

Combating Phytopathogens by Integration of Metagenomics and Phototrophic Biotechnologies: Toward Sustainable Agricultural Practices

Assemgul K. Sadvakasova, Bekzhan D. Kossalbayev, Dilnaz Zaletova, Meruyert O. Bauenova, Zhiyong Huang, Sergey K. Zharmukhamedov, Sergey Shabala & Suleyman I. Allakhverdiev

To cite this article: Assemgul K. Sadvakasova, Bekzhan D. Kossalbayev, Dilnaz Zaletova, Meruyert O. Bauenova, Zhiyong Huang, Sergey K. Zharmukhamedov, Sergey Shabala & Suleyman I. Allakhverdiev (2025) Combating Phytopathogens by Integration of Metagenomics and Phototrophic Biotechnologies: Toward Sustainable Agricultural Practices, *Critical Reviews in Plant Sciences*, 44:2, 70-87, DOI: [10.1080/07352689.2025.2494872](https://doi.org/10.1080/07352689.2025.2494872)

To link to this article: <https://doi.org/10.1080/07352689.2025.2494872>



© 2025 The Author(s). Published with license by Taylor & Francis Group, LLC.



Published online: 24 Apr 2025.



[Submit your article to this journal](#)



Article views: 1953



[View related articles](#)



[View Crossmark data](#)



Citing articles: 2 [View citing articles](#)

Combating Phytopathogens by Integration of Metagenomics and Phototrophic Biotechnologies: Toward Sustainable Agricultural Practices

Assemgul K. Sadvakasova^a, Bekzhan D. Kossalbayev^{b,c}, Dilnaz Zaletova^a, Meruyert O. Bauenova^a, Zhiyong Huang^d, Sergey K. Zharmukhamedov^e, Sergey Shabala^f  and Suleyman I. Allakhverdiev^{e,g,h} 

^aFaculty of Biology and Biotechnology, Al-Farabi Kazakh National University, Almaty, Kazakhstan; ^bDepartment of Chemical and Biochemical Engineering, Institute of Geology and Oil-Gas Business Institute Named After K. Turyssov, Satbayev University, Almaty, Kazakhstan; ^cEcology Research Institute, Khoja Akhmet Yassawi International Kazakh-Turkish University, Turkistan, Kazakhstan; ^dTianjin Institute of Industrial Biotechnology, Chinese Academy of Sciences, Tianjin Airport Economic Area, Tianjin, China; ^eInstitute of Basic Biological Problems, FRC PSCBR RAS, Pushchino, Russia; ^fSchool of Biological Science, University of Western Australia, Crawley, Australia; ^gK.A. Timiryazev Institute of Plant Physiology, Moscow, Russia; ^hFaculty of Engineering and Natural Sciences, Bahçeşehir University, Istanbul, Turkey

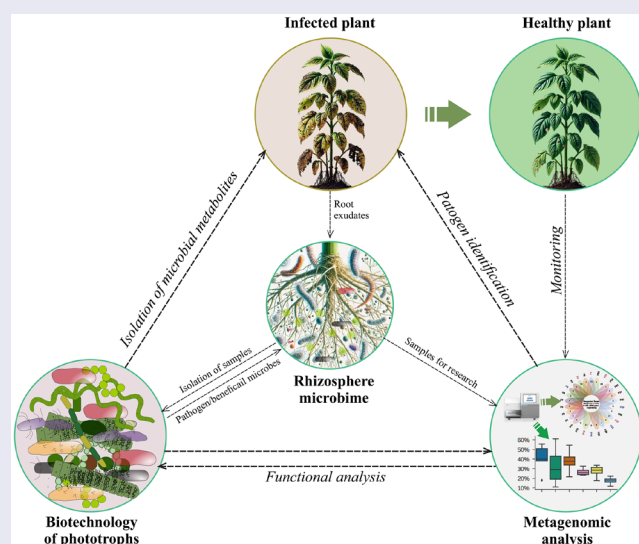
ABSTRACT

Rising global food demand amid climate change presents unprecedented challenges for modern agriculture. The spread of phytopathogens and the degradation of agroecosystems necessitate the development of innovative plant protection solutions. Traditional chemical pesticides are losing their effectiveness due to the emergence of resistant pathogens and their adverse environmental impacts, thereby intensifying interest in biological control methods. This study examines the integration of metagenomic analysis and phototrophic biotechnology as a promising approach to biocontrol. Metagenomics enables the precise identification of phytopathogens and beneficial microorganisms, laying the groundwork for the development of targeted biopesticides. Phototrophic microorganisms, including microalgae and cyanobacteria, exhibit antimicrobial properties and contribute to the restoration of soil ecosystems. The convergence of these technologies offers opportunities to form adaptive microbial consortia that ensure the long-term sustainability of agroecosystems. The paper discusses key challenges, including data processing complexities, the scalability of technologies, and regulatory barriers, and underscores the need for standardized methodologies and interdisciplinary collaboration. The integration of metagenomics and phototrophic biotechnology represents a promising direction for creating environmentally safe and sustainable agricultural production systems.

KEYWORDS

Biopesticides; biocontrol; cyanobacteria; metagenomics; microalgae; microbial communities; phototrophic biotechnology; sustainable agriculture

GRAPHICAL ABSTRACT



CONTACT Sergey Shabala  Sergey.Shabala@uwa.edu.au  suleyman.allakhverdiev@gmail.com 

This article has been corrected with minor changes. These changes do not impact the academic content of the article.

© 2025 The Author(s). Published with license by Taylor & Francis Group, LLC.

This is an Open Access article distributed under the terms of the Creative Commons Attribution-NonCommercial-NoDerivatives License (<http://creativecommons.org/licenses/by-nc-nd/4.0/>), which permits non-commercial re-use, distribution, and reproduction in any medium, provided the original work is properly cited, and is not altered, transformed, or built upon in any way. The terms on which this article has been published allow the posting of the Accepted Manuscript in a repository by the author(s) or with their consent.

Abbreviations: DNA: Deoxyribonucleic Acid; RNA: Ribonucleic Acid; PCR: Polymerase Chain Reaction; ITS: Internal Transcribed Spacer; ISR: Induced Systemic Resistance; SAR: Systemic Acquired Resistance; SA: Salicylic Acid; JA: Jasmonic Acid; PBP: Phycobiliproteins; FOL: *Fusarium oxysporum* f. sp. *lycopersici*; Foc: *Fusarium oxysporum* f. sp. *cubense*; H₂O₂: Hydrogen Peroxide; NGS: Next-Generation Sequencing; BUSCO: Benchmarking Universal Single-Copy Orthologs; MEGAN: Metagenome Analyzer; RDP: Ribosomal Database Project; SynCon: Synthetic Consortium.I. Introduction

Agricultural lands occupy approximately 40% of the Earth's terrestrial surface, with their significant expansion over the past three centuries driven by the need to provide food for a rapidly growing global population (Lal, 2023). However, the intensive utilization of these lands, accompanied by an increasing demand for food to sustain this population growth, has led to substantial environmental and social challenges (Adisa *et al.*, 2024).

One of the most significant threats to agricultural production, resulting in substantial crop losses, is the outbreak of plant diseases (Singh *et al.*, 2023). Currently, bacterial pathogens are responsible for over 7% of infectious plant diseases, while viruses and phytoplasmas account for approximately 9%. Most plant diseases, approximately 83%, are caused by fungal pathogens, which annually reduce crop yields by 10%–15% (Peng *et al.*, 2021; Khakimov *et al.*, 2022). A striking historical example of catastrophic consequences is the Irish Potato Famine caused by fungus *Phytophthora infestans* (Wang *et al.*, 2024). In addition to direct economic losses, phytopathogens degrade product quality by increasing the levels of toxins such as aflatoxins and mycotoxins (Gullino *et al.*, 2022).

Traditional approaches to managing phytopathogens, primarily relying on chemical pesticides, have proven effective but come with significant limitations. The intensive application of pesticides results in soil, water, and air pollution, while also destroying beneficial microbial communities, including nitrogen-fixing bacteria, thereby disrupting the nitrogen cycle and reducing soil fertility (Pahalvi *et al.*, 2021; Zhou *et al.*, 2025). Microbial diversity in the rhizosphere is a critical element of agricultural system resilience, as beneficial microorganisms in the root zone actively participate in nutrient cycling, stimulate plant growth, and suppress phytopathogens (Hakim *et al.*, 2021; Lahlali *et al.*, 2022). However, intensive farming practices, accompanied by the extensive use of agrochemicals and the disruption of agronomic practices, degrade soil microbiota, thereby weakening the protective functions of the rhizosphere community (Collinge *et al.*, 2022). Furthermore, pesticide residues in the environment and food pose risks to human health (Deguine *et al.*, 2023).

The issue of plant disease outbreaks is further exacerbated by global climate change, which promotes the expansion of pathogen ranges and enhances their virulence (Garrett *et al.*, 2021; Etherton *et al.*, 2024). Rising average temperatures, altered precipitation patterns, and extreme weather events contribute to the evolution of new strains with increased virulence (Hunjan and Lore, 2020; Roussin-Léveillé *et al.*, 2024). *Fusarium graminearum*, which thrives in warm and humid climates, is gradually displacing the less aggressive *Fusarium culmorum* in northern regions due to climate warming (Karlsson *et al.*, 2021). Notably, shifts in temperature and humidity directly affect plant immune mechanisms, making them more susceptible to infection (Kim *et al.*, 2022). The rapid escalation in plant disease incidence undermines food security and destabilizes global trade networks, thereby underscoring the urgent need for comprehensive protective strategies capable of adapting to pathogens' evolving characteristics.

Faced with these challenges, researchers have turned to alternative; environmentally sound management strategies, such as biological control, to restore microbiological balance while safeguarding both the environment and human health. In this context, special attention is directed toward integrating innovative technologies—metagenomics and phototrophic microorganisms (microalgae and cyanobacteria). Metagenomic analysis reveals the dynamics of microbial communities, providing valuable insights for disease management and overcoming the limitations of traditional culture-based methods (Newberry *et al.*, 2020). Phototrophic microorganisms, in turn, produce a wide spectrum of bioactive compounds that inhibit phytopathogen growth while simultaneously stimulating plant physiological processes, thereby enhancing their tolerance to adverse environmental factors such as drought, salinity, and temperature fluctuations (Lee and Ryu, 2021; Song *et al.*, 2022; Bauenova *et al.*, 2024).

This article provides a detailed analysis of the potential for combining metagenomic approaches with phototrophic biotechnology to combat phytopathogens in the face of current ecological challenges. Emphasis is placed on assessing the possible synergistic effects of jointly applying these methods, which may enhance

plant resistance to pathogens, restore soil fertility, and reduce environmental impact. Existing challenges and prospects for utilizing these technologies are examined, alongside directions for further research. This review serves as a methodological foundation for the development of specialized bioproducts and plant protection systems, offering novel solutions aimed at promoting sustainable agriculture through reduced chemical inputs, the preservation of biodiversity, and the maintenance of long-term productivity.

II. Metagenomics as a tool for studying phytopathogens and their microbial communities

A. Metagenomics in the diagnosis and biocontrol of phytopathogens

Effective management of phytopathogens is impossible without timely and accurate diagnostics, as early detection of infections is crucial for preventing significant crop losses (Nazarov *et al.*, 2020). Traditional diagnostic methods, including visual observation, microscopy, mycological analysis, and indicator plant assays, rely on external manifestations of plant diseases and often face significant limitations due to the similarity of symptoms caused by different phytopathogens (Prasanna *et al.*, 2024). Over the past decade, molecular techniques, such as advanced polymerase chain reaction (PCR) methods (nested, multiplex, and quantitative), isothermal amplification, and DNA- or RNA-based probe technologies have markedly improved the accuracy and speed of identifying soilborne phytopathogens (Jayalakshmi *et al.*, 2023; Kumar *et al.*, 2023). However, these approaches require specific primers or probes, limiting their applicability in detecting novel or poorly characterized species (Piombo *et al.*, 2021). Unlike traditional and molecular methods, metagenomics offers a fundamentally new level of microbial community analysis, enabling the identification of even uncultivable and previously unknown microorganisms (Gökdemir *et al.*, 2022; Navgire *et al.*, 2022). Next-generation sequencing (NGS) technologies such as Illumina, PacBio, and Oxford Nanopore have greatly expanded our capacity to explore microbial diversity, providing high accuracy and scalability in metagenomic research (Akaçin *et al.*, 2022).

Metagenomics has revolutionized our understanding of microbial diversity and metabolic processes, offering new insights into the microbial world and its interactions with the environment (Nam *et al.*, 2023). Metagenomic analysis facilitates the determination of taxonomic composition in microbial communities, the

detection of phytopathogens via their specific genetic markers, and the examination of functional genes associated with virulence and pathogenicity (Fenibo *et al.*, 2022; Nwachukwu and Babalola, 2022). The ability of metagenomics to identify microorganisms at the strain level substantially enhances the development of reliable biopesticides, providing more effective plant protection (Anyansi *et al.*, 2020). These data enable the targeted selection of microorganisms, including phototrophic species that can produce antimicrobial compounds and immunomodulators required for the creation of effective bioproducts.

B. Classification of metagenomics analysis

Metagenomic studies are broadly categorized into structural and functional metagenomics, each offering unique advantages in the study of microbial communities (Diwan *et al.*, 2022).

Structural metagenomics focuses on the taxonomic profiling of microbial communities and the identification of phytopathogens through amplicon sequencing of phylogenetic markers, including 16S/18S/26S rRNA genes and internal transcribed spacer (ITS) regions (Navgire *et al.*, 2022; Clagnan *et al.*, 2024). Metagenomic amplicon sequencing has been applied to analyze microbial communities in cases of pea root rot, revealing shifts in microbiome structure and increased relative abundance of taxa such as *Rhizobium*, *Fusarium*, and *Pythium* (Hossain *et al.*, 2021). Studies on the microbiota of Welsh onion demonstrated the effectiveness of ITS1 rRNA amplicon sequencing in detecting the phytopathogens *Stemphylium* and *Colletotrichum*, which are associated with leaf blight, and showed significant changes in both phyllosphere and rhizosphere microbiomes following infection (Jayasinghe *et al.*, 2024). The research presented in Table 1 highlights the potential of structural metagenomics methods for investigating phytopathogens and assessing their impact on plant microbiomes.

Functional metagenomics involves sequencing fragments of the entire genome to annotate active genes and biochemical pathways associated with pathogenicity and other key microbial community functions (Diwan *et al.*, 2022). This approach analyzes all DNA fragments in a sample, regardless of their origin, thereby expanding the capacity to identify microorganisms, assess genetic composition, and explore functional pathways (Pérez-Cobas *et al.*, 2020). The studies shown in Table 2 confirm the high efficacy of functional metagenomic analysis in identifying key genes and enzymes involved in plant-phytopathogen interactions and in beneficial microorganism activity.

Table 1. Studies in structural metagenomics for managing phytopathogens.

Research objective	Direction of structural metagenomics	Study results	Metabolic pathways influencing pathogenicity	References
Determination of wheat virome composition (<i>Triticum aestivum</i> L.)	Identification of known and novel viral sequences associated with plants and fungi	Identified known wheat viruses (WSMV, TriMV, HPWMoV, BYDV-PAV, CYDV) and novel viral sequences, including wheat umbra-like virus (WULV), wheat-associated vipovirus (WaVPV), tobamo-like virus (WaTBLV), and a new mitovirus	Viral sequences affect host metabolism by activating RNA interference (RNAi) defense mechanisms and altering physiological processes to facilitate replication and pathogenicity	Redila <i>et al.</i> (2021)
Study of viruses associated with papaya ringspot disease (PRSD)	Identification of viruses causing PRSD	Detected Moroccan watermelon mosaic virus (MWMV) and three <i>Carlavirus</i> species, including known CpMMV and novel PaMV and PaMMV; PRSV was not detected	MWMV strongly linked to PRSD symptoms in papaya fruits; viruses damage leaf and fruit tissues, altering physiological processes and reducing yield	Mumo <i>et al.</i> (2020)
Analysis of fungal communities associated with grapevine trunk diseases (GTD)	Identification of pathogenic fungi influencing GTD symptom development	Identified 258 taxa, including 10 species linked to GTD, with <i>Diplodia</i> sp., <i>N. cordaticola</i> , and <i>Diaporthe</i> sp. most common. Symptomatic vines showed greater fungal diversity (9 species) compared to asymptomatic ones (4 species)	Release of phytotoxins and secondary metabolites by pathogenic fungi contributes to GTD symptoms	Patanita <i>et al.</i> (2022)
Study of bacterial diversity in symptomatic and asymptomatic banana plants affected by bacterial wilt	Comparative analysis of microbiota in healthy and infected plants	Taxonomic analysis revealed 17 bacterial types in asymptomatic plants and 9 in symptomatic ones. Unique to asymptomatic plants were 102 bacterial genera. Cyanobacteria and Proteobacteria accounted for >99% of bacterial fragments in both	High species diversity of endophytic bacteria in asymptomatic plants likely creates antagonistic pressure on pathogens via competition for nutrients and niches; reduced diversity in infected plants may facilitate pathogen spread	Suhaimi <i>et al.</i> (2017)
Development of a workflow for precise fungal pathogen identification in wheat	Identification of species composition and distribution of fungal pathogens and microbial communities	Detected all fungal diseases present in infected samples, including stripe rust (<i>Puccinia striiformis</i> f. sp. <i>tritici</i>), Septoria tritici blotch (<i>Zymoseptoria tritici</i>), and tan spot (<i>Pyrenophora tritici-repentis</i>), along with one additional disease (Septoria nodorum blotch caused by <i>Parastagonospora nodorum</i>)	Leaves infected by <i>Puccinia</i> and <i>Zymoseptoria</i> showed co-presence of <i>Pseudomonas</i> bacteria, potentially playing a role in pathogenesis	Hu <i>et al.</i> (2019)
Identification of phytopathogenic viral sequences in fresh and wastewater samples and sludge in tropical areas of Mexico	Analysis of aquatic ecosystems to identify viruses threatening agriculture	Identified 15 phytopathogenic viruses of the <i>Virgaviridae</i> family and <i>Tobamovirus</i> genus, including pepper mild mottle virus, tomato brown rugose fruit virus, and tropical soda apple mosaic virus	<i>Tobamovirus</i> likely infects plants via waterborne transmission pathways	Lopez-Roblero <i>et al.</i> (2024)

Integrating structural and functional approaches provides a comprehensive understanding of microbial community composition and functional mechanisms. Research on *Plasmodiophora brassicae* in Chinese cabbage revealed how environmental factors and microbial interactions influence resistance to clubroot disease (Liu *et al.*, 2024). Metagenomic analysis has shown that combined applications of *Bacillus velezensis* VB7 and *Trichoderma koningiopsis* TK increase fungal abundance and diversity in tomato rhizospheres, effectively suppressing root-knot nematode infections by altering microbiome structure

(Kamalanathan *et al.*, 2023). Consequently, metagenomic approaches lay the groundwork for developing more effective and long-term strategies for biocontrol and microbial community management.

C. Challenges and prospects for using metagenomics in the biocontrol of plant phytopathogens

Metagenomics offers new opportunities for precise diagnosis of phytopathogens and for analyzing their

Table 2. Functional metagenomic studies as a key approach in phytopathogen control.

Research objective and methodology	Key phytopathogens and their functions	Key microbial interactions	Metabolic pathways influencing pathogenicity	References
Study of soil microbial response to <i>Ralstonia solanacearum</i> and its correlation with soil properties	<i>Ralstonia solanacearum</i> causes bacterial wilt, negatively correlates with phosphorus levels and plant health	Healthy soils enriched with <i>Comamonadaceae</i> (e.g., <i>Ramlibacter tataouinensis</i>) and <i>Halobacteriaceae</i> show antagonism to the pathogen; infected soils favor <i>Halostagnicola larsenii</i>	Observed 468 horizontal gene transfer events enhancing microbial adaptation and affecting colonization and pathogenicity in soils	Xiao <i>et al.</i> (2024)
Analysis of microbial diversity and functional traits in suppressive and conducive soils for banana Fusarium wilt suppression	<i>Fusarium oxysporum</i> f.sp. <i>cubense</i> (Foc) attacks the vascular system of banana plants	<i>Pseudomonas</i> , <i>Burkholderia</i> , and <i>Streptomyces</i> dominate suppressive soils, while conducive soils harbor <i>Bacillus</i> and more <i>Streptomyces</i>	High levels of zinc and manganese transporters enhance siderophore synthesis in suppressive soils, increasing pathogen resistance and nutrient uptake in plants	Nisrina <i>et al.</i> (2021)
Study of endophytic root microbiome response to Fusarium infection	<i>Fusarium oxysporum</i> f. sp. <i>cubense</i> (Foc)	Dominance of <i>Proteobacteria</i> , <i>Bacteroidetes</i> , and <i>Actinobacteria</i> with antagonistic interactions involving <i>Pseudomonadales</i> and <i>Streptomycetaceae</i>	Infected root microbiomes engage in carbohydrate metabolism, cell wall degradation, and symbiotic nutrient acquisition	Kaushal <i>et al.</i> (2020)
Analysis of rhizosphere microbiome in wild ginseng (<i>Panax ginseng</i>) and its role in resistance to fungal diseases	<i>Ilyonectria robusta</i> causes root rot, reducing water and nutrient uptake	Dominant taxa include <i>Pseudomonadota</i> , <i>Actinomycetota</i> , and <i>Acidobacteriota</i> . Enriched <i>Streptomyces</i> spp. suppress fungal pathogens	Denitrification genes reduce soil fertility, while ring-hydroxylating dioxygenase (RHD) genes degrade aromatic allelochemicals. Actinomycins D and Y6 exhibit antifungal activity	Huang <i>et al.</i> (2024)
Carbon cycle analysis in oat (<i>Avena fatua</i>) roots grown under labeled ¹³ CO ₂ conditions in rhizosphere and bulk soils	<i>Burkholderiales</i> , a potential plant pathogen using carbon from root exudates	Phages associated with <i>Burkholderiales</i> and <i>Catenulispora</i> sp. in the rhizosphere modulate growth and carbon cycling	Genes for hormone modulation, plant pathogenicity, and microeukaryote defense highlight microbial and phage roles in carbon flux regulation	Starr <i>et al.</i> (2021)
Role of rhizosphere microbes in tomato resistance to <i>Ralstonia solanacearum</i> using resistant and susceptible varieties	<i>Ralstonia solanacearum</i> , a soilborne pathogen disrupting vascular function	Microbiota transplantation from resistant to susceptible varieties suppresses symptoms; isolated <i>Flavobacterium</i> TRM1 suppresses pathogen	TRM1 genomic features, including monosaccharide transporters, limit sugar availability for pathogen colonization	Kwak <i>et al.</i> (2018)
Mechanisms underpinning suppressive soil resistance to Panama disease in bananas	<i>Fusarium oxysporum</i> f.sp. <i>cubense</i> TR4	Suppressive soils enriched with <i>Myxococcales</i> , <i>Pseudomonadales</i> , and <i>Xanthomonadales</i> ; <i>Pseudomonas</i> spp. display antagonism toward Foc4	Quorum sensing, biofilm formation, and antimicrobial compound synthesis genes are enriched in suppressive soil microbiomes	Shen <i>et al.</i> (2022)
Microbial differences in healthy and diseased pepper plants to understand pathogen response and beneficial microbe roles	<i>Fusarium</i> spp. produce toxins affecting plant health	Diseased plants enriched with chemotaxis MCP genes attract beneficial bacteria (<i>Bacillus subtilis</i> , <i>Pseudomonas</i> spp.); diseased microbiomes lack alkaline phosphatase phoD genes	UDP-glucuronosyltransferase and LuxR CsgD regulatory genes promote biofilm formation and pathogen tolerance	Gao <i>et al.</i> (2021)
Impact of <i>Fusarium oxysporum</i> (fox) on rhizosphere and endosphere microbiomes in susceptible and resistant bean varieties	<i>Fusarium oxysporum</i> causes root infections and alters microbiome structure	Rhizosphere of resistant varieties enriched with <i>Flavobacterium</i> , <i>Bacillus</i> , and <i>Dyadobacter</i> ; endosphere enriched with <i>Sinorhizobium</i> and <i>Ensifer</i>	Terpenoid biosynthesis genes enriched in resistant varieties enhance fungal pathogen suppression	Mendes <i>et al.</i> (2023)

interactions with plant microbiomes. However, the implementation of this approach faces several difficulties. One key challenge is the complexity of data processing, including quality control, assembly, and binning—the process of grouping sequence fragments to reconstruct genomes. Although tools such as BUSCO, CheckM, Kraken, MetaPhlAn, MEGAN, and MetaBAT have been successfully applied to genome

assembly and microorganism identification, their effectiveness diminishes when dealing with highly fragmented datasets or heterogeneous communities containing closely related species (Aragona *et al.*, 2022; Iquebal *et al.*, 2022). This issue is compounded by the fact that existing reference databases (GenBank, Ribosomal Database Project, Greengenes, SILVA, and UNITE) used for annotation and identification are

often incomplete and fail to adequately capture the true biodiversity of phytopathogenic microorganisms in diverse ecosystems. Such gaps lead to the omission of key phytopathogens, thereby reducing the accuracy and informativeness of diagnostic efforts and hindering timely plant protection measures (Crandall *et al.*, 2020; Piombo *et al.*, 2021; Iquebal *et al.*, 2022). One promising solution to these problems is the application of machine-learning methods for classifying individual reads based on unique sequence features, enabling researchers to differentiate samples from infected and healthy plants independently of reference databases (Johnson *et al.*, 2023).

Successful implementation of metagenomic analysis requires the prior development of standardized protocols with clear criteria for data selection, processing, and unambiguous interpretation of results. Of particular importance is the establishment and validation of threshold values for read counts to identify functional genes and pathogenicity factors, which will ensure consistent data interpretation and comparability of results across different research groups (Roman-Reyna and Crandall, 2024).

Prospects for metagenomics involve its integration with other omics technologies, such as metatranscriptomics, metaproteomics, and metabolomics. A comprehensive omics-based approach will provide a holistic view of the activity and functional status of microbial consortia, deepening our understanding of their interactions with host plants (De Corato, 2020). Especially relevant is the advancement of interaction-network analysis of phytopathogens and beneficial microorganisms, which will facilitate the formation of stable, resilient microbial communities capable of effectively protecting plants. Finally, metagenomics lays the groundwork for microbial engineering by enabling the isolation of valuable microorganisms from complex communities – organisms that produce bioactive compounds with antiphytopathogenic properties. In this way, targeted metagenomic strategies shift the focus from merely studying microbial diversity to developing innovative biological products that enhance crop resistance to a wide range of phytopathogens (Masenya *et al.*, 2024).

III. Application of phototrophic biotechnology for sustainable phytopathogen management

A. Mechanisms of action of phototrophic microorganisms against phytopathogens

The use of phototrophic microorganisms, such as microalgae and cyanobacteria, has emerged as a

promising solution for environmentally friendly agriculture, owing to their capacity to serve as biofertilizers, biostimulants, and biopesticides (Sadvakasova *et al.*, 2022; Nawaz *et al.*, 2024; Vermelho *et al.*, 2024). The antimicrobial and insecticidal properties of cyanobacteria *Anabaena*, *Nostoc*, *Fischerella*, and others have proven effective in the biocontrol of various phytopathogens (Purushothaman and Irfana-Mol, 2020). In one study, the antifungal activity of 280 microbial strains was tested against six fungal and three oomycete strains. Among these, the best results were observed with aqueous extracts of the cyanobacteria *Tolypothrix tenuis* MACC-205 and *Trichormus variabilis* MACC-304, which inhibited the growth of 6 phytopathogens, and *Nostoc linckia* MACC-612, which suppressed 4 phytopathogens (Horváth *et al.*, 2023). In addition, cyanobacteria such as *Anabaena* and *Nostoc* enhance soil fertility by fixing nitrogen and carbon, while also contributing to the restoration of beneficial rhizosphere microbiomes (Bao *et al.*, 2021). Water extracts of the microalga *Chlorella vulgaris* inhibit the development of phytopathogens, strengthening plant defenses and thereby aiding agriculture in adapting to climate change (Alvarez *et al.*, 2021; Čmiková *et al.*, 2024). Jokel *et al.* (2023) demonstrated the antimicrobial potential of microalgae, specifically *Chlorella sorokiniana*, whose extract exhibited high efficacy against the phytopathogen *Phytophthora cactorum*, inhibiting its growth on strawberry leaves. In the study by Schmid *et al.* (2022), extracts from microalgae (*Nannochloropsis sp.*, *Phaeodactylum tricornutum*, *Scenedesmus obliquus*, *Chlorella vulgaris*, and *Spirulina sp.*) were tested for their antagonistic activity against the phytopathogens *Sclerotium rolfii*, *Rhizoctonia solani*, *Botrytis cinerea*, and *Alternaria alternata*. The most significant results were obtained against *S. rolfii* with extracts from *S. obliquus*, *Nannochloropsis sp.*, and *P. tricornutum*.

The application of phototrophic microorganisms for plant protection is based on multifaceted mechanisms, encompassing both direct suppression of phytopathogen growth and indirect effects related to the activation of systemic plant resistance and the regulation of soil microbial communities. Understanding these mechanisms is key to optimizing the use of microalgae and cyanobacteria in sustainable agriculture, which aims to conserve natural resources and maintain ecological balance (Berthon *et al.*, 2021). Figure 1 presents a general overview of the antimicrobial mechanisms of phototrophic microorganisms.

The direct mechanism involves suppressing phytopathogens through the synthesis of bioactive compounds that effectively disrupt the cell walls of pathogenic fungi and bacteria, thereby limiting their

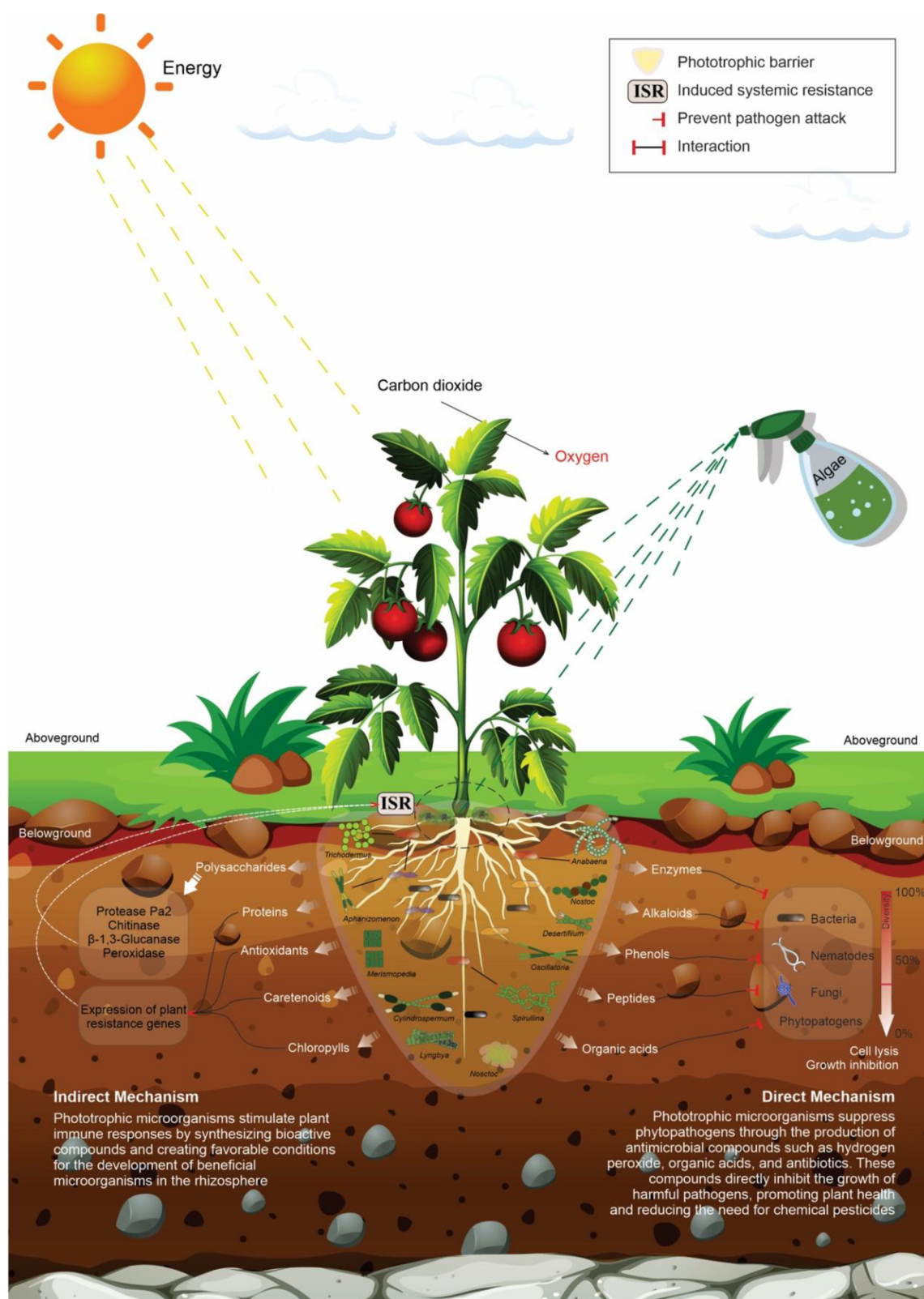


Figure 1. Mechanisms of action of phototrophic microorganisms in the fight against phytopathogens. Abbreviations: ISR: Induced Systemic Resistance; Pa2: Protease enzyme; β -1,3-Glucanase: Beta-1,3-glucanase enzyme; CO_2 : Carbon Dioxide; O_2 : Oxygen.

growth and reducing the likelihood of plant infections (Berthon *et al.*, 2021; Shah *et al.*, 2021; Akmukhanova *et al.*, 2023). Numerous studies have shown that

cyanobacterial extracts, owing to their production of abundant biologically active compounds, effectively inhibit the growth of pathogenic fungi. El-Sheekh *et al.*

(2022) demonstrated that foliar application of extracts from *Nostoc calcicola* and *Nostoc linckia*, which contain high levels of chlorophyll *a*, carotenoids and total phenols, significantly suppressed the pathogenic fungus *Fusarium oxysporum* f. sp. *lycopersici* in tomatoes. According to findings reported by Águila-Carricondo *et al.* (2024), cyanobacteria *Nostoc commune*, *Scytonema hyalinum*, and *Tolypothrix distortiona*, isolated from erosion-prone soils, showed strong inhibitory activity against phytopathogens *Phytophthora capsici*, *Pythium aphanidermatum*, and *Fusarium oxysporum* f. sp. *radicis-cucumerinum*, attributable to elevated production of hydrolytic enzymes that degrade the cellulose walls of phytopathogens and secondary metabolites synthesized under conditions of limited nitrogen and carbon availability. In another study, extracts from *Oscillatoria nigro-viridis* HSSASE 15, *Anabaena* sp. HSSASE11, and *Dunaliella* sp. HSSASE13 demonstrated significant antifungal activity against phytopathogens *Pythium ultimum*, *Fusarium solani*, and *Botryodiplodia theobromae*. The highest efficacy correlated with the elevated content of flavonoids, phenols, proteins, xylanase, glucanase and total neutral sugars (Senousy *et al.*, 2022). Furthermore, the cyanobacteria *Anabaena* sp. IPPAS B-2020 exhibited high fungicidal activity against *Fusarium culmorum*, *F. graminearum*, and *F. sporotrichioides*, attributed to the synthesis of bioactive compounds, including citric, lactic and acetic acids, terpenes, alkanes, alcohols and other low-molecular-weight organic substances (Bataeva *et al.*, 2024). *Neowestiellopsis persica* A1387 cyanobacterium exopolysaccharide extract demonstrated significant antifungal activity against *Fusarium oxysporum* *in vitro* and *in vivo*, reducing the severity of fusarium wilt in cucumbers, increasing their biomass and inhibiting the activity of antioxidant enzymes (Nowruzi and Beiranvand 2024).

Despite extensive research on cyanobacteria as sources of antifungal compounds, there is growing interest in microalgae, whose biologically active extracts also demonstrate notable antibacterial and antifungal activity, effectively suppressing phytopathogens (Ferreira *et al.*, 2023). In the study by Al-Nazwani *et al.* (2021), a methanolic extract of *Chlorella vulgaris*, containing palmitic and oleic acids, glycine and phenol, showed significant antifungal activity against *Rhizoctonia solani*, reducing the pathogenicity of this fungus on potatoes both *in vitro* and under greenhouse conditions. In another study, the diethyl ether extract of *Chlorella vulgaris*, rich in fatty acids, alcohols, esters, demonstrated high antifungal activity against *Fusarium oxysporum*, *Fusarium* sp., *Fusarium solani*, *Aspergillus flavus*, and *Aspergillus niger* (Perveen

et al., 2022). Analyses of *in vitro* and *in vivo* experiments indicate that polyphenols in aqueous suspensions of *Chlorella vulgaris* and *Tetrademus obliquus* can suppress the growth of the pathogenic fungus *Fusarium oxysporum* in spinach (Viana *et al.*, 2024). Scaglioni *et al.* (2019) investigated phenolic, and carotenoid extracts from *Nannochloropsis* sp. and *Spirulina* sp., which significantly inhibited the growth of a *Fusarium* complex, with natural phenolic acid extracts proving more effective than their synthetic counterparts. Bencheikh *et al.* (2022) showed that an aqueous extract of *Arthrospira platensis* grown in a modified medium exhibited high antifungal activity against *Fusarium culmorum*, *Alternaria solani*, and *Cladosporium* sp., as well as antibacterial activity, predominantly against Gram-positive bacteria, due to the presence of γ -linolenic acid and the synergistic effects of lauric and palmitoleic acids. Ambrico *et al.* (2020) reported that the hexane extract from the microalga *Dunaliella salina*, rich in β -carotene, demonstrated strong antibacterial activity both *in vitro* and *in vivo* against phytopathogenic bacteria *Pseudomonas syringae* pv. *tomato* and *Pectobacterium carotovorum* subsp. *carotovorum*, significantly reducing the incidence and severity of bacterial spot and soft rot symptoms in tomatoes and zucchinis.

The indirect mechanism by which phototrophic microorganisms act against phytopathogens is through stabilizing the structure and biodiversity of rhizosphere microbial communities and activating nutrient cycling processes (Berthon *et al.*, 2021; Shah *et al.*, 2021). Plants respond to localized infections through a salicylic acid (SA)-mediated signaling cascade, that triggers systemic acquired resistance (SAR), conferring prolonged protection against a variety of phytopathogens, including fungi, bacteria, and viruses (Kamle *et al.*, 2020). This process is further enhanced by root exudates, which serve as chemical signals to attract beneficial microorganisms and mediate interactions within the rhizosphere. Consequently, induced systemic resistance (ISR) is formed against phytopathogens, activating plant defense responses through jasmonic acid (JA) and ethylene signaling pathways (Zehra *et al.*, 2021). Root treatment with a *Scenedesmus*-677 extract effectively suppressed bacterial infections in tomato seedlings caused by *Clavibacter michiganensis*, whereas the application of *Leptolyngbya*-1267 enhanced plant resistance by activating defense responses through the SA signaling pathway (Toribio *et al.*, 2021).

In addition, phototrophic microorganisms that form symbiotic relationships with plants synthesize biologically active compounds that stimulate plant defense

systems and enhance systemic resistance to phytopathogens, as demonstrated by numerous studies. Polysaccharides boost defense mechanisms by activating enzymes such as phenylalanine ammonia-lyase, chitinase, β -1,3-glucanase, and peroxidase (Riseh *et al.*, 2022). Righini *et al.* (2019) demonstrated that aqueous extracts and polysaccharides from the cyanobacteria *Anabaena* sp. and the algae *Ecklonia* sp. and *Jania* sp. effectively suppressed the growth and sporulation of *Botrytis cinerea*, while indirectly activating plant defense mechanisms and reducing the likelihood of gray mold infection during preharvest treatments. Polysaccharides from microalgae such as *Porphyridium* sp., *Phaeodactylum tricornutum*, *Desmodesmus* sp., and *Dunaliella salina* effectively stimulated tomato plant defense mechanisms by activating antioxidant enzymes and pathogenesis-related proteins, modulating the metabolite profiles, and strengthening cell membrane structures (Rachidi *et al.*, 2021). In another study, polysaccharides isolated from *Chlorella vulgaris*, *C. sorokiniana*, *Dunaliella salina*, *Chlamydomonas reinhardtii* demonstrated significant biostimulatory effects on plant defense enzymes such as β -1,3-glucanase and phenylalanine ammonia-lyase (Farid *et al.*, 2019). The chloroform extract of the microalga *Tetraselmis rubens* demonstrated high antibacterial activity *in vitro* and *in vivo* against *Pseudomonas corrugata* due to a complex of bioactive compounds, including fatty acid esters, which effectively reduced the incidence of bacterial leaf spot in tomatoes (Ouaddi *et al.*, 2025).

Proteins, antioxidants, phenols, flavonoids, and other metabolites also provide substantial indirect protective effects by inhibiting the growth of diverse phytopathogens. Righini *et al.* (2020) reported that aqueous extracts of the cyanobacteria *Anabaena minutissima* and the algae *Ecklonia maxima* and *Jania adhaerens* exhibit strong antifungal effects against *Podosphaera xanthii*, the causal agent of cucumber powdery mildew. Extracts from *A. minutissima* and *J. adhaerens*, which contain proteins, phycobiliproteins (PBP), chlorophylls, carotenoids, and antioxidants, induced the expression of plant defense-related genes by activating SA and JA signaling pathways. These authors also investigated aqueous extracts and PBP from *A. minutissima*, which demonstrated potent antifungal activity against *Botrytis cinerea* on tomato fruits by inhibiting mycelial growth and colony formation. Moreover, PBPs preserved the integrity of cutin and pectin structures in treated fruits (Righini *et al.*, 2021). In another study, treating tomato seeds with PBPs from *A. minutissima* promoted seeds germination and growth by activating the defense enzymes

such as chitinase and β -1,3-D-glucanase, through elevated phenol and flavonoid contents, thereby conferring resistance to the phytopathogen *Rhizoctonia solani* (Righini *et al.*, 2023). Furthermore, aqueous extracts of *A. minutissima*, rich in proteins and carbohydrates, effectively protected tomato plants from soilborne phytopathogens *R. solani* and *Pythium ultimum* by enhancing plant resistance, including increased activity of endochitinase and glucanase defense enzymes and higher levels of carotenoids and chlorophyll (Righini *et al.*, 2025). Abdelaziz *et al.* (2022) applied aqueous extracts of the cyanobacteria *Desmonostoc muscorum*, *Anabaena oryzae*, and *Arthrospira platensis* to bolster pepper (*Capsicum annuum*) immunity against Fusarium wilt. Their findings revealed that cyanobacterial treatment conferred protection from phytopathogens by elevating the levels of photosynthetic pigments, osmoprotectants, and antioxidant enzymes while reducing hydrogen peroxide (H_2O_2) and lipid peroxidation. In a study by Ghareeb *et al.* (2022), extracts from the *Oscillatoria* sp. MT790332, containing flavonoid, phenolic, and quinone compounds, displayed significant nematocidal activity against the root-knot nematode *Meloidogyne incognita*, suppressing its development and simultaneously improving soybean growth, biomass, and chlorophyll content. These effects were associated with enhanced expression of plant defense genes linked to pathogenesis. Elsharkawy *et al.* (2022) demonstrated that extracts from microalgae and cyanobacteria such as *Chlorella vulgaris*, *Anabaena oryzae*, *Nostoc linckia*, *Spirulina platensis*, and *Dunaliella salina* effectively mitigate the severity of tomato mosaic virus. This protective effect is attributed to the induction of plant resistance mechanisms, evidenced by elevated peroxidase and polyphenol oxidase activity, as well as increased expression of the PR1 and PAL genes involved in SA and JA pathways (Elsharkawy *et al.*, 2022).

B. Limitations to the development of phototrophic biotechnology in the biocontrol of phytopathogens

Phototrophic biotechnology offers effective biocontrol methods aimed at suppressing phytopathogens through bioactive compounds produced by microalgae and cyanobacteria. However, its widespread adoption remains constrained by various technological, economic, and environmental factors.

Although microalgae and cyanobacteria themselves can serve as relatively low-cost raw materials, the industrial-scale cultivation and extraction of

biologically active compounds still pose a major financial challenge (Gonçalves, 2021). Research focused on optimizing technological processes and developing more efficient extraction methods has the potential to substantially lower overall costs (Righini *et al.*, 2022).

Despite numerous studies demonstrating the high biological activity of microalgae and cyanobacteria, the number of commercially available products derived from these organisms remains limited. Many promising compounds with biopesticidal properties are patented, yet only a few reach the market (Berthon *et al.*, 2021). One barrier in this regard is the adaptation of phototrophic microorganisms to environmental conditions during field trials (Parmar *et al.*, 2023). A thorough understanding of soil biological and ecological characteristics can significantly enhance the efficacy of phototrophic biocontrol agents, including improvements in sampling procedures, considerations of soil biota interactions, and adaptation to agroecological conditions (Lahlali *et al.*, 2022).

Although extracts from microalgae and cyanobacteria have proven effective against numerous phytopathogens, they may contain metabolites that are toxic to certain crop species (Ramakrishnan *et al.*, 2023). To improve both the efficacy and safety of microalgae- and cyanobacteria-based biocontrol agents, it is critical to account for their selective action against phytopathogens to avoid inadvertently promoting harmful organisms. Before these biopesticides are deployed on a large scale, it is essential to identify specific targets and select phototrophic microorganism strains with selective antimicrobial activity (Schmid *et al.*, 2022). In this context, metagenomics can serve as a powerful tool for the comprehensive analysis of phototrophic communities, enabling the identification of their composition and functional activity while evaluating potential ecosystem risks. This approach ensures the safety of microalgae- and cyanobacteria-based products, guarantees their long-term efficacy under field conditions, and minimizes adverse impacts on agroecosystems.

Equally important is the regulatory dimension of bioproduct application. With the introduction of new regulations, such as EU Regulation 2019/1009, procedures for registering and bringing microalgae- and cyanobacteria-based bioproducts to market are expected to become more streamlined (Berthon *et al.*, 2021). Nevertheless, the current level of regulatory oversight continues to require further research and confirmation of the safety and selectivity of these bioproducts for successful use in agriculture.

Consequently, overcoming these limitations through a comprehensive approach – encompassing production optimization, selectivity studies, and the development

of effective regulatory frameworks is essential for the successful and safe integration of phototrophic microorganisms into agricultural practice.

IV. Challenges and prospects of integrating metagenomics and phototrophic biotechnology in biopesticide development

In recent years, significant progress in biological control has been made possible by advances in computational technologies, molecular biology, and biotechnology. These tools have enabled researchers to delve deeper into the interactions between biocontrol agents, phytopathogens, and host plants at molecular, cellular, and ecological levels (Tariq *et al.*, 2020). However, despite these achievements, there remains a pressing need for integrated approaches to achieve more sustainable management of agroecosystems. One promising avenue involves combining metagenomic technologies with phototrophic biotechnology to enhance the biocontrol of phytopathogens and restore soil ecosystem functions.

Metagenomic techniques facilitate the identification and characterization of both pathogenic microorganisms and beneficial phototrophic microorganisms that possess antimicrobial and immunomodulatory properties. This integration offers the possibility of creating targeted bioproducts adapted to specific agroecosystem conditions, ensuring their effective performance in the soil and rhizosphere.

The application of specialized metagenomic analysis methods alongside detailed investigations of marker genes and the monitoring of changes in microbial diversity significantly expands our understanding of the dynamics and structure of soil microbial communities. This not only enables the identification of the most promising microbial strains but also paves the way for the design of optimized synthetic consortia (SynCon) specifically engineered to enhance plant resilience against phytopathogens and environmental stressors (Martins *et al.*, 2023). The introduction of phototrophic microorganisms into these consortia helps suppress phytopathogens, supply nutrients to plants, and boost their tolerance to unfavorable conditions (Sadvakasova *et al.*, 2023). Continuous monitoring and dynamic management of microbial community composition via a metagenomic approach maintains the stability, functionality, and high adaptability of these consortia under changing agroecosystem conditions (Rainey and Quistad, 2020).

Figure 2 illustrates the concept of integrating metagenomic analysis with phototrophic biotechnology in agriculture. The diagram highlights the key

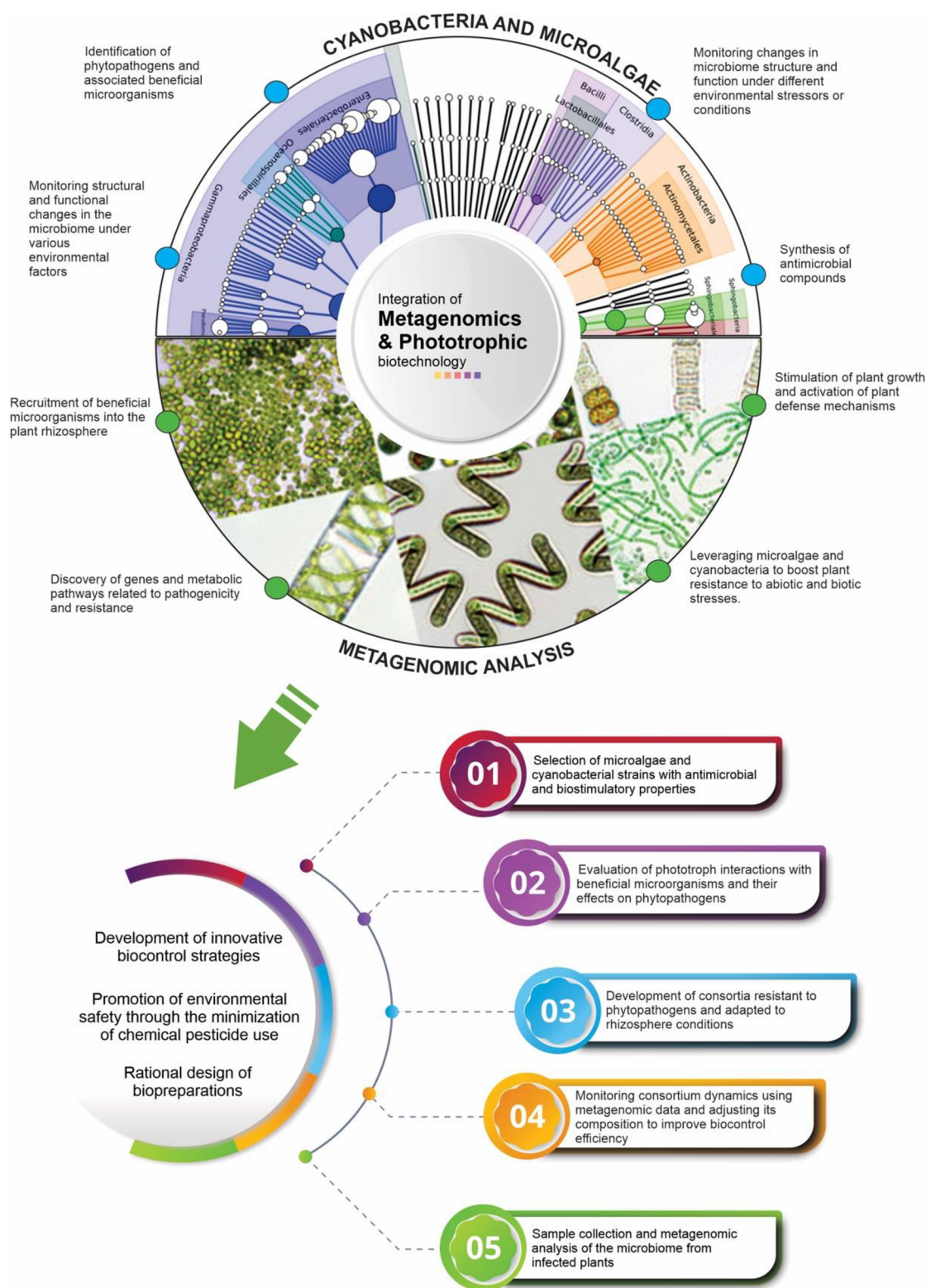


Figure 2. Prospects for the integration of metagenomics and phototrophic technology for biocontrol of phytopathogens.

advantages of these approaches and their synergistic application to microbial community management, including sequential steps for selecting, analyzing, optimizing, and deploying bioproducts. This integrated strategy aims to reduce dependence on chemical

pesticides while strengthening agroecosystem resilience to a range of biotic and abiotic stress factors.

The successful integration of metagenomics and phototrophic biotechnology into agriculture requires careful consideration of both scientific and socioeconomic

factors. Major technical challenges include the high costs of developing new methods for processing and interpreting large-scale metagenomic data, difficulties in scaling up laboratory research for practical field applications, and the need to maintain the stability and activity of phototrophic microorganisms under field conditions. Addressing these challenges demands the standardization of metagenomic analysis methodologies, as well as the development of uniform and reliable protocols for cultivating phototrophic microorganisms. In addition, it is essential to establish accessible and effective systems for monitoring and managing microbial consortia directly in agroecosystems.

Despite growing interest in biological control, challenges remain in demonstrating its profitability and practical value (Barratt *et al.*, 2018). The lack of compelling economic data on biocontrol effectiveness limits governmental support and narrows academic interest in developing new solutions. Farmers, particularly those with limited experience in biocontrol systems, often perceive them as less cost-effective than chemical pesticides, which complicates the adoption of innovative technologies (Barratt *et al.*, 2018; Deguine *et al.*, 2021). The advancement of biopreparations is further impeded by the intricacy of the registration procedures and the absence of unified international regulations. Establishing a global regulatory framework is crucial for streamlining the production and application of biopesticides (Koul, 2023). Effective coordination among government agencies, industrial organizations, and the scientific community is a critical factor for success. Significant investment in public research is needed to fill gaps often overlooked by the private sector. Policy supports through subsidies, regulatory standardization, and international collaboration will expedite the implementation of these technologies. Interdisciplinary approaches that integrate scientific knowledge with the practical needs of farmers can further facilitate adoption. Outreach and education for farmers demonstrating the long-term economic benefits and environmental safety of bioproducts along with effective marketing strategies are equally vital (Lee *et al.*, 2024). Systematic research dedicated to developing specialized bioproducts and gaining an in-depth understanding of microbial community interactions with plants and the environment is essential for the successful realization of this promising concept.

V. Conclusion

The application of metagenomics for the targeted selection of resilient phototrophic strains adapted to

various climatic and soil conditions ensure high precision and effectiveness in biocontrol. These microorganisms form the basis of new biopreparations that exhibit resilience to stress and function effectively across diverse agroecosystems. Functional metagenomics offers detailed insights into the mechanisms driving phototroph antagonism against phytopathogens, while also enhancing their efficacy. Furthermore, the development of synergistic microbial consortia facilitates the establishment of multi-component systems capable of adaptive biocontrol, even in dynamic environmental conditions. However, several critical challenges must be overcome to enable the widespread implementation of these technologies. Current limitations in metagenomic methods, such as sequencing accuracy and the complexity of data annotation, require further advancements to improve the analysis of complex microbial communities. Economic costs associated with the production of microalgal biomass and the extraction of bioactive compounds remain significant barriers, underscoring the need for more cost-effective and scalable methods. These challenges define the direction for future research aimed at improving cultivation technologies, reducing production costs, and increasing the accessibility of biopreparations for farmers. The successful implementation of innovative biotechnologies also depends on systemic support from governmental and international institutions and the establishment of an appropriate regulatory framework. Broad adoption of environmentally friendly biopreparations requires coordinated efforts by scientists, policymakers, and agricultural producers. Thus, the integration of metagenomics and phototrophic biotechnology lays the foundation for the future of sustainable agriculture, aimed at reducing environmental impacts, improving soil health, and strengthening plant protection. This approach is not only a promising direction for biotechnological research but also a strategic initiative with the potential to transform agricultural practices and ensure the long-term sustainability of agroecosystems.

Acknowledgments

We thank Dr. Huma Balouch for her valuable discussions and helpful feedback during the preparation of this manuscript.

Authors' contributions

Assemgul K. Sadvakasova: Data curation, Formal analysis, Validation, Writing – original draft; Dilnaz Zaletova: Data curation, Formal analysis, Validation; Meruyert O. Bauenova:

Resources, Investigation; Zhiyong Huang: Visualization, Software, Data curation; Bekzhan D. Kossalbayev and Sergey K. Zharmukhamedov: Resources, Investigation; Sergey Shabala and Suleyman I. Allakhverdiev: Supervision, Writing – review & editing.

Disclosure statement

The authors declare no conflict of interest.

Funding

This research has been funded by the Committee of Science of the Ministry of Science and Higher Education of the Republic of Kazakhstan: BR24992814. SKZ and SIA were supported by the grant from Russian Science Foundation (No: 24-14-00033). Table 1 was obtained within the state assignment of the Ministry of Science and Higher Education of the Russian Federation (theme No. 122050400128–1).

ORCID

Sergey Shabala  <http://orcid.org/0000-0003-2345-8981>
Suleyman I. Allakhverdiev  <http://orcid.org/0000-0002-0452-232X>

References

- Abdelaziz, A. M., Attia, M. S., Salem, M. S., Refaay, D. A., Alhoqail, W. A., and Senousy, H. H. 2022. Cyanobacteria-mediated immune responses in pepper plants against fusarium wilt. *Plants (Basel)* 11: 2049. doi:10.3390/plants11152049
- Adisa, N. O., Ilugbusi, N. B. S., Adelekan, N. O. A., Asuzu, N. O. F., and Ndubuisi, N. N. L. 2024. A comprehensive review of redefining agricultural economics for sustainable development: Overcoming challenges and seizing opportunities in a changing world. *World J. Adv. Res. Rev.* 21: 2329–1241. doi:10.30574/wjarr.2024.21.1.0322
- Águila-Carricondo, P., Román, R., Marín-Guirao, J. I., Cantón, Y., and de Cara, M. 2024. Native biocrust cyanobacteria strains showing antagonism against three soil-borne pathogenic fungi. *Pathogens* 13: 579. doi:10.3390/pathogens13070579
- Akaçin, İ., Ersoy, Ş., Doluca, O., and Güngörmüşler, M. 2022. Comparing the significance of the utilization of next generation and third generation sequencing technologies in microbial metagenomics. *Microbiol. Res.* 264: 127154. doi:10.1016/j.micres.2022.127154
- Akmukhanova, N. R., Leong, Y. K., Seilbek, S. N., Konysbay, A., Zayadan, B. K., Sadvakasova, A. K., Sarsekeyeva, F. K., Bauenova, M. O., Bolatkhan, K., Alharby, H. F., Chang, J., and Allakhverdiev, S. I. 2023. Eco-friendly biopesticides derived from CO₂-Fixing cyanobacteria. *Environ. Res.* 239: 117419. doi:10.1016/j.envres.2023.117419
- Al-Nazwani, M. S., Aboshosha, S. S., El-Saedy, M. A. M., Ghareeb, R. Y., and Komeil, D. A. 2021. Antifungal activities of *Chlorella vulgaris* extract on black scurf disease, growth performance and quality of potato. *Arch. Phytopathol. Plant Prot.* 54: 2171–2190. doi:10.1080/03235408.2021.1925434
- Alvarez, A. L., Weyers, S. L., Goemann, H. M., Peyton, B. M., and Gardner, R. D. 2021. Microalgae, soil and plants: A critical review of microalgae as renewable resources for agriculture. *Algal Res.* 54: 102200. doi:10.1016/j.algal.2021.102200
- Ambrico, A., Trupo, M., Magarelli, R., Balducchi, R., Ferraro, A., Hristoforou, E., Marino, T., Musmarra, D., Casella, P., and Molino, A. 2020. Effectiveness of *Dunaliella salina* extracts against *Bacillus subtilis* and bacterial plant pathogens. *Pathogens* 9: 613. doi:10.3390/pathogens9080613
- Anyansi, C., Straub, T. J., Manson, A. L., Earl, A. M., and Abeel, T. 2020. Computational methods for strain-level microbial detection in colony and metagenome sequencing data. *Front. Microbiol.* 11: 1925. doi:10.3389/fmicb.2020.01925
- Aragona, M., Haegi, A., Valente, M. T., Riccioni, L., Orzali, L., Vitale, S., Luongo, L., and Infantino, A. 2022. New-generation sequencing technology in diagnosis of fungal plant pathogens: A dream comes true? *J. Fungi (Basel)* 8: 737. doi:10.3390/jof8070737
- Bao, J., Zhuo, C., Zhang, D., Li, Y., Hu, F., Li, H., Su, Z., Liang, Y., and He, H. 2021. Potential applicability of a cyanobacterium as a biofertilizer and biopesticide in rice fields. *Plant Soil* 463: 97–112. doi:10.1007/s11104-021-04899-9
- Barratt, B. I. P., Moran, V. C., Bigler, F., and Van Lenteren, J. C. 2018. The status of biological control and recommendations for improving uptake for the future. *BioControl* 63: 155–167. doi:10.1007/s10526-017-9831-y
- Bataeva, Y. V., Sinetova, M. A., Kurashov, E. A., Krylova, J. V., Kolombet, L. V., and Grigoryan, L. N. 2024. Characterization of biological activity and evaluation of exogenous metabolites of cyanobacteria “*Anabaena*” sp. IPPAS B-2020. *Microbiology* 93: 537–550. doi:10.1134/S0026261724604871
- Bauenova, M. O., Sarsekeyeva, F. K., Sadvakasova, A. K., Kossalbayev, B. D., Mammadov, R., Token, A. I., Balouch, H., Pashkovskiy, P., Leong, Y. K., Chang, J., and Allakhverdiev, S. I. 2024. Assessing the efficacy of cyanobacterial strains as *Oryza sativa* growth biostimulants in saline environments. *Plants (Basel)* 13: 2504. doi:10.3390/plants13172504
- Bencheikh, A., Mamache, W., Gharzouli, A., Kouachi, A., Khadidja, H., Daichi, M. B., and Rouag, N. 2022. Evaluation of the *Spirulina* (*Arthrospira platensis* Gomont) antimicrobial activity. *Turkish JAF. SciTech.* 10: 2051–2055. doi:10.24925/turjaf.v10i10.2051-2055.5307
- Berthon, J., Michel, T., Wauquier, A., Joly, P., Gerbore, J., and Filaire, E. 2021. Seaweed and microalgae as major actors of blue biotechnology to achieve plant stimulation and pest and pathogen biocontrol: a review of the latest advances and future prospects. *J. Agric. Sci.* 159: 523–534. doi:10.1017/S0021859621000885
- Clagnan, E., Costanzo, M., Visca, A., Di Gregorio, L., Tabacchioni, S., Colantoni, E., Sevi, F., Sbarra, F., Bindo, A., Nolfi, L., Magarelli, R. A., Trupo, M., Ambrico, A., and Bevivino, A. 2024. Culturomics- and metagenomics-based insights into the soil microbiome preservation and application for sustainable agriculture. *Front. Microbiol.* 15: 1473666. doi:10.3389/fmicb.2024.1473666

- Čmíková, N., Paulen, O., Mankovecký, J., and Kačániová, M. 2024. Potential use of algae and seaweed extracts as protection against peach leaf curl. *Acta Hort. Regiotect.* 27: 124–130. doi:10.2478/ahr-2024-0019
- Collinge, D. B., Jensen, D. F., Rabiey, M., Sarrocco, S., Shaw, M. W., and Shaw, R. H. 2022. Biological control of plant diseases: What has been achieved and what is the direction? *Plant Pathol.* 71: 1024–1047. doi:10.1111/ppa.13555
- Crandall, S. G., Gold, K. M., Del Mar Jiménez-Gasco, M., Filgueiras, C. C., and Willett, D. S. 2020. A multi-omics approach to solving problems in plant disease ecology. *PLoS One.* 15: e0237975. doi:10.1371/journal.pone.0237975
- De Corato, U. 2020. Soil microbiota manipulation and its role in suppressing soil-borne plant pathogens in organic farming systems under the light of microbiome-assisted strategies. *Chem. Biol. Technol. Agric.* 7. doi:10.1186/s40538-020-00183-7
- Deguine, J., Aubertot, J., Bellon, S., Côte, F., Lauri, P., Lescourret, F., Ratnadass, A., Scopel, E., Andrieu, N., Bàrberi, P., Becker, N., Bouyer, J., Brévault, T., Cerdan, C., Cortesero, A., Dangles, O., Delatte, H., Dinh, P. T. Y., Dreyer, H., et al. 2023. Agroecological crop protection for sustainable agriculture. *Adv. Agron.* 178: 1–59. doi:10.1016/bs.agron.2022.11.002
- Deguine, J., Aubertot, J., Flor, R. J., Lescourret, F., Wyckhuys, K. A., and Ratnadass, A. 2021. Integrated pest management: good intentions, hard realities. a review. *Agron. Sustain. Dev.* 41. doi:10.1007/s13593-021-00689-w
- Diwan, D., Rashid, M. M., and Vaishnav, A. 2022. Current understanding of plant-microbe interaction through the lenses of multi-omics approaches and their benefits in sustainable agriculture. *Microbiol. Res.* 265: 127180. doi:10.1016/j.micres.2022.127180
- Elsharkawy, M. M., El-Okkiah, S., Elsadany, A. Y., Bedier, M. Y., Omara, R. I., Behiry, S. I., Hassan, S., and Abdelkhalek, A. 2022. Systemic resistance induction of tomato plants against tomato mosaic virus by microalgae. *Egypt. J. Biol. Pest Control.* 32. doi:10.1186/s41938-022-00538-2
- El-Sheekh, M. M., Deyab, M. A., Hasan, R. S. A., Abu Ahmed, S. E. A., and Elsadany, A. Y. 2022. Biological control of Fusarium tomato-wilt disease by cyanobacteria *Nostoc* spp. *Arch. Microbiol.* 204: 116. doi:10.1007/s00203-021-02673-0
- Etherton, B. A., Choudhury, R. A., Briseño, R. I. A., Mouafo-Tchinda, R. A., Sulá, A. I. P., Choudhury, M., Adhikari, A., Lei, S. L., Kraistudomsook, N., Buritica, J. R., Cerbaro, V. A., Ogero, K., Cox, C. M., Walsh, S. P., Andrade-Piedra, J. L., Omondi, B. A., Navarrete, I., McEwan, M. A., and Garrett, K. A. 2024. Disaster plant pathology: Smart solutions for threats to global plant health from natural and human-driven disasters. *Phytopathology* 114: 855–868. doi:10.1094/phyto-03-24-0079-fi
- Farid, R., Mutale-Joan, C., Redouane, B., Najib, E. M., Abderahime, A., Laila, S., and Hicham, E. A. 2019. Effect of microalgae polysaccharides on biochemical and metabolomics pathways related to plant defense in *Solanum lycopersicum*. *Appl. Biochem. Biotechnol.* 188: 225–240. doi:10.1007/s12010-018-2916-y
- Fenibo, E. O., Ijoma, G. N., Nurmahomed, W., and Matambo, T. 2022. The potential and green chemistry attributes of biopesticides for sustainable agriculture. *Sustainability* 14: 14417. doi:10.3390/su142114417
- Ferreira, A., Bastos, C. R. V., Marques-Dos-Santos, C., Acién-Fernandez, F. G., and Gouveia, L. 2023. Algaeculture for agriculture: from past to future. *Front. Agron.* 5. doi:10.3389/fagro.2023.1064041
- Gao, M., Xiong, C., Gao, C., Tsui, C. K. M., Wang, M., Zhou, X., Zhang, A., and Cai, L. 2021. Disease-induced changes in plant microbiome assembly and functional adaptation. *Microbiome* 9: 187. doi:10.1186/s40168-021-01138-2
- Garrett, K., Nita, M., De Wolf, E., Esker, P., Gomez-Montano, L., and Sparks, A. 2021. Plant pathogens as indicators of climate change. *Clim. Change: Observed Impact Planet Earth Third Edition.* 499–513. doi:10.1016/b978-0-12-821575-3.00024-4
- Ghareeb, R. Y., Abdelsalam, N. R., Maghraby, D. M. E., Ghozlan, M. H., El-Argawy, E., and Abou-Shanab, R. A. I. 2022. *Oscillatoria* sp. as a potent anti-phytopathogenic agent and plant immune stimulator against root-knot nematode of Soybean cv. Giza 111. *Front. Plant Sci.* 13: 870518. doi:10.3389/fpls.2022.870518
- Gökdemir, F. Ş., İşeri, Ö. D., Sharma, A., Achar, P. N., and Eyidoğan, F. 2022. Metagenomics next generation sequencing (mNGS): an exciting tool for early and accurate diagnostic of fungal pathogens in plants. *J. Fungi (Basel)* 8: 1195. doi:10.3390/jof8111195
- Gonçalves, A. L. 2021. The use of microalgae and cyanobacteria in the improvement of agricultural practices: a review on their biofertilising, biostimulating and biopesticide roles. *Appl. Sci.* 11: 871. doi:10.3390/app11020871
- Gullino, M. L., Albajes, R., Al-Jboory, I., Angelotti, F., Chakraborty, S., Garrett, K. A., Hurley, B. P., Juroszek, P., Lopian, R., Makkouk, K., Pan, X., Pugliese, M., and Stephenson, T. 2022. Climate change and pathways used by pests as challenges to plant health in agriculture and forestry. *Sustainability* 14: 12421. doi:10.3390/su141912421
- Hakim, S., Naqqash, T., Nawaz, M. S., Laraib, I., Siddique, M. J., Zia, R., Mirza, M. S., and Imran, A. 2021. Rhizosphere engineering with plant growth-promoting microorganisms for agriculture and ecological sustainability. *Front. Sustain. Food Syst.* 5. doi:10.3389/fsufs.2021.617157
- Horváth, Á. N., Németh, L., Vörös, L., Stirk, W. A., Van Staden, J., and Ördög, V. 2023. Cataloguing microalgae and cyanobacteria strains from the mosonmagyaróvár algal culture collection with in vitro antagonistic activity against phytopathogenic fungi and oomycetes. *Phytoparasitica* 51: 747–762. doi:10.1007/s12600-023-01045-2
- Hossain, Z., Hubbard, M., Gan, Y., and Bainard, L. D. 2021. Root rot alters the root-associated microbiome of field pea in commercial crop production systems. *Plant Soil.* 460: 593–607. doi:10.1007/s11104-020-04779-8
- Hu, Y., Green, G. S., Milgate, A. W., Stone, E. A., Rathjen, J. P., and Schwessinger, B. 2019. Pathogen detection and microbiome analysis of infected wheat using a portable DNA sequencer. *Phytobiomes J.* 3: 92–101. doi:10.1094/PBIOMES-01-19-0004-R
- Huang, J., Wu, Y., Gao, Q., Li, X., Zeng, Y., Guo, Y., Zhang, H., and Qin, Z. 2024. Metagenomic exploration of the rhizosphere soil microbial community and their significance in facilitating the development of wild-simulated ginseng. *Appl. Environ. Microbiol.* 90: e02335-23. doi:10.1128/aem.02335-23

- Hunjan, M. S., and Lore, J. S. 2020. Climate change: impact on plant pathogens, diseases, and their management. In *Crop Protection under Changing Climate*, Jabran, K., Florentine, S., Chauhan, B. Eds. Cham: Springer, pp 85–100. doi:10.1007/978-3-030-46111-9_4
- Iqbal, M. A., Jagannadham, J., Jaiswal, S., Prabha, R., Rai, A., and Kumar, D. 2022. Potential use of microbial community genomes in various dimensions of agriculture productivity and its management: a review. *Front. Microbiol.* **13**: 708335. doi:10.3389/fmicb.2022.708335
- Jayalakshmi, K., Manzar, N., Namriboi, B. K., Kashyap, A. S., Sahu, P. K., Saranya, R., Nagaraju, Y., Sharath, N., Gupta, A., and Singh, A. K. 2023. Detection and diagnosis of important soil-borne pathogens. In *Detection, Diagnosis and Management of Soil-Borne Phytopathogens*, Singh, U.B., Kumar, R., Singh, H.B., Eds. Singapore: Springer, pp 101–126. doi:10.1007/978-981-19-8307-8_5
- Jayasinghe, H., Chang, H., Knobloch, S., Yang, S., Hendalage, D. P. B., Ariyawansa, K. G. S. U., Liu, P., Stadler, M., and Ariyawansa, H. A. 2024. Metagenomic insight to apprehend the fungal communities associated with leaf blight of Welsh onion in Taiwan. *Front. Plant Sci.* **15**: 1352997. doi:10.3389/fpls.2024.1352997
- Johnson, M. A., Liu, H., Bush, E., Sharma, P., Yang, S., Mazloom, R., Heath, L. S., Nita, M., Li, S., and Vinatzer, B. A. 2022. Investigating plant disease outbreaks with long-read metagenomics: sensitive detection and highly resolved phylogenetic reconstruction applied to *Xylella fastidiosa*. *Microb. Genom.* **8**. doi:10.1099/mgen.0.000822
- Johnson, M. A., Vinatzer, B. A., and Li, S. 2023. Reference-free plant disease detection using machine learning and long-read metagenomic sequencing. *Appl. Environ. Microbiol.* **89**: e0026023. doi:10.1128/aem.00260-23
- Jokel, M., Salazar, J., Chovancek, E., Sirin, S., and Allahverdiyeva, Y. 2023. Screening of several microalgae revealed biopesticide properties of *Chlorella sorokiniana* against the strawberry pathogen *Phytophthora cactorum*. *J. Appl. Phycol.* **35**: 2675–2687. doi:10.1007/s10811-023-03015-x
- Kamalanathan, V., Sevugapperumal, N., Nallusamy, S., Ashraf, S., Kailasam, K., and Afzal, M. 2023. Metagenomic approach deciphers the role of community composition of mycobiome structured by *Bacillus velezensis* VB7 and *Trichoderma koningiopsis* TK in tomato rhizosphere to suppress root-knot nematode infecting tomato. *Microorganisms* **11**: 2467. doi:10.3390/microorganisms11102467
- Kamle, M., Borah, R., Bora, H., Jaiswal, A. K., Singh, R. K., and Kumar, P. 2020. Systemic acquired resistance (SAR) and induced systemic resistance (ISR): role and mechanism of action against phytopathogens. In *Fungal Biotechnology and Bioengineering. Fungal Biology*, Hesham, A.L., Upadhyay, R., Sharma, G., Manoharachary, C., Gupta, V., Eds. Cham: Springer, pp 457–470. doi:10.1007/978-3-030-41870-0_20
- Karlsson, I., Persson, P., and Friberg, H. 2021. Fusarium head blight from a microbiome perspective. *Front. Microbiol.* **12**: 628373. doi:10.3389/fmicb.2021.628373
- Kaushal, M., Mahuku, G., and Swennen, R. 2020. Metagenomic insights of the root colonizing microbiome associated with symptomatic and non-symptomatic bananas in fusarium wilt infected fields. *Plants (Basel)* **9**: 263. doi:10.3390/plants9020263
- Khakimov, A., Salakhutdinov, I., Omolikhov, A., and Utaganov, S. 2022. Traditional and current-prospective methods of agricultural plant diseases detection: a review. *IOP Conf. Ser. Earth Environ. Sci.* **951**: 012002. doi:10.1088/1755-1315/951/1/012002
- Kim, J. H., Castroverde, C. D. M., Huang, S., Li, C., Hilleary, R., Seroka, A., Sohrabi, R., Medina-Yerena, D., Huot, B., Wang, J., Nomura, K., Marr, S. K., Wildermuth, M. C., Chen, T., MacMicking, J. D., and He, S. Y. 2022. Increasing the resilience of plant immunity to a warming climate. *Nature* **607**: 339–344. doi:10.1038/s41586-022-04902-y
- Koul, O. 2023. Biopesticides: commercial opportunities and challenges. In *Development and Commercialization of Biopesticides, Costs and Benefits*, Koul, O., Eds. Academic Press: Elsevier, pp 1–23. doi:10.1016/B978-0-323-95290-3.00009-1
- Kumar, R., Srivastava, S., Kumar, S., Singh, U. B., Chosdon, T., Yadav, M. K., Kumar, A., Sagwal, A., Tiwari, R., and Singh, G. P. 2023. Diagnosis and detection of soil-borne fungal phytopathogens in major crops. in: Singh, U.B., Kumar, R., Singh, H.B. (Eds.), *Detection, Diagnosis and Management of Soil-Borne Phytopathogens*. Singapore: Springer, pp 67–99. doi:10.1007/978-981-19-8307-8_4
- Kwak, M., Kong, H. G., Choi, K., Kwon, S., Song, J. Y., Lee, J., Lee, P. A., Choi, S. Y., Seo, M., Lee, H. J., Jung, E. J., Park, H., Roy, N., Kim, H., Lee, M. M., Rubin, E. M., Lee, S., and Kim, J. F. 2018. Rhizosphere microbiome structure alters to enable wilt resistance in tomato. *Nat. Biotechnol.* **36**: 1100–1109. doi:10.1038/nbt.4232
- Lahlali, R., Ezrari, S., Radouane, N., Kenfaoui, J., Esmaeel, Q., Hamss, H. E., Belabess, Z., and Barka, E. A. 2022. Biological control of plant pathogens: a global perspective. *Microorganisms* **10**: 596. doi:10.3390/microorganisms10030596
- Lal, R. 2023. Farming systems to return land for nature: It's all about soil health and re-carbonization of the terrestrial biosphere. *Farm. Syst.* **1**: 100002. doi:10.1016/j.farsys.2023.100002
- Lee, K., McDermott, S., and Fernandez, L. 2024. Using economics to inform and evaluate biological control programs: opportunities, challenges, and recommendations for future research. *BioControl* **69**: 237–252. doi:10.1007/s10526-024-10244-7
- Lee, S., and Ryu, C. 2021. Algae as new kids in the beneficial plant microbiome. *Front. Plant Sci.* **12**. doi:10.3389/fpls.2021.599742
- Liu, Y., Lai, J., Sun, X., Huang, L., Sheng, Y., Zhang, Q., Zeng, H., Zhang, Y., Ye, P., and Wei, S. 2024. Comparative metagenomic analysis reveals rhizosphere microbiome assembly and functional adaptation changes caused by clubroot disease in Chinese cabbage. *Microorganisms* **12**: 1370. doi:10.3390/microorganisms12071370
- Lopez-Roblero, A., Cano, D. J. M., Diego-García, E., Guillén-Navarro, G. K., Iša, P., and Zarza, E. 2024. Metagenomic analysis of plant viruses in tropical fresh and wastewater. *Environ. DNA* **6**. doi:10.1002/edn3.416
- Martins, S. J., Pasche, J., Silva, H. A. O., Seltén, G., Savastano, N., Abreu, L. M., Bais, H. P., Garrett, K. A., Kraisitudomsook, N., Pieterse, C. M. J., and Cernava, T.

2023. The use of synthetic microbial communities to improve plant health. *Phytopathology* **113**: 1369–1379. doi:10.1094/phyto-01-23-0016-ia
- Maseny, K., Manganyi, M. C., and Dikobe, T. B. 2024. Exploring cereal metagenomics: unravelling microbial communities for improved food Security. *Microorganisms* **12**: 510. doi:10.3390/microorganisms12030510
- Mendes, L. W., Raaijmakers, J. M., De Hollander, M., Sepo, E., Expósito, R. G., Chiorato, A. F., Mendes, R., Tsai, S. M., and Carrión, V. J. 2023. Impact of the fungal pathogen *Fusarium oxysporum* on the taxonomic and functional diversity of the common bean root microbiome. *Environ. Microbiome*. **18**: 68. doi:10.1186/s40793-023-00524-7
- Mumo, N. N., Mamati, G. E., Ateka, E. M., Rimberia, F. K., Asudi, G. O., Boykin, L. M., Machuka, E. M., Njuguna, J. N., Pelle, R., and Stomeo, F. 2020. Metagenomic analysis of plant viruses associated with papaya ringspot disease in carica papaya L. in Kenya. *Front. Microbiol.* **11**: 205. doi:10.3389/fmicb.2020.00205
- Nam, N., Do, H., Trinh, K. L., and Lee, N. 2023. Metagenomics: an effective approach for exploring microbial diversity and functions. *Foods* **12**: 2140. doi:10.3390/foods12112140
- Navigre, G. S., Goel, N., Sawhney, G., Sharma, M., Kaushik, P., Mohanta, Y. K., Mohanta, T. K., and Al-Harrasi, A. 2022. Analysis and Interpretation of metagenomics data: an approach. *Biol. Proced. Online*. **24**: 18. doi:10.1186/s12575-022-00179-7
- Nawaz, T., Fahad, S., Saud, S., Hassan, S., Gu, L., Fahad, S., Saud, S., Nawaz, T., and L., Ahmad. 2024. Cyanobacterial solutions for climate-resilient agriculture and global food security. In *Environment, Climate, Plant and Vegetation Growth*. Gu M., Zhou, R., Eds. Cham: Springer, pp 1–39. doi:10.1007/978-3-031-69417-2_1
- Nazarov, P. A., Baleev, D. N., Ivanova, M. I., Sokolova, L. M., and Karakozova, M. V. 2020. Infectious plant diseases: etiology, current status, problems and prospects in plant protection. *Acta Naturae*. **12**: 46–59. doi:10.32607/actanaturae.11026
- Newberry, E., Bhandari, R., Kemble, J., Sikora, E., and Potnis, N. 2020. Genome-resolved metagenomics to study co-occurrence patterns and intraspecific heterogeneity among plant pathogen metapopulations. *Environ. Microbiol.* **22**: 2693–2708. doi:10.1111/1462-2920.14989
- Nisrina, L., Effendi, Y., and Pancoro, A. 2021. Revealing the role of plant Growth promoting Rhizobacteria in suppressive soils against *Fusarium oxysporum* f.sp. cubense based on metagenomic analysis. *Heliyon* **7**: e07636. doi:10.1016/j.heliyon.2021.e07636
- Nowruz, B., and Beiranvand, H. 2024. In vitro and in vivo study of the antifungal activity of extracellular products of cyanobacterium *Neowestiellospira persica* strain A1387 against *Fusarium wilt* disease of cucumber. *Rev. Argent. Microbiol.* **S0325-7541(24)00132-9**. doi:10.1016/j.ram.2024.10.011
- Nwachukwu, B. C., and Babalola, O. O. 2022. Metagenomics: a tool for exploring key microbiome with the potentials for improving sustainable agriculture. *Front. Sustain. Food Syst.* **6**: doi:10.3389/fsufs.2022.886987
- Ouaddi, O., Oukarroum, A., Bouharroud, R., Alouani, M., Altaf, E. B., Qessaoui, R., Drissi, B. E., Radouane, N., Errafii, K., Hijri, M., Hamadi, F., Sobeh, M., and Hassi, M. 2025. A study of antibacterial efficacy of *Tetraselmis rubens* extracts against tomato phytopathogenic *Pseudomonas corrugata*. *Algal Res.* **86**: 103956. doi:10.1016/j.algal.2025.103956
- Pahalvi, H. N., Rafiya, L., Rashid, S., Nisar, B., and Kamili, A. N. 2021. Chemical fertilizers and their impact on soil health. In *Microbiota and Biofertilizers*. Dar, G.H., Bhat, R.A., Mehmood, M.A., Hakeem, K.R., Eds. Cham: Springer, Vol 2; pp 1–20. doi:10.1007/978-3-030-61010-4_1
- Parmar, P., Kumar, R., Neha, Y., and Srivatsan, V. 2023. Microalgae as next generation plant growth additives: Functions, applications, challenges and circular bioeconomy based solutions. *Front. Plant Sci.* **14**. doi:10.3389/fpls.2023.1073546
- Patanita, M., Albuquerque, A., Campos, M. D., Materatski, P., Varanda, C. M. R., Ribeiro, J. A., and Félix, M. D. R. 2022. Metagenomic assessment unravels fungal microbiota associated to grapevine trunk diseases. *Horticulturae* **8**: 288. doi:10.3390/horticulturae8040288
- Peng, Y., Li, S. J., Yan, J., Tang, Y., Cheng, J. P., Gao, A. J., Yao, X., Ruan, J. J., and Xu, B. L. 2021. Research progress on phytopathogenic fungi and their role as biocontrol agents. *Front. Microbiol.* **12**: 670135. doi:10.3389/fmicb.2021.670135
- Pérez-Cobas, A. E., Gomez-Valero, L., and Buchrieser, C. 2020. Metagenomic approaches in microbial ecology: an update on whole-genome and marker gene sequencing analyses. *Microb. Genom.* **6**. doi:10.1099/mgen.0.000409
- Perveen, K., Bukhari, N. A., Masoudi, L. M. A., Alqahtani, A. N., Alruways, M. W., and Alkhattaf, F. S. 2022. Antifungal potential, chemical composition of *Chlorella vulgaris* and SEM analysis of morphological changes in *Fusarium oxysporum*. *Saudi J. Biol. Sci.* **29**: 2501–2505. doi:10.1016/j.sjbs.2021.12.033
- Piombo, E., Abdelfattah, A., Droby, S., Wisniewski, M., Spadaro, D., and Schena, L. 2021. Metagenomics approaches for the detection and surveillance of emerging and recurrent plant pathogens. *Microorganisms* **9**: 188. doi:10.3390/microorganisms9010188
- Prasanna, N. L., Choudhary, S., Kumar, S., Choudhary, M., Meena, P. K., Samreen, N., Saloni, S., Ghanghas, R., 2024. Advances in plant disease diagnostics and surveillance- a review. *Plant Cell Biotech. Mol. Biol.* **25**: 137–150. doi:10.56557/pcbmb/2024/v25i11-128918
- Purushothaman, T., and Irfana-Mol, K. 2020. Micro-algae as biopesticides for the development of sustainable agriculture. *Wide Spectrum* **8**: 5–22. URL https://www.researchgate.net/publication/346494756_Micro-algae_as_bio-pesticides_for_the_development_of_sustainable_agriculture.
- Rachidi, F., Benhima, R., Kasmi, Y., Sbabou, L., and Arroussi, H. E. 2021. Evaluation of microalgae polysaccharides as biostimulants of tomato plant defense using metabolomics and biochemical approaches. *Sci. Rep.* **11**: 930. doi:10.1038/s41598-020-78820-2
- Rainey, P. B., and Quistad, S. D. 2020. Toward a dynamical understanding of microbial communities. *Philos. Trans. R Soc. Lond. B Biol. Sci.* **375**: 20190248. doi:10.1098/rstb.2019.0248
- Ramakrishnan, B., Maddela, N. R., Venkateswarlu, K., and Megharaj, M. 2023. Potential of microalgae and cyanobacteria to improve soil health and agricultural produc-

- tivity: a critical view. *Environ. Sci. Adv.* **2**: 586–611. doi:10.1039/D2VA00158F
- Redila, C. D., Prakash, V., and Nouri, S. 2021. Metagenomics analysis of the wheat virome identifies novel plant and fungal-associated viral sequences. *Viruses* **13**: 2457. doi:10.3390/v13122457
- Righini, H., Baraldi, E., García Fernández, Y., Quintana, A. M., and Roberti, R. 2019. Different antifungal activity of *Anabaena* sp., *Ecklonia* sp., and *Jania* sp. against *Botrytis cinerea*. *Mar. Drug.* **17**: 299. doi:10.3390/md17050299
- Righini, H., Francioso, O., Di Foggia, M., Quintana, A. M., and Roberti, R. 2021. Assessing the potential of the terrestrial cyanobacterium *Anabaena minutissima* for controlling *Botrytis cinerea* on tomato fruits. *Horticulturae* **7**: 210. doi:10.3390/horticulturae7080210
- Righini, H., Francioso, O., Quintana, A. M., Pinchetti, J. L. G., Zuffi, V., Cappelletti, E., and Roberti, R. 2023. New insight on tomato seed priming with *Anabaena minutissima* phycobiliproteins in relation to *Rhizoctonia solani* root rot resistance and seedling growth promotion. *Phytoparasitica* **51**: 763–781. doi:10.1007/s12600-023-01056-z
- Righini, H., Francioso, O., Quintana, A. M., and Roberti, R. 2022. Cyanobacteria: a natural source for controlling agricultural plant diseases caused by fungi and oomycetes and improving plant growth. *Horticulturae* **8**: 58. doi:10.3390/horticulturae8010058
- Righini, H., Galletti, S., Cianchetta, S., Quintana, A. M., Francioso, O., and Roberti, R. 2025. A new autoclave extract from *Anabaena minutissima* for seed priming improves tomato plantlets growth and protects against soilborne pathogens. *J. Appl. Phycol.* **37**: 67–81. doi:10.1007/s10811-024-03285-z
- Righini, H., Somma, A., Cetrullo, S., D'Adamo, S., Flamigni, F., Quintana, A. M., and Roberti, R. 2020. Inhibitory activity of aqueous extracts from *Anabaena minutissima*, *Ecklonia maxima* and *Jania adhaerens* on the cucumber powdery mildew pathogen in vitro and in vivo. *J. Appl. Phycol.* **32**: 3363–3375. doi:10.1007/s10811-020-02160-x
- Riseh, R. S., Vazvani, M. G., Ebrahimi-Zarandi, M., and Skorik, Y. A. 2022. Alginate-induced disease resistance in plants. *Polymers. (Basel)* **14**: 661. doi:10.3390/polym14040661
- Roman-Reyna, V., and Crandall, S. G. 2024. Seeing in the dark: a metagenomic approach can illuminate the drivers of plant disease. *Front. Plant Sci.* **15**. doi:10.3389/fpls.2024.1405042
- Roussin-Léveillé, C., Rossi, C. A., Castroverde, C. D. M., and Moffett, P. 2024. The plant disease triangle facing climate change: a molecular perspective. *Trends Plant Sci.* **29**: 895–914. doi:10.1016/j.tplants.2024.03.004
- Sadvakasova, A. K., Bauenova, M. O., Kossalbayev, B. D., Zayadan, B. K., Huang, Z., Wang, J., Balouch, H., Alharby, H. F., Chang, J., and Allakhverdiev, S. I. 2023. Synthetic algocyanobacterial consortium as an alternative to chemical fertilizers. *Environ. Res.* **233**: 116418–116418. doi:10.1016/j.envres.2023.116418
- Sadvakasova, A. K., Kossalbayev, B. D., Token, A. I., Bauenova, M. O., Wang, J., Zayadan, B. K., Balouch, H., Alwasel, S., Leong, Y. K., Chang, J., and Allakhverdiev, S. I. 2022. Influence of Mo and Fe on photosynthetic and nitrogenase activities of nitrogen-fixing cyanobacteria under nitrogen starvation. *Cells* **11**: 904. doi:10.3390/cells11050904
- Scaglioni, P. T., Pagnussatt, F. A., Lemos, A. C., Nicolli, C. P., Del Ponte, E. M., and Badiale-Furlong, E. 2019. *Nannochloropsis* sp. and *Spirulina* sp. as a source of antifungal compounds to mitigate contamination by *Fusarium graminearum* species complex. *Curr. Microbiol.* **76**: 930–938. doi:10.1007/s00284-019-01663-2
- Schmid, B., Coelho, L., Schulze, P. S. C., Pereira, H., Santos, T., Maia, I. B., Reis, M., and Varela, J. 2022. Antifungal properties of aqueous microalgal extracts. *Bioresour. Technol. Rep.* **18**: 101096. doi:10.1016/j.biteb.2022.101096
- Senousy, H. H., El-Sheekh, M. M., Saber, A. A., Khairy, H. M., Said, H. A., Alhoqail, W. A., and Abu-Elsoud, A. M. 2022. Biochemical analyses of ten cyanobacterial and microalgal strains isolated from Egyptian habitats, and screening for their potential against some selected phytopathogenic fungal strains. *Agronomy* **12**: 1340. doi:10.3390/agronomy12061340
- Shah, S. T., Basit, A., Ullah, I., and Mohamed, H. I. 2021. Cyanobacteria and algae as biocontrol agents against fungal and bacterial plant pathogens. In *Plant Growth-Promoting Microbes for Sustainable Biotic and Abiotic Stress Management*. Mohamed, H.I., El-Beltagi, H.E.D.S., Abd-Elsalam, K.A., Eds. Cham: Springer, pp 1–23. doi:10.1007/978-3-030-66587-6_1
- Shen, Z., Thomashow, L. S., Ou, Y., Tao, C., Wang, J., Xiong, W., Liu, H., Li, R., Shen, Q., and Kowalchuk, G. A. 2022. Shared core microbiome and functionality of key taxa suppressive to banana *Fusarium* wilt. *Research* **2022**. doi:10.34133/2022/9818073
- Singh, B. K., Delgado-Baquerizo, M., Egidi, E., Guirado, E., Leach, J. E., Liu, H., and Trivedi, P. 2023. Climate change impacts on plant pathogens, food security and paths forward. *Nat. Rev. Microbiol.* **21**: 640–656. doi:10.1038/s41579-023-00900-7
- Song, X., Bo, Y., Feng, Y., Tan, Y., Zhou, C., Yan, X., Ruan, R., Xu, Q., and Cheng, P. 2022. Potential applications for multifunctional microalgae in soil improvement. *Front. Environ. Sci.* **10**. doi:10.3389/fenvs.2022.1035332
- Starr, E., Shi, S., Blazewicz, S. J., Koch, B., Probst, A. J., Hungate, B. A., Pett-Ridge, J., Firestone, M. K., and Banfield, J. F. 2021. Stable-isotope-informed, genome-resolved metagenomics uncovers potential cross-kingdom interactions in rhizosphere soil. *mSphere* **6**: e0008521. doi:10.1128/msphere.00085-21
- Suhaimi, N. S. M., Goh, S., Ajam, N., Othman, R. Y., Chan, K., and Thong, K. L. 2017. Diversity of microbiota associated with symptomatic and non-symptomatic bacterial wilt-diseased banana plants determined using 16S rRNA metagenome sequencing. *World J. Microbiol. Biotechnol.* **33**: 168. doi:10.1007/s11274-017-2336-0
- Tariq, M., Khan, A., Asif, M., Khan, F., Ansari, T., Shariq, M., and Siddiqui, M. A. 2020. Biological control: a sustainable and practical approach for plant disease management. *Acta Agric. Scand. B Soil Plant Sci.* **70**: 507–524. doi:10.1080/09064710.2020.1784262
- Toribio, A. J., Jurado, M. M., Suárez-Estrella, F., López-González, J. A., Martínez-Gallardo, and López, M. J. 2021. Application of sonicated extracts of cyanobacteria and microalgae for the mitigation of bacterial canker in tomato seedlings. *J. Appl. Phycol.* **33**: 3817–3829. doi:10.1007/s10811-021-02599-6

- Vermelho, A. B., Moreira, J. V., Akamine, I. T., Cardoso, V. S., and Mansoldo, F. R. P. **2024**. Agricultural pest management: the role of microorganisms in biopesticides and soil bioremediation. *Plants (Basel)* **13**: 2762. doi:[10.3390/plants13192762](https://doi.org/10.3390/plants13192762)
- Viana, C., Genevace, M., Gama, F., Coelho, L., Pereira, H., Varela, J., and Reis, M. **2024**. *Chlorella vulgaris* and *Tetrademus obliquus* Protect Spinach (*Spinacia oleracea* L.) against *Fusarium oxysporum*. *Plants (Basel)* **13**: 1697. doi:[10.3390/plants13121697](https://doi.org/10.3390/plants13121697)
- Wang, N., Sundin, G. W., De La Fuente, L., Cubero, J., Tatineni, S., Brewer, M. T., Zeng, Q., Bock, C. H., Cunneffe, N. J., Wang, C., Candresse, T., Chappell, T., Coleman, J. J., and Munkvold, G. **2024**. Key challenges in plant pathology in the next decade. *Phytopathology* **114**: 837–842. doi:[10.1094/phyto-04-24-0137-kc](https://doi.org/10.1094/phyto-04-24-0137-kc)
- Xiao, Y., Zhang, S., Li, H., Teng, K., Wu, S., Liu, Y., Yu, F., He, Z., Li, L., Li, L., Meng, D., Yin, H., and Wang, Y. **2024**. Metagenomic insights into the response of soil microbial communities to pathogenic *Ralstonia solanacearum*. *Front. Plant Sci.* **15**. doi:[10.3389/fpls.2024.1325141](https://doi.org/10.3389/fpls.2024.1325141)
- Zehra, A., Raytekar, N. A., Meena, M., and Swapnil, P. **2021**. Efficiency of microbial bio-agents as elicitors in plant defense mechanism under biotic stress: a review. *Curr. Res. Microb. Sci.* **2**: 100054. doi:[10.1016/j.crmicro.2021.100054](https://doi.org/10.1016/j.crmicro.2021.100054)
- Zhou, W., Li, M., and Achal, V. **2025**. A comprehensive review on environmental and human health impacts of chemical pesticide usage. *Emerg. Contam.* **11**: 100410–100410. doi:[10.1016/j.emcon.2024.100410](https://doi.org/10.1016/j.emcon.2024.100410)