

Developing guidelines for quality control measures at various stages of the HTS process, from sample preparation to data analysis, is crucial. These guidelines will help ensure the reproducibility and reliability of HTS results, thereby facilitating their interpretation and application in plant disease management.

Data sharing

Establishing policies for data sharing and management will foster research collaboration and knowledge exchange. This may involve the development of data-sharing platforms, repositories, and data standards, along with data access, privacy, and security guidelines.

Intellectual property rights

To safeguard the intellectual property rights associated with HTS technologies and their applications in plant disease management, it is crucial to establish regulatory frameworks. This may require the development of

policies and agreements concerning patenting, licensing, and benefit-sharing, ensuring that the interests of various stakeholders, including researchers, institutions, and communities, are safeguarded.

By adhering to the best practices and regulatory frameworks for HTS in plant disease management, the scientific community can ensure this powerful technology's responsible and effective utilization. This will help maintain data integrity, protect intellectual property rights, and contribute to more effective and sustainable plant disease management strategies, ultimately enhancing global food security.

Conclusions

HTS has the potential to revolutionize plant disease management with its rapid and precise pathogen identification capabilities. It can also aid in discovering new and emerging pathogens and support disease surveillance, plant breeding, and genetic engineering efforts. With continuous advancements in HTS technologies, we can expect more affordable, accessible, and efficient applications in plant disease management. However, to fully tap into the potential of HTS, we must navigate a number of challenges, including technical and logistical barriers, data analysis and interpretation issues, legal considerations, and economic factors. Building capacity and fostering global collaboration, particularly in resource-limited settings and developing countries, is crucial for extending HTS benefits to a broader array of researchers and institutions. Moreover, establishing best practices and regulatory frameworks is essential for the responsible and effective implementation of HTS in plant disease management. This integrated approach, along with the incorporation of other omics approaches and advanced imaging techniques, will allow the scientific community to contribute to more effective and sustainable plant disease management strategies, with the ultimate goal of ensuring global food security and well-being for future generations. Continued investment in research, capacity building, and collaboration will be pivotal in realizing the full potential of HTS, transforming plant disease management, and safeguarding our agricultural systems. The future of plant disease management hinges on our ability to harness the power of these advanced technologies, fostering a new era of discovery and application in plant pathology.

Abbreviations

CBD	Convention on Biological Diversity
ddPCR	Droplet digital polymerase chain reaction
GBIF	Global Biodiversity Information Facility
GSC	Genomic standards consortium
HTS	High-throughput sequencing

IPR	Intellectual property rights
ITPGRFA	International Treaty on Plant Genetic Resources for Food and Agriculture
PAMPs	Pathogen-associated molecular patterns
PCR	Polymerase chain reaction
PRRs	Pattern recognition receptors
PSTVd	<i>Potato spindle tuber viroid</i>
PTI	PAMP-triggered immunity
rep-PCR	Repetitive extragenic palindromic polymerase chain reaction
SOPs	Standard operating procedures
TSWV	<i>Tomato spotted wilt tospovirus</i>
TYLCV	<i>Tomato yellow leaf curl virus</i>

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Author contributions

MMN and QZ conceptualized, developed the research questions, and designed the study framework. Conducted a comprehensive literature review and synthesized the information. Wrote and revised the manuscript. GM reviewed and provided constructive feedback on the manuscript. YW conceptualized and contributed to the overall direction and scope of the review paper. Reviewed and provided feedback on the manuscript, including suggestions for improvements in organization and clarity. All authors read and approved the final version of the manuscript.

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Declarations

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Not applicable.

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Competing interests

The authors declare that they have no competing interests.

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