INTERNATIONAL JOURNAL OF INTELLECTUAL ADVANCES FOR MULTIDISCIPLINARY SCIENCES

IJIAMS.COM

Volume 01, Issue 01 : Year 2025

UNRAVELING PLANT-MICROBE INTERACTIONS: A NEW ERA IN BOTANICAL STUDIES

Priyanka Dahiya[1]
Manjeet Kaur[2]
Department of Biotechnology, University Institute of Engineering and Technology
Maharshi Dayanand University, Rohtak-124001, Haryana,India
***E-mail:* manjeet.kundu@gmail.com**[2]

Submitted: 20/08/2025 **Accepted : 24/08/2025**

Abstract:

The plants and microbe intricate relationships have long been a focal point of botanical studies, yet recent advancements are ushering in a new era of understanding. This paper explores the multifaceted interactions between plant hosts and their microbial partners, highlighting the significance of these relationships in ecological balance, plant health, and agricultural productivity. We delve into the mechanisms through which microbes influence plant growth, disease resistance, and nutrient acquisition, emphasizing the role of beneficial microorganisms in enhancing plant resilience to environmental stressors. Furthermore, we discuss cutting-edge research methodologies that are revolutionizing our approach to studying these interactions, including genomic and metabolomic analyses. By unraveling the complexities of pslant-microbe interactions, this work aims to foster innovative strategies for sustainable cultivation and ecosystem protection, ultimately contributing to the preservation of biodiversity and ecosystem health.

Keywords: Plant–microbe interactions, rhizosphere microbiome, symbiotic relationships, endophytes, epiphytes, plant growth-promoting rhizobacteria (PGPR), mycorrhizal associations, sustainable agriculture

1. Introduction

Microbial associations with plants are crucial ecological as well as evolutionary processes that involve a wide range of relationships between plants and microorganisms, including bacteria, fungi, and oomycetes. These relationships can be either mutually beneficial or commensal, or pathogenic, significantly influencing plant health, growth, and survival. Historically, the study of plant-microbe interactions began with observations of notable symbiotic interactions that include plant associations with Rhizobium for nitrogen fixation and with mycorrhizal fungi, which enhance nutrient uptake and confer stress resistance to plants (Kaur & Kaur, 2018) (Provorov, 2009). Early research relied on traditional methods such as culturing and microscopy to understand these interactions (Dass & Mallick, 2019). However, the advent of molecular biology and advanced imaging techniques has revolutionized the field, allowing for detailed insights into the cellular and molecular mechanisms underlying these interactions. Modern techniques such as next-generation sequencing, PCR, and high-resolution microscopy have uncovered the complex molecular dialogues that occur at the plant-microbe interface, including the role of microbial effectors and plant immune responses (Panstruga & Kuhn, 2015) (Dass & Mallick, 209). These interactions are crucial for nutrient acquisition and secondary metabolites formation that enhance plant defense and stress tolerance (Çetiz & Memon, 2021) (Babar et al., 2016). The rhizosphere, a critical zone of interaction, is where plants modulate root exudates to recruit beneficial microbes and repel pathogens, thus shaping the microbial community and influencing the health of plant (Yang et al., 2024). The evolutionary aspect of these interactions is highlighted by the ancestral role of arbuscular mycorrhizae in plant colonization of land, which set the stage for the development of more complex symbiotic relationships (Provorov, 2009).

Plant-microbe interactions encompass a diverse range of relationships which includes pathogenic, symbiotic, and commensal interactions, each playing immensable role in ecosystem dynamics. Symbiotic interactions enhance nutrient availability and plant growth, while commensal interactions with endophytic microbes support plant health by producing growth-promoting substances and offering protection against pathogens (Mohapatra et al., 2024)(Ramasamy & Kumar, n.d.). Pathogenic interactions, on the other hand, pose significant challenges by triggering complex plant immune responses and causing diseases that threaten agricultural productivity (Sahoo et al., 2024)(Mahadevakumar & Sridhar, 2020). Recent technological advances have significantly enhanced our understanding of these interactions. Techniques such as next-generation sequencing, high-resolution microscopy, and various molecular assays have provided deeper insights into the molecular dialogues and signaling pathways that facilitate these interactions (Dass & Mallick, 2019). These breakthroughs have facilitated the design of novel approaches for safeguarding crops, including the application of biocontrol agents and microbial inoculants.They have also guided improvements in plant breeding and genetic modification aimed at introducing resistance genes. Furthermore, such progress has supported efforts to alter and strengthen plant immune responses (Sahoo et al., 2024) (Pathma et al., 2020). The future scope of this field involves combining multi-omics techniques to gain deeper insights. It also includes employing synthetic microbial communities (SynComs) for enhanced plant–microbe interactions. Additionally, CRISPR tools hold promise for the targeted editing of both plant and microbial genes (Sahoo et al., 2024) (Shi et al., 2023). Moreover, microbiome engineering offers potential for fostering beneficial microbial assemblages in plants. It can enhance crop resilience while minimizing reliance on chemical fertilizers and pesticides. In turn, this contributes to sustainable farming practices and strengthens global food security (Sahoo et al., 2024) (Kaur & Saxena, 2024). Addressing challenges such as field variability, crop compatibility issues, and environmental concerns related to introducing non-native microbes will require a multidisciplinary approach combining genomics, biotechnology, and sustainable management practices (Mohapatra et al., 2024).

2. Types of Plant-Microbe Interactions

Symbiotic interaction, including those between legumes, rhizobia, and mycorrhizal fungi., are pivotal for nutrient exchange and nitrogen fixation, enhancing plant growth and soil fertility. Arbuscular mycorrhizal fungi (AMF) and rhizobia form a tripartite symbiosis with legumes, facilitating phosphorus and nitrogen acquisition, respectively, which is crucial for plant growth in soils which are deficient in nutrients (Chang et al., 2017) (Duan et al., 2024). The molecular pathways underlying these interactions involve complex signaling pathways. For instance, legume root exudates, including strigolactones and flavonoids, play an important role in signaling and recognition, activating mycorrhizal and nodulation factors that facilitate symbiosis (Chang et al., 2017) (Biate et al., 2015). In the rhizobia-legume symbiosis, rhizobia fix atmospheric nitrogen into ammonia within root nodules, a process regulated by Nod factors and their receptors on the plant cell membrane, which activate signaling pathways essential for nodule formation (Feki et al., 2020) (Basu & Kumar, 2020). Through improving soil health and lowering chemical fertilizer usage, this symbiotic nitrogen fixation underpins sustainable agricultural practices (Chellem et al., 2024) (Srivastava et al., 2024). The interaction between AMF and rhizobia is synergistic, often resulting in increased nutrient uptake and plant yield compared to single symbioses (Javaid, 2010). Environmental challenges like soil salinity and drought can disrupt these symbiotic associations. This underscores the necessity for deeper research to optimize such interactions across diverse conditions (Duan et al., 2024) (Chen & Zhou, 2024). Emerging tools in genetic engineering together with biofertilizer innovations hold great promise for strengthening these beneficial relationships, potentially extending nitrogen-fixing capabilities to non-leguminous crops (Chellem et al., 2024). Understanding the molecular and environmental factors that regulate these mutualistic interactions is crucial for improving agricultural productivity and sustainability (Gorgia & Tsikou, 2025).

Arbuscular mycorrhizal (AM) fungi and ectomycorrhizal (EM) fungi are two predominant types of mycorrhizal associations that significantly contribute to terrestrial ecosystems through enhanced nutrient cycling, greater ecosystem adaptability and increased plant productivity. AM fungi, which form symbiotic relationships with the roots of most land plants, are particularly effective in phosphorus uptake and improving overall growth of plant growth along with tolerance to stress conditions (Mundra & Morsy, 2024) (Gayathry et al., 2024). In contrast, EM fungi are primarily associated with trees and are known for their ability to access mineral phosphorus through mineral weathering, a process facilitated by the acidification of the rhizosphere (Koele et al., 2014). The ecological significance of these fungi is underscored by their contribution to soil health and carbon sequestration (Vishwakarma, 2024). The diversity and community composition of these fungi can vary significantly across different ecosystems, as demonstrated in the Indian subcontinent, where both AM and EM fungi exhibit distinct patterns of abundance and diversity (Beggi & Dasgupta, 2021). The interaction between AM and EM fungi is complex, with studies showing that mixing tree species associated with these fungi can lead to dual mycorrhization and affect fungal community composition, although the richness of AM fungi may be suppressed in the presence of EM trees (Heklau et al., 2021). This interaction is further complicated by the presence of invasive species, such as the AM fungus Funneliformis mosseae, which has been found in ectomycorrhizal forests, indicating potential adaptability and ecological impact (Zambounis et al., 2016). The evolutionary history of these fungi reveals distinct genomic adaptations that have facilitated their symbiotic lifestyles, with AM fungi showing unique gene content that supports their obligate symbiosis with plants (Rosling et al., 2023).

Plant-pathogen interactions are complex processes involving a dynamic interplay between pathogenic effectors and plant immune responses. Pathogens, including bacteria, fungi, oomycetes, and viruses, deploy effectors as key virulence factors to drive infection by manipulating host processes while inhibiting plant defense mechanisms**.** Effectors may be protein-based, including type-III secretion system effectors in bacteria, RXLR and CRN motif effectors in oomycetes, and LysM domain effectors in fungi. They can also be non-protein in nature, such as toxins and small RNAs (Liu et al., 2023) (Todd et al., 2023). The primary role of these effectors is to interfere with plant immune signaling, disrupt physical barriers, and create conditions conducive to pathogen survival and proliferation (Zhang et al., 2022) (Sun et al., 2023). To counter pathogens, plants have developed complex immune systems that include pattern-triggered immunity (PTI) and effector-triggered immunity (ETI). PTI is activated when pattern recognition receptors (PRRs) detect pathogen-associated molecular patterns (PAMPs). This recognition initiates a broad-spectrum defense response against invading microbes (Agarrwal et al., 2024). However, pathogens often overcome PTI by secreting effectors that directly target host cells. To counteract this, plants have developed ETI, which involves the recognition of specific effectors by resistance (R) genes, triggering a more robust and specific immune response, often culminating in a hypersensitive response to localize and restrict pathogen spread (Prihatna, 2009) (Agarrwal et al., 2024). Notable examples of plant-pathogen interactions include Phytophthora infestans, which uses RXLR effectors to manipulate host immunity, and Xanthomonas spp., which employs type-III effectors to suppress host defenses (Liu et al., 2023) (Todd et al., 2023).

Grasping these interactions is essential for designing sustainable approaches to disease control. Such strategies include breeding resistant plant varieties and applying integrated pest management practices (Montoya-Martínez et al., 2024) (Poudel & KC, 2024). Ongoing genomic studies are contributing to fresh approaches aimed at enhancing crop resistance and supporting agricultural sustainability (Kalita et al., 2024) (Todd et al., 2022).

Endophytic bacteria and fungi are integral to plant health. These microorganisms, including notable examples like *Bacillus subtilis* and *Trichoderma* spp., enhance plant growth, stress tolerance, and secondary metabolite production through various mechanisms. Endophytic bacteria belonging to genera like *Bacillus* and *Pseudomonas* support plant growth through multiple mechanisms. They synthesize phytohormones, improve nutrient uptake, and function as biocontrol agents against plant pathogens (Endophytic Microbes and Their Role in Plant Health, 2023) (Santos et al., 2018) (Singh et al., 2020 (Singh et al., 2020) (Bind et al., 2021). Similarly, endophytic fungi, including Trichoderma spp., play a crucial role in plant growth and stress management. They produce secondary metabolites and hydrolytic enzymes that protect plants from phytopathogens and enhance tolerance to environmental stresses such as heavy metals and high temperatures (Carvalho et al., 2020) (Sharma & Singh, 2021). These fungi also facilitate the accumulation of secondary metabolites, which are beneficial for plant resilience and growth (Wang et al., 2024) (Choudhury et al., 2022). The interaction between endophytes and plants is complex, involving mutualistic and commensalistic relationships that have evolved over time, allowing these microorganisms to colonize plant tissues effectively and confer various benefits (Endophytic Microbes and Their Role in Plant Health, 2023) (Vandana et al., 2021). The potential of endophytes as biofertilizers and biostimulants is significant, offering sustainable solutions for agriculture by improving plant growth and resilience in an eco-friendly manner (Choudhury et al., 2022) (Wu et al., 2021).

3. Advances in Research Methodologies

Omics technologies, encompassing genomics, transcriptomics, and proteomics, play a crucial role in elucidating plant-microbe interactions by providing comprehensive insights into the genetic, transcriptional, and protein-level dynamics of these interactions. Genomic research helps pinpoint crucial genes that regulate plant–microbe interactions.This provides valuable insights into the genetic capacities of both plants and their microbial partners (Kaur et al., 2022) (Jain et al., 2024). Transcriptomics further reveals the the shifts in gene expression, aiding in understanding plant–microbe responses under varying environmental stresses. (Jain et al., 2024) (Omics Technologies for Agricultural Microbiology Research, 2022). Proteomics complements these approaches by identifying proteins that are crucial for these interactions, thereby providing a functional perspective (Kaur et al., 2022) (Jain et al., 2024). Metagenomics, particularly, has revolutionized the study of microbial communities in the rhizosphere and phyllosphere by enabling the analysis of uncultivable microbes and their functional genes, thus offering a holistic view of microbial diversity and function (Tett et al., 2012)(Sudhakar, 2022)(Boparai & Sharma, 2021). This approach is crucial for understanding the complex microbial ecosystems that influence plant health and productivity (Tett et al., 2012)(Archana et al., 2023). Case studies involving model plants like Arabidopsis and maize have utilized these omics technologies to profile their microbiomes, revealing the intricate interactions between plants and their associated microbial communities (Rosselli & Squartini, 2015). Research has emphasized the importance of certain microbial groups and their genes in supporting plant growth. These findings also reveal their contribution to enhancing plant resilience under stress conditions (Sudhakar, 2022)(Rosselli & Squartini, 2015). The integration of multi-omics data, including metabolomics, further enhances our understanding by linking genetic and functional data to metabolic pathways, thus providing a comprehensive picture of plant-microbe interactions (Mishra et al., 2022).

Fluorescence microscopy and live imaging have become indispensable tools for studying interaction dynamics at the cellular level. These techniques allow researchers to visualize and manipulate genetic and molecular interactions in real-time. These approaches offer valuable understanding of the spatial and temporal regulation of cellular processes. For example, combining CRISPR/Cas9 with live imaging enables precise spatiotemporal control over gene editing in plants, as demonstrated in Arabidopsis thaliana, where domain-specific CRISPR-Cas9 systems were used to study the PIN1 protein's role in tissue patterning and mechanical stress responses analyzed at single-cell scale (Li et al., 2019). Similarly, the ANCHOR labeling strategy combined with CRISPR/Cas9 allows for the discreet labeling of chromatin in living cells, facilitating the study of chromatin dynamics and gene transcription regulation (Fok et al., 2021). Advances in single-cell RNA sequencing, such as the smLiveFISH technique, have further enhanced the spatial resolution of interactions by enabling the real-time tracking of individual RNA molecules, revealing distinct localization mechanisms of mRNA transcripts in living cells (Xia et al., 2024). Additionally, dual CRISPR/Cas9 strategies coupled with high-resolution fluorescence in situ hybridization (sm-FISH) have been employed to monitor gene deletions and their effects on cellular processes, such as cholesterol accumulation in adrenal and testis cells (Lee & Jefcoate, 2017). CRISPR-based imaging techniques, such as those utilizing deactivated Cas9 (dCas9) and dCas13, have broadened the tools available for cellular visualization. These methods allow the tracking of chromatin, genomic loci, RNAs, and proteins, greatly advancing our understanding of chromatin structure and dynamics (Singh & Jain, 2021).

Fluorescence microscopy and live imaging have become indispensable tools for studying interaction dynamics at the cellular level. These methods enable real-time visualization and manipulation of genetic and molecular interactions. They also provide crucial insights into the spatial and temporal dynamics of cellular processes. For instance, the use of CRISPR/Cas9 in conjunction with live imaging has enabled the precise spatiotemporal control of gene editing in plants, as demonstrated in Arabidopsis thaliana, where domain-specific CRISPR-Cas9 systems were used to study the PIN1 protein's role in tissue morphogenesis and mechanical stress response at a single-cell resolution (Li et al., 2019). Similarly, the ANCHOR labeling strategy combined with CRISPR/Cas9 allows for the discreet labeling of chromatin in living cells, facilitating the study of chromatin dynamics and gene transcription regulation (Fok et al., 2021). Advances in single-cell RNA sequencing, such as the smLiveFISH technique, have further enhanced the spatial resolution of interactions by enabling the real-time tracking of individual RNA molecules, revealing distinct localization mechanisms of mRNA transcripts in living cells (Xia et al., 2024). Additionally, dual CRISPR/Cas9 strategies coupled with high-resolution fluorescence in situ hybridization have been employed to monitor gene deletions and their effects on cellular processes, such as cholesterol accumulation in adrenal and testis cells (Lee & Jefcoate, 2017). Advances in CRISPR-based imaging, particularly with deactivated Cas9 (dCas9) and dCas13, have greatly expanded molecular visualization tools.

These approaches enable detailed imaging of chromatin, genomic loci, RNAs, and proteins, providing deeper insights into chromatin structure and dynamics (Singh & Jain, 2021).

4. Molecular Mechanisms of Plant-Microbe Interactions

Chemical signaling in plants involves a complex interplay of molecules such as strigolactones, flavonoids, and microbial quorum-sensing molecules, which are crucial for plant-microbe interactions. Strigolactones, a group of phytohormones synthesized from carotenoids, are key regulators of plant signaling. They mediate communication with symbiotic fungi and bacteria, while also influencing interactions with parasitic plants. They regulate plant architecture and are involved in processes like seed germination and nodulation, highlighting their importance in both plant development and microbial symbiosis (Marzec, 2017) (Faizan et al., 2020). Flavonoids, another group of secondary metabolites, are part of root exudates that mediate interactions with rhizosphere microbes, influencing microbial behavior and plant immunity (Implication of Microbial Signals: Plant Communication, 2022). Microbial quorum-sensing molecules, such as N-acyl-homoserine lactones (AHLs), facilitate interspecies and interkingdom communication (Yajima, 2014) (Zaytseva et al., 2019). Plant hormones such as salicylic acid and jasmonic acid are pivotal in regulating these interactions, modulating plant responses to both beneficial and pathogenic microbes. These hormones are involved in nodulation, arbuscular mycorrhizal symbioses, and stress adaptation, often through complex signaling networks that integrate signals from both plant and microbial origins (Aalhus, 2022) (Singh et al., 2021) (Foo et al., 2019). Cross-kingdom signaling, a process where signaling molecules from one kingdom affect another, is exemplified by the interaction between plant hormones and microbial signals, which can modulate gene expression and plant immunity. This interkingdom communication is crucial for establishing symbiotic relationships and enhancing plant disease resistance, offering potential strategies for agricultural improvement (Kan et al., 2017)(Yajima, 2016).

Genetic control together with epigenetic processes are central to plant–microbe interactions particularly in symbiosis and defense mechanisms. Epigenetic modifications, such as DNA methylation and histone modifications, are pivotal in regulating plant responses to microbial interactions, influencing both symbiotic and defensive pathways. For instance, in legumes, nodulation genes are tightly regulated by epigenetic mechanisms, which are essential for the root nodules formation during Rhizobium symbiosis. This process involves the demethylase gene DEMETER, which regulates genes necessary for nodule organogenesis in Medicago truncatula, highlighting the role of DNA methylation in symbiotic interactions (Zimmermann & Gaillard, 2023). Similarly, in the legume-rhizobia symbiosis, effector-triggered immunity (ETI) is a critical component, where specific host genes, such as the Rj4 gene in soybeans, restrict nodulation by certain rhizobia strains through ETI pathways, demonstrating the intersection of immune responses and symbiotic regulation (Yasuda et al., 2016). Epigenetic regulation is also crucial in plant defense against pathogens, where modifications like DNA methylation and histone changes facilitate transcriptional reprogramming in response to pathogen attacks, contributing to both pathogen-associated molecular pattern-triggered immunity (PTI) and ETI (Xie & Duan, 2023) (Huang & Jin, 2022). These modifications can lead to systemic acquired resistance (SAR) and priming, where plants maintain a poised state for rapid defense activation upon subsequent pathogen exposure (Espinas et al., 2016). Furthermore, epigenetic changes can be heritable, providing transgenerational memory that enhances plant resilience to biotic stresses (Huang & Jin, 2022). In microbial interactions, epigenetic modifications are not limited to plants; they also affect microbial genomes, influencing symbiotic and pathogenic interactions. For example, in poplar and its ectomycorrhizal fungus Laccaria bicolor, hypomethylation in the host plant leads to altered fungal methylomes, affecting symbiotic efficiency (Zimmermann & Gaillard, 2023). These findings underscore the complexity and significance of epigenetic regulation in plant-microbe interactions

(Tao et al., 2023) (Epigenetic Modifications and Regulation in Infection, 2023).

5. Ecological and Evolutionary Perspectives

The metabolic interplay between plants and microbes in the rhizosphere is a complex and dynamic process that significantly influences plant health and soil ecology. Root exudates, which include a diverse array of primary and secondary metabolites such as sugars, organic acids, flavonoids, and terpenes, contribute to the organization of rhizosphere microbial assemblies through their role as nutrient providers and signaling agents (Korenblum et al., 2022) (Yetgin, 2023) (Chen & Liu, 2024). These exudates not only provide energy sources for microbial growth but also mediate communication between plants and microbes, influencing microbial composition and function (Yetgin, 2023) (Jain et al., 2020). In return, the rhizosphere microbiome supports plant health through multiple mechanisms. These include nutrient cycling, hormone production, and the modulation of plant defense responses (Poria et al., 2021) (Bhagat et al., 2023). For example, microbes release siderophores—molecules that chelate and solubilize iron, improving its availability to plants. This process boosts plant growth strengthens resilience against stress (Poria et al., 2021). The interactions between root exudates and microbes are strongly shaped by environmental conditions. Factors such as soil type, plant genotype, and abiotic stresses influence both the composition and the amount of exudates secreted (Yetgin, 2023) (Chen & Liu, 2024). Moreover, specific metabolites in root exudates can have differential effects on microbial communities, as seen in medicinal plants where compounds like carvone and zymosterol distinctly affect bacterial and fungal populations (Qu et al., 2024). Advanced approaches like metagenomics and metabolomics are now widely applied to investigate these interactions. They reveal key metabolic pathways and shed light on their broader ecological significance (Mishra et al., 2022). Understanding these complex interactions is essential for developing sustainable agricultural practices that leverage plant-microbe symbiosis to enhance crop productivity and soil health (Khade & Sruthi, 2024) (Wu et al., 2024).

The co-evolution of plants and microbes, particularly in the context of mutualism and pathogenicity, is a complex process driven by various evolutionary mechanisms, including horizontal gene transfer (HGT). Plant-microbe interactions form an evolutionary continuum, with mutualistic relationships such as arbuscular mycorrhizae (AM) and nitrogen-fixing symbioses playing crucial roles in plant adaptation and survival on land (Provorov, 2009) (Delaux & Schornack, 2021). The evolution of nitrogen-fixing symbioses, particularly in legumes, is a prime example of mutualism where plants and microbes have co-evolved to enhance soil fertility and crop yields. This co-evolution is driven by reciprocal selective pressures, leading to specialized symbiotic relationships facilitated by genetic adaptations in both plants and microbes (Chellem et al., 2024). Horizontal gene transfer has played a pivotal role in shaping symbiotic relationships. It enables the exchange of symbiotic traits among rhizobial strains, enhancing their adaptability and ecological success (Bailly et al., 2007). The emergence of nitrogen-fixing symbionts is hypothesized to have originated from soil diazotrophs and AM fungi, with subsequent bacterial migration into plant tissues leading to the development of nodular symbioses (Provorov et al., 2016)(Provorov et al., 2017). This process involved the integration of microbial consortia with ancestral land plants, resulting in the selection of genotypes capable of independent multiplication and symbiotic activity within plant tissues (Provorov et al., 2016). Case studies, such as the evolution of nitrogen-fixing symbioses in Medicago species, demonstrate how HGT and homologous recombination have driven the diversification and specialization of symbionts, allowing them to adapt to different host plants while maintaining gene flow among host-specific biovars (Bailly et al., 2007). The evolutionary trajectory of these symbioses reflects a balance between mutualistic benefits and the potential for pathogenicity, with plants evolving mechanisms to support beneficial microbes while defending against pathogens (Delaux & Schornack, 2021).

Abiotic stressors such as drought, salinity, and temperature significantly impact plant-microbe interactions, which are crucial for plant resilience in the face of climate change. These stressors disrupt cellular homeostasis and impair plant growth, posing a serious threat to agriculture and food security (Plant-Microbiota Interactions in Abiotic Stress Environments, 2022) (Omae & Tsuda, 2022). Microorganisms, especially those inhabiting the rhizosphere, are key players in alleviating plant stresses. They do so by improving nutrient availability, regulating plant metabolism, and modifying physiological responses (Sharma et al., 2021) (Anas et al., 2024). Plant growth-promoting rhizobacteria (PGPR), arbuscular mycorrhizal fungi (AMF), and endophytes are widely recognized for their beneficial effects on crops. They enhance both agricultural productivity and plant tolerance to stress (Inbaraj, 2021) (Singh et al., 2023). For instance, PGPR can activate plant antioxidant defense mechanisms, regulate reactive oxygen species (ROS), and produce enzymes like ACC deaminase, which help plants withstand abiotic stresses (Sharma et al., 2021). Drought stress, a major concern, can be alleviated by microbial communities that produce phytohormones and stress-combating enzymes, enhancing plant tolerance and improving crop yields (Negi et al., 2023). Microbial consortia, including synthetic ones, are being explored for their potential to reinforce plant defense capacity in fluctuating environments, although challenges remain in translating lab findings to field applications (Anas et al., 2024). The microbial mitigation of abiotic stress is a promising strategy for sustainable agriculture, offering an eco-friendly alternative to genetic engineering, which faces acceptance issues globally (Inbaraj, 2021). As climate change exacerbates the frequency and intensity of abiotic stresses, leveraging plant-microbe interactions becomes increasingly vital for developing climate-resilient crop species and ensuring global food security (Hayat et al., 2023) (“Microbial Mitigation of Abiotic Stress in Crops,” 2023).

6. Applications in Agriculture and Conservation

The use of beneficial microbes such as Pseudomonas fluorescens and Bacillus thuringiensis in biocontrol strategies offers a promising alternative to chemical pesticides for plant protection. These microbes function as biocontrol agents (BCAs), using diverse strategies to suppress plant pathogens and support plant health. For example, *Pseudomonas fluorescens* produces antibiotics and secondary metabolites that restrict pathogen growth, while also colonizing roots to create a protective barrier against infections (Mahapatra et al., 2024) (Fischer et al., 2013). This bacterium is also capable of solubilizing phosphates and fixing atmospheric nitrogen, thereby supplying vital nutrients to plants. In addition, it stimulates systemic acquired resistance, enhancing plant defense mechanisms (Mahapatra et al., 2024). Bacillus thuringiensis, on the other hand, is widely used as a biopesticide due to its production of insecticidal proteins that target specific pests without harming beneficial organisms (Chernin & Chet, 2002). Both Pseudomonas and Bacillus species are integral to sustainable agriculture, as they reduce the reliance on synthetic chemicals, which are associated with environmental and health hazards (Ayaz et al., 2023) (Kim et al., 2023). The effectiveness of these microbes is further enhanced when used in microbial consortia, which combine different organisms to interact synergistically, thereby enhancing plant growth and protection against a broad spectrum of phytopathogens (Use of Microbial Consortia for Broad Spectrum Protection of Plant Pathogens, 2022). In India, for example, commercialized biopesticides such as those containing Pseudomonas fluorescens and Bacillus thuringiensis are regulated and widely used, demonstrating their practical application in agriculture (Use of Microbial Consortia for Broad Spectrum Protection of Plant Pathogens, 2022). Despite their potential, challenges remain in the mass production, formulation, and application of these BCAs to ensure their stability and efficacy in diverse environmental conditions (Use of Microbial Consortia for Broad Spectrum Protection of Plant Pathogens, 2022) (Joshi et al., 2024).

Biofertilizers, especially microbial inoculants, are vital for sustainable farming as they improve nutrient absorption and enrich soil fertility. This reduces dependence on chemical fertilizers and helps lessen their negative environmental effects. These biofertilizers consist of diverse microorganisms, including nitrogen-fixing bacteria, phosphate-solubilizing microbes, and mycorrhizal fungi. Each group plays a unique role in enhancing soil health and promoting plant growth. Rhizobia-based biofertilizers, for instance, are well-documented for their ability to fix atmospheric nitrogen, making it available to plants, which is particularly beneficial for leguminous crops. This not only improves plant growth but also enhances soil fertility over time (Beleri, 2023) (Sharma et al., 2024). Mycorrhizal fungi, particularly arbuscular mycorrhizal fungi (AMF), establish symbiotic associations with plant roots. They help plants absorb phosphorus and other vital nutrients efficiently. AMF are especially beneficial in low-input and organic farming systems. They enhance plant nutrition, improve soil structure, and increase resilience to environmental stresses (Chen, 2022) (Dukare et al., 2021). Case studies indicate that using these biofertilizers can substantially enhance crop yields. They also contribute to improved soil health and fertility. For example, the use of rhizobial inoculants in various agroecosystems has demonstrated enhanced nitrogen availability and improved plant growth, while mycorrhizal applications have been successful in increasing phosphorus uptake and improving plant resistance to abiotic stresses (Giri et al., 2019)("Nutrient Acquisition and Soil Fertility: Contribution of Rhizosphere Microbiomes in Sustainable Agriculture," 2022). Despite their benefits, the widespread adoption of biofertilizers faces challenges such as limited farmer awareness, quality control issues, and the need for effective application techniques (Beleri, 2023)(Biofertilizers for Sustainable Agriculture, 2022).

Plant-microbe interactions play a crucial role in ecosystem restoration and phytoremediation, particularly in the context of heavy metal contamination. These interactions enhance the efficiency of phytoremediation by facilitating the uptake and stabilization of heavy metals in contaminated soils. Beneficial soil microorganisms, such as Plant Growth-Promoting Rhizobacteria (PGPR) and Arbuscular Mycorrhizal Fungi (AMF), are instrumental in this process. They enhance plant growth and resilience against heavy metal stress, making them vital components of sustainable phytoremediation strategies. For instance, AMF species like Glomus and Rhizophagus, along with PGPR species such as Bacillus and Pseudomonas, have been shown to significantly enhance the phytoremediation capabilities of plants by improving their growth and metal uptake efficiency (Hnini et al., 2024) (Sorour et al., 2022). The synergistic interaction between plants and microbes not only improves the bioavailability of metals but also aids in their transformation into less toxic forms through processes like biotransformation, biosorption, and redox reactions (Arshad et al., 2024) (Islam et al., 2021). This interaction is particularly effective in hyperaccumulator plants, which can sequester and stabilize heavy metals more efficiently when supported by microbial partners (Khatoon et al., 2024). Moreover, microbial contributions such as the production of siderophores, organic acids, and phytohormones enhance the mobility and bioavailability of heavy metals, thereby accelerating the phytoremediation process (Plant-Microbe Association to Improve Phytoremediation of Heavy Metal, 2022). Incorporating plant–microbe interactions into phytoremediation helps in cleaning up contaminated environments. This approach also improves soil fertility and plant health, making it a sustainable strategy for managing heavy metal-polluted sites (Upadhyay et al., 2019). Future studies should aim to optimize plant–microbe interactions for maximum effectiveness. Efforts should also focus on applying laboratory insights to real-world field conditions to fully utilize these partnerships in ecosystem restoration (Montreemuk et al., 2023) (Gul et al., 2021).

7. Challenges and Limitations

Current methodologies in omics, while revolutionary, face significant limitations, particularly in scalability and field applicability. The integration of genomics, transcriptomics, proteomics, and metabolomics has advanced our understanding of plant-microbe interactions, yet these techniques often struggle with scalability due to the vast data they generate and the computational power required to process it (Carper et al., 2022) (Tarazona et al., 2021). Multi-omics approaches, although promising, are still nascent and face challenges in data integration and interpretation, which can lead to potentially incorrect conclusions if not carefully managed (Tarazona et al., 2021) (Jiang et al., 2019). The complexity of studying multi-species interactions is compounded by the need for interdisciplinary approaches that can bridge the gap between descriptive and quantitative understanding, particularly in marine ecosystems where environmental changes impact microbial communities (Mock et al., 2016). Long-term ecological impacts remain poorly understood due to the inherent complexity and uncertainty in predicting ecosystem responses to climate change, which requires integrating quantitative models with expert insights to better assess biological responses (Rangwala et al., n.d.). Ethical and regulatory issues in microbial applications are also critical, as the deployment of microbial technologies in environmental and industrial settings must consider potential ecological disruptions and the need for robust regulatory frameworks to manage these risks (Sood et al., 2023). Furthermore, the challenges in microbial ecology, such as building predictive models of community function and dynamics, highlight the need for better integration of experimental data with mathematical models to enhance our understanding of microbial community dynamics (Widder et al., 2016). Overall, while omics technologies offer unprecedented insights, their application is limited by technical, interpretative, and regulatory challenges that must be addressed to fully realize their potential in ecological and microbial studies.

8. Future Directions

The integration of synthetic biology, microbiome engineering, and artificial intelligence (AI) is paving the way for innovative approaches to developing climate-resilient crops and sustainable agricultural practices. Synthetic biology provides powerful tools to design and modify plant systems along with their associated microbiomes. This enables improved stress tolerance, nutrient absorption, and overall plant productivity (Iram et al., 2024) (Singla, 2020). Microbiome engineering specifically targets the alteration of microbial communities associated with plants. This approach aims to enhance plant health and stress resilience, which is vital under changing climate conditions (Tan et al., 2022) (Kaul et al., 2021) (Hayat et al., 2023). This strategy entails the targeted manipulation of microbial communities to boost plant functions like disease resistance and tolerance to abiotic stress. By doing so, it lowers dependence on agrochemicals and supports sustainable agricultural practices (Orukotan et al., 2023) (Trivedi et al., 2021). The use of AI and big data analytics further enhances these efforts by enabling predictive modeling of plant-microbe interactions, thus facilitating the design of more effective microbiome interventions (Iram et al., 2024) (Zhang et al., 2024). AI-powered synthetic biology offers advanced tools for designing genetic circuits in plants.This approach supports the development of crops with improved photosynthesis and greater adaptability to environmental challenges (Zhang et al., 2024). The success of these technologies relies heavily on interdisciplinary collaboration, combining expertise from botany, microbiology, ecology, and computational sciences to address the complex challenges of plant-microbe interactions and their applications in agriculture (Tan et al., 2022) (Lawson, 2021) (Kozaeva et al., 2024). This collaborative approach is essential for translating scientific insights into practical solutions that can be adopted by farmers and integrated into existing agricultural systems (Trivedi et al., 2021). As these technologies continue to evolve, they hold the promise of significantly advancing the development of climate-resilient crops and contributing to global food security in a sustainable manner.

Conclusion

Investigating interactions between plants and microbes is a crucial area of study.This research represents a key frontier in advancing plant health and productivity in botanical studies, integrating ecological, molecular, and evolutionary perspectives to enhance our understanding of these complex relationships. The advancements in research methodologies, particularly through omics technologies and innovative imaging techniques, have illuminated the intricate signaling pathways and molecular dialogues that underpin these interactions, revealing their profound implications for plant health, sustainability of ecosystem and agricultural productivity. In addressing climate change and environmental degradation, it is vital to harness the advantages of beneficial plant-microbe interactions. At the same time, managing harmful microbial relationships is crucial for promoting sustainable agricultural practices. Future directions in synthetic biology, microbiome engineering, and artificial intelligence provides promising tools to leverage plant-microbe interactions for crop improvement. This approach can help develop climate-resilient crops and strengthen global food security. Continued interdisciplinary collaboration and research will be crucial in translating these insights into practical applications that benefit both agriculture and the environment.

References

Kaur, S., & Kaur, G. (2018).*Morphological and Physiological Aspects of Symbiotic Plant–Microbe Interactions and Their Significance*. https://doi.org/10.1007/978-3-319-75910-4_15

Provorov, N. A. (2009). [Plant-microbe symbioses as an evolutionary continuum].*Zhurnal Obshchei Biologii*.

Dass, R. S., & Mallick, R. (2019).*A Concise Compilation of the Diverse Detection Methods to Study Plant-Microbe Interfaces at the Cellular and Molecular Level: The Past, Present and Future*. https://doi.org/10.1007/978-3-030-19831-2_13

Panstruga, R., & Kuhn, H. (2015). Introduction to a Virtual Special Issue on cell biology at the plant–microbe interface.*New Phytologist*. https://doi.org/10.1111/NPH.13551

Çetiz, M. V., & Memon, A. (2021). Effect of The Plant- Microbe Interaction on Secondary Metabolites.*Turkish Journal of Agriculture: Food Science and Technology*.

https://doi.org/10.24925/TURJAF.V9I2.281-287.3775

Babar, M. M., Babar, M. M., Khan, S. F., Zargaham, M. K., Zaidi, N.-S. S., & Gul, A. (2016).*Plant-Microbe Interactions: A Molecular Approach*. https://doi.org/10.1007/978-3-319-29573-2_1

Yang, L., Qian, X., Zhao, Z., Wang, Y., Ding, G., & Xing, X. (2024). Mechanisms of rhizosphere plant-microbe interactions: molecular insights into microbial colonization.*Frontiers in Plant Science*. https://doi.org/10.3389/fpls.2024.1491495

Mohapatra, R., Saritha, B., Jhankar, J., Sumitha, J., Jainab, B., & Pal, S. K. (2024). Plant Microbe Interactions an Implications for Sustainable Agriculture.*Uttar Pradesh Journal of Zoology*. https://doi.org/10.56557/upjoz/2024/v45i184417

Ramasamy, K., & Kumar, K. (n.d.).*Plant-Microbe Interactions*. https://doi.org/10.59317/9789389547580

Sahoo, S., Panda, S. S., Kumar, S., Nigam, R., Sarangi, S. N., Choudhary, M., Yuvarani, R., & Shivam, S. (2024). A Review on Plant-microbe Interactions and its Defence Mechanism.*PLANT CELL BIOTECHNOLOGY AND MOLECULAR BIOLOGY*. https://doi.org/10.56557/pcbmb/2024/v25i11-128920

Mahadevakumar, S., & Sridhar, K. R. (2020).*Plant-Microbe Interaction: Current Developments and Future Challenges*. https://doi.org/10.1007/978-981-15-3208-5_1

Pathma, J., Raman, G., Kennedy, R. K., & Bhushan, L. S. (2020).*Recent Advances in Plant-Microbe Interaction*. https://doi.org/10.1007/978-981-15-4099-8_2

Shi, X., Zhao, Y., Xu, M., Ma, L., Adams, J. M., & Shi, Y. (2023).*Insight into Plant-Microbe Interactions in rhizosphere for Sustainable Agriculture in the New Crops Era*. https://doi.org/10.1016/j.ncrops.2023.11.002

Kaur, M., & Saxena, R. (2024).*Review on plant-microbe interactions, applications and future aspects*. https://doi.org/10.1016/b978-0-443-18446-8.00005-x

Chang, C., Nasir, F., Nasir, F., Ma, L., & Tian, C. (2017).*Molecular Communication and Nutrient Transfer of Arbuscular Mycorrhizal Fungi, Symbiotic Nitrogen-Fixing Bacteria, and Host Plant in Tripartite Symbiosis*. https://doi.org/10.1007/978-3-319-55729-8_9

Duan, H.-X., Luo, C., Wang, X., Cheng, Y.-S., Abrar, M., & Batool, A. (2024). Responses of Legumes to Rhizobia and Arbuscular Mycorrhizal Fungi Under Abiotic Stresses: A Global Meta-Analysis.*Agronomy*. https://doi.org/10.3390/agronomy14112597

Biate, D. L., Kumari, A., Annapurna, K., Kumar, L. V., Ramadoss, D., Reddy, K. K., & Naik, S. (2015).*Legume Root Exudates: Their Role in Symbiotic Interactions*. https://doi.org/10.1007/978-81-322-2068-8_13

Feki, K., Brini, F., Mrabet, M., & Mhadhbi, H. (2020).*Legume Symbiotic Interaction from Gene to Whole Plant*. https://doi.org/10.1007/978-3-030-53017-4_7

Basu, S., & Kumar, G. (2020).*Nitrogen Fixation in a Legume-Rhizobium Symbiosis: The Roots of a Success Story*. https://doi.org/10.1007/978-3-030-36248-5_3

Chellem, S. R., Kishore, C. V. L., Reddy, G., Akshay, D. V. S., Kalpana, K., Lavanya, P., & Choragudi, K. H. (2024). Symbiotic Relationships between Nitrogen-fixing Bacteria and Leguminous Plants Ecological and Evolutionary Perspectives: A Review.*Uttar Pradesh Journal of Zoology*. https://doi.org/10.56557/upjoz/2024/v45i134143

Srivastava, P. S., Sahgal, M., & Paul, S. (2024).*Nitrogen-fixing Rhizobium-legume symbiosis in agroecosystems*. https://doi.org/10.1016/b978-0-443-13365-7.00016-6

Javaid, A. (2010).*Role of Arbuscular Mycorrhizal Fungi in Nitrogen Fixation in Legumes*. https://doi.org/10.1007/978-3-211-99753-6_17

Chen, Y., & Zhou, X. (2024). Symbiotic Nitrogen Fixation: The Role of Rhizobia in Enhancing Legume Growth and Soil Fertility.*Molecular Microbiology Research*. https://doi.org/10.5376/mmr.2024.14.0012

Gorgia, P., & Tsikou, D. (2025). Tripartite Symbiosis Between Legumes, Arbuscular

Mycorrhizal Fungi and Nitrogen Fixing Rhizobia: Interactions and Regulation.*Plant Cell and Environment*. https://doi.org/10.1111/pce.15341

Mundra, S., & Morsy, M. (2024). Editorial: Applicative and ecological aspects of mycorrhizal symbioses.*Frontiers in Plant Science*. https://doi.org/10.3389/fpls.2024.1510941

Gayathry, G., Natarajan, K., Jayalakshmi, T., Radha, R. V., Sugumaran, M. P., Sunitha, R., & Kumutha, K. (2024). Mycorrhizae: A Rhizolive Symbiotic Fungi in Organic Agriculture.*Archives of Current Research International*. https://doi.org/10.9734/acri/2024/v24i9881

Koele, N., Dickie, I. A., Dickie, I. A., Blum, J. D., Gleason, J. D., & Graaf, L. de. (2014). Ecological significance of mineral weathering in ectomycorrhizal and arbuscular mycorrhizal ecosystems from a field-based comparison.*Soil Biology & Biochemistry*. https://doi.org/10.1016/J.SOILBIO.2013.10.041

Vishwakarma, R. (2024). The Role of Plant-Mycorrhizal-Fungal Interactions in Soil Health and Carbon Sequestration in Agroecosystems.*International Journal for Research in Applied Science and Engineering Technology*. https://doi.org/10.22214/ijraset.2024.63575

Beggi, F., & Dasgupta, D. (2021).*Arbuscular and ectomycorrhizal fungi diversity in the Indian subcontinent*. https://doi.org/10.7910/dvn/hxah87

Heklau, H., Schindler, N., Buscot, F., Eisenhauer, N., Ferlian, O., Salcedo, L. D. P., & Bruelheide, H. (2021). Mixing tree species associated with arbuscular or ectotrophic mycorrhizae reveals dual mycorrhization and interactive effects on the fungal partners.*Ecology and Evolution*. https://doi.org/10.1002/ECE3.7437

Zambounis, A., Xanthopoulou, A., Aravanopoulos, F. A., Tsaftaris, A., & Barbas, E. (2016).*First report of an arbuscular mycorrhizal fungus funneliformis mosseae associated with thuja plicata in an ectomycorrhizal forest in greece*. https://doi.org/10.33687/PHYTOPATH.005.01.1601

Rosling, A., Sahraei, S. E., Khan, F. K., Desirò, A., Bryson, A. E., Mondo, S. J., Grigoriev, I. V., Bonito, G., & Sánchez-García, M. (2023).*Evolutionary history of arbuscular mycorrhizal fungi and genomic signatures of obligate symbiosis*. https://doi.org/10.21203/rs.3.rs-3092996/v1

Liu, T., Chen, Y., Tian, S., & Li, B. (2023). Crucial Roles of Effectors in Interactions between Horticultural Crops and Pathogens.*Horticulturae*. https://doi.org/10.3390/horticulturae9020250

Todd, J. N. A., Carreón-Anguiano, K. G., Couoh-Dzul, O. J., Santos-Briones, C. D. L., & Canto-Canché, B. (2023). Effectors: key actors in phytopathology.*Revista Mexicana de Fitopatología*. https://doi.org/10.18781/r.mex.fit.2210-4

Zhang, S., Li, C., Si, J., Han, Z., & Chen, D. (2022). Action Mechanisms of Effectors in Plant-Pathogen Interaction.*International Journal of Molecular Sciences*. https://doi.org/10.3390/ijms23126758

Sun, L., Wu, X., Diao, J., & Zhang, J. (2023). Pathogenesis mechanisms of phytopathogen effectors.*Wires Mechanisms Of Disease*. https://doi.org/10.1002/wsbm.1592

Agarrwal, R., Ahire, T. P., Manjunatha, N., Pokhare, S. S., Ojha, R., & Salvi, P. (2024).*Imperative Role of R-Genes and Associated Molecular Mechanisms in Plant Disease Resistance*. https://doi.org/10.1007/978-981-99-8874-7_4

Prihatna, C. (2009). The Plant - Pathogen Interactions.*Microbiology Indonesia*. https://doi.org/10.5454/MI.3.3.1

Montoya-Martínez, A. C., Ruiz, V. V., Chávez-Luzanía, R. A., Parra-Cota, F. I., & Santos-Villalobos, S. de los. (2024).*Plant–pathogen interactions: Mechanisms involved in plant diseases*. https://doi.org/10.1016/b978-0-443-18855-8.00003-5

Poudel, A., & KC, S. (2024). Interplay of plant pathogens and host defenses: Unveiling the mechanisms and strategies for crop protection.*Archives of Agriculture and Environmental Science*. https://doi.org/10.26832/24566632.2024.0901014

Kalita, P., Mohapatra, B., & Maruthi, M. (2024).*Role of Effectors in Plant–Pathogen Interactions*. https://doi.org/10.1007/978-981-99-8874-7_15

Todd, J. N. A., Carreón-Anguiano, K. G., Islas-Flores, I., & Canto-Canché, B. (2022). Microbial Effectors: Key Determinants in Plant Health and Disease.*Microorganisms*. https://doi.org/10.3390/microorganisms10101980

Endophytic Microbes and Their Role in Plant Health. (2023). https://doi.org/10.1007/978-981-99-0030-5_12

Santos, M. L. dos, Berlitz, D. L., Wiest, S. L. F., Schünemann, R., Knaak, N., & Fiuza, L. M. (2018). Benefits Associated with the Interaction of Endophytic Bacteria and Plants.*Brazilian Archives of Biology and Technology*. https://doi.org/10.1590/1678-4324-2018160431

Singh, S., Kumar, V., Dhanjal, D. S., Sidhu, G. K., Datta, S., Kumar, S., & Singh, J. (2020).*Endophytic microbes in abiotic stress management*. https://doi.org/10.1016/B978-0-12-818734-0.00005-X

Bind, S., Bind, S., & Chandra, D. (2021).*An Endophytic Bacterial Approach: A Key Regulator of Drought Stress Tolerance in Plants*. https://doi.org/10.1007/978-981-16-3840-4_28

Carvalho, J. O. de, Broll, V., Martinelli, A. H. S., & Lopes, F. C. (2020).*Endophytic fungi: positive association with plants*. https://doi.org/10.1016/B978-0-12-818469-1.00026-2

Sharma, P., & Singh, S. P. (2021).*Role of the endogenous fungal metabolites in the plant growth improvement and stress tolerance*. https://doi.org/10.1016/B978-0-12-821734-4.00002-2

Wang, L., Zhang, S., Xie, Q., Tao, J., Jia, Y., Xiao, Y., Tang, Z., Li, Q., Yuan, M., & Bu, T. (2024). Exploring Plant Growth-Promoting Traits of Endophytic Fungi Isolated from Ligusticum chuanxiong Hort and Their Interaction in Plant Growth and Development.*Journal of Fungi*. https://doi.org/10.3390/jof10100713

Choudhury, D., Tarafdar, S., Parvin, N., Rit, R., Roy, S., Sadhu, S. Kr., & Dutta, S. (2022). Endophytic microbes and their diverse beneficial aspects in various sectors: A critical insight.*Plant Science Today*. https://doi.org/10.14719/pst.1877

Vandana, U. K., Rajkumari, J., Singha, L. P., Satish, L., Alavilli, H., Sudheer, P. D. V. N., Chauhan, S., Ratnala, R., Satturu, V., Mazumder, P. B., & Pandey, P. (2021). The Endophytic Microbiome as a Hotspot of Synergistic Interactions, with Prospects of Plant Growth Promotion.*Biology*. https://doi.org/10.3390/BIOLOGY10020101

Wu, W., Chen, W., Liu, S., Wu, J., Zhu, Y., Qin, L., & Zhu, B. (2021). Beneficial Relationships Between Endophytic Bacteria and Medicinal Plants.*Frontiers in Plant Science*. https://doi.org/10.3389/FPLS.2021.646146

Kaur, M., Kaur, R., & Sodhi, H. S. (2022).*Utilization of omics approaches for underpinning plant-microbe interaction*. https://doi.org/10.1016/b978-0-323-85577-8.00009-3

Jain, A., Sarsaiya, S., Singh, R., Gong, Q., Wu, Q., & Shi, J. (2024). Omics approaches in understanding the benefits of plant-microbe interactions.*Frontiers in Microbiology*. https://doi.org/10.3389/fmicb.2024.1391059

Omics technologies for agricultural microbiology research. (2022). https://doi.org/10.1016/b978-0-323-91595-3.00015-x

Tett, A. J., Turner, T. R., & Poole, P. S. (2012).*Genomics and the Rhizosphere*. https://doi.org/10.1002/9780470015902.A0023728

Sudhakar, P. (2022).*Metagenomic Approaches for Studying Plant–Microbe Interactions*. https://doi.org/10.1007/978-981-19-3696-8_12

Boparai, J. K., & Sharma, P. K. (2021).*Metagenomics and Metatranscriptomics Approaches in Understanding and Discovering Novel Molecules in Rhizosphere Environment*. https://doi.org/10.1007/978-981-16-0889-6_3

Archana, T. S., Kumar, D., Kumar, V., Singh, S., Shukuru, N. B., & Kumar, G. (2023).*Rhizospheric microbiome: organization and bioinformatics studies*. https://doi.org/10.1016/b978-0-443-16030-1.00016-x

Rosselli, R., & Squartini, A. (2015).*Metagenomics of Plant–Microbe Interactions*. https://doi.org/10.1007/978-3-319-17157-9_9

Mishra, A. K., Sudalaimuthuasari, N., Hazzouri, K. M., Saeed, E. E., Shah, I., & Amiri, K. M. A. (2022). Tapping into Plant–Microbiome Interactions through the Lens of Multi-Omics

Techniques.*Cells*. https://doi.org/10.3390/cells11203254

Li, T., Yan, A., & Meyerowitz, E. M. (2019). Live imaging-assisted domain-specific CRISPR genome editing at single cell resolution in plants.*bioRxiv*. https://doi.org/10.1101/793240

Fok, E. T., Fanucchi, S., Fanucchi, S., Bystricky, K., Mhlanga, M. M., & Mhlanga, M. M. (2021).*Visualization of Chromatin Dynamics by Live Cell Microscopy Using CRISPR/Cas9 Gene Editing and ANCHOR Labeling*.https://doi.org/10.1007/978-1-0716-0664-3_11

Xia, C., Colognori, D., Jiang, X., Xu, K., & Doudna, J. A. (2024).*Single-molecule live-cell RNA imaging with CRISPR-Csm*. https://doi.org/10.1101/2024.07.14.603457

Lee, J., & Jefcoate, C. R. (2017). Monitoring of Dual CRISPR/Cas9-Mediated Steroidogenic Acute Regulatory Protein Gene Deletion and Cholesterol Accumulation Using High-Resolution Fluorescence In Situ Hybridization in a Single Cell.*Frontiers in Endocrinology*. https://doi.org/10.3389/FENDO.2017.00289

Singh, V., & Jain, M. K. (2021). Recent advancements in CRISPR-Cas toolbox for imaging applications.*Critical Reviews in Biotechnology*. https://doi.org/10.1080/07388551.2021.1950608

Marzec, M. (2017).*Strigolactone Signaling in Plants*. https://doi.org/10.5772/INTECHOPEN.68497

Faizan, M., Faraz, A., Sami, F., Siddiqui, H., Yusuf, M., Gruszka, D., & Hayat, S. (2020). Role of strigolactones: Signalling and crosstalk with other phytohormones.*Central European Journal of Biology*. https://doi.org/10.1515/BIOL-2020-0022

Implication of Microbial Signals: Plant Communication. (2022). https://doi.org/10.1201/9781003171416-3

Yajima, A. (2014). Recent Progress in the Chemistry and Chemical Biology of Microbial Signaling Molecules: Quorum-Sensing Pheromones and Microbial Hormones.*ChemInform*. https://doi.org/10.1002/CHIN.201424283

Zaytseva, Yu. V., Sidorov, A. V., Marakaev, O. A., & Khmel, I. A. (2019). Plant-Microbial Interactions Involving Quorum Sensing Regulation.*Microbiology*. https://doi.org/10.1134/S0026261719040131

Aalhus, J. L. (2022). Role of Phytohormones in Plant-Microbial Interaction.*Signaling and Communication in Plants*. https://doi.org/10.1007/978-3-031-05427-3_14

Singh, S., Kumar, V., Datta, S., Ramamurthy, P. C., & Singh, J. (2021).*Molecular mechanism and signaling pathways interplay between plant hormones during plant-microbe crosstalk*. https://doi.org/10.1016/B978-0-323-85193-0.00004-8

Foo, E., Plett, J. M., López-Ráez, J. A., & Reid, D. (2019). Editorial: The role of plant hormones in plant-microbe symbioses.*Frontiers in Plant Science*. https://doi.org/10.3389/FPLS.2019.01391

Kan, J., Fang, R., & Jia, Y. (2017). Interkingdom signaling in plant-microbe interactions.*Science China-Life Sciences*. https://doi.org/10.1007/S11427-017-9092-3

Yajima, A. (2016).*Recent Advances in the Chemistry and Chemical Biology of Quorum-Sensing Pheromones and Microbial Hormones*. https://doi.org/10.1016/B978-0-444-63603-4.00010-3

Zimmermann, S., & Gaillard, I. (2023). Epigenetic control is involved in molecular dialogue in plant-microbe symbiosis.*New Phytologist*. https://doi.org/10.1111/nph.18916

Yasuda, M., Miwa, H., Masuda, S., Takebayashi, Y., Sakakibara, H., & Okazaki, S. (2016). Effector-Triggered Immunity Determines Host Genotype-Specific Incompatibility in Legume-Rhizobium Symbiosis.*Plant and Cell Physiology*. https://doi.org/10.1093/PCP/PCW104

Xie, S.-S., & Duan, C. (2023). Epigenetic regulation of plant immunity: from chromatin codes to plant disease resistance.*aBIOTECH*. https://doi.org/10.1007/s42994-023-00101-z

Huang, C. Y., & Jin, H. (2022). Coordinated Epigenetic Regulation in Plants: A Potent Managerial Tool to Conquer Biotic Stress.*Frontiers in Plant Science*. https://doi.org/10.3389/fpls.2021.795274

Espinas, N. A., Saze, H., & Saijo, Y. (2016). Epigenetic control of defense signaling and priming in plants.*Frontiers in Plant Science*. https://doi.org/10.3389/FPLS.2016.01201

Tao, Z., Yan, F.-H., Hahn, M., & Ma, Z. (2023).*Regulatory roles of epigenetic modifications in plant-phytopathogen interactions*. https://doi.org/10.1007/s44297-023-00003-y

Epigenetic modifications and regulation in infection. (2023). https://doi.org/10.1016/b978-0-12-823931-5.00002-5

Korenblum, E., Massalha, H., & Aharoni, A. (2022). Plant-microbe interactions in the rhizosphere via a circular metabolic economy.*The Plant Cell*. https://doi.org/10.1093/plcell/koac163

Yetgin, A. (2023). The dynamic interplay of root exudates and rhizosphere microbiome.*Soil Studies*. https://doi.org/10.21657/soilst.1408089

Chen, L., & Liu, Y. (2024). The Function of Root Exudates in the Root Colonization by Beneficial Soil Rhizobacteria.*Biology*. https://doi.org/10.3390/biology13020095

Jain, A., Chakraborty, J., & Das, S. (2020). Underlying mechanism of plant–microbe crosstalk in shaping microbial ecology of the rhizosphere.*Acta Physiologiae Plantarum*. https://doi.org/10.1007/S11738-019-3000-0

Poria, V., Singh, S., Nain, L., Singh, B., & Saini, J. K. (2021).*Rhizospheric Microbial Communities: Occurrence, Distribution, and Functions*. https://doi.org/10.1007/978-981-15-9758-9_12

Bhagat, S., Shete, P., & Jain, A. (2023).*Plant health: Feedback effect of root exudates and rhizobiome interactions*. https://doi.org/10.1016/b978-0-443-16030-1.00007-9

Qu, P., Wang, B., Qi, M., Lin, R., Chen, H., Xie, C., Zhang, Z., Qiu, J., Du, H., & Ge, Y. (2024). Medicinal Plant Root Exudate Metabolites Shape the Rhizosphere Microbiota.*International Journal of Molecular Sciences*. https://doi.org/10.3390/ijms25147786

Khade, O. S., & Sruthi, K. (2024).*The rhizosphere microbiome: A key modulator of plant health and their role in secondary metabolites production*. https://doi.org/10.1016/b978-0-443-15397-6.00016-4

Wu, D., He, X., Jiang, L., Li, W., Wang, H., & Lv, G. (2024). Root exudates facilitate the regulation of soil microbial community function in the genus Haloxylon.*Frontiers in Plant Science*. https://doi.org/10.3389/fpls.2024.1461893

Delaux, P.-M., & Schornack, S. (2021). Plant evolution driven by interactions with symbiotic and pathogenic microbes.*Science*. https://doi.org/10.1126/SCIENCE.ABA6605

Bailly, X., Olivieri, I., Brunel, B., Cleyet-Marel, J.-C., & Béna, G. (2007). Horizontal gene transfer and homologous recombination drive the evolution of the nitrogen-fixing symbionts of Medicago species.*Journal of Bacteriology*. https://doi.org/10.1128/JB.00105-07

Provorov, N. A., Shtark, O. Yu., & Dolgikh, E. A. (2016). [Evolution of nitrogen-fixing symbioses based on the migration of bacteria from mycorrhizal fungi and soil into the plant tissues].*Zhurnal Obshchei Biologii*.

Provorov, N. A., Shtark, O. Yu., & Dolgikh, E. A. (2017). Evolution of nitrogen-fixing symbioses on the basis of bacterial migration from mycorrhizal fungi and soil into plant tissues.*Biology Bulletin Reviews*. https://doi.org/10.1134/S2079086417050061

Plant-Microbiota Interactions in Abiotic Stress Environments. (2022). https://doi.org/10.1094/mpmi-11-21-0281-fi

Omae, N., & Tsuda, K. (2022). Plant-Microbiota Interactions in Abiotic Stress Environments.*Molecular Plant-Microbe Interactions*. https://doi.org/10.1094/MPMI-11-21-0281-FI

Anas, M., Khalid, A., Saleem, M. H., Khan, K. A., Khattak, W. A., & Fahad, S. (2024). Symbiotic Synergy: Unveiling Plant-Microbe Interactions in Stress Adaptation.*Deleted Journal*. https://doi.org/10.1007/s10343-024-01070-z

Sharma, S. D., Chandra, D., & Sharma, A. K. (2021).*Rhizosphere Plant–Microbe Interactions Under Abiotic Stress*. https://doi.org/10.1007/978-981-15-6125-2_10

Inbaraj, M. P. (2021).*Plant-Microbe Interactions in Alleviating Abiotic Stress—A Mini Review*. https://doi.org/10.3389/FAGRO.2021.667903

Singh, P., Rayeen, F., Singh, R., Pathak, N., Singh, R. P., Tiwari, V., Tripathi, M., & Singh, P. K. (2023). Enhancing Agricultural Sustainability through Microbial-Mediated Abiotic Stress Tolerance.*Journal of Ecophysiology and Occupational Health*. https://doi.org/10.18311/jeoh/2023/34777

Negi, N. P., Narwal, P., & Sharma, A. (2023).*Plant–microbe interaction in alleviating drought stress*. https://doi.org/10.1016/b978-0-323-91734-6.00022-3

Hayat, K., Menhas, S., Ullah, S., Hayat, S., Khan, A., Aftab, T., & Liu, W. (2023).*Plant–Microbe Interaction in Developing Climate-Resilient Crop Species*. https://doi.org/10.1007/978-3-031-43729-8_20

Microbial Mitigation of Abiotic Stress in Crops. (2023).*Sustainable Agriculture Reviews*. https://doi.org/10.1007/978-3-031-24181-9_9

Mahapatra, B., Ghosh, D., & Mukhopadhyay, R. (2024). Biocontrol potential of Trichoderma and Pseudomonas: A review.*International Journal of Advanced Biochemistry Research*. https://doi.org/10.33545/26174693.2024.v8.i4sb.933

Fischer, S., Príncipe, A., Alvarez, F., Cordero, P., Castro, M., Godino, A., Jofré, E., & Mori, G. (2013).*Fighting Plant Diseases Through the Application of Bacillus and Pseudomonas Strains*. https://doi.org/10.1007/978-3-642-39317-4_9

Chernin, L., & Chet, I. (2002).*Microbial enzymes in the biocontrol of plant pathogens and pests.*https://doi.org/10.1201/9780203904039-14

Ayaz, M., Li, C.-H., Ali, Q., Chi, Y.-K., Shafiq, M., Ali, F., Yu, X.-Y., & Qi, R.-D. (2023). Bacterial and Fungal Biocontrol Agents for Plant Disease Protection: Journey from Lab to Field, Current Status, Challenges, and Global Perspectives.*Molecules*. https://doi.org/10.3390/molecules28186735

Kim, S. C., Koo, B.-K., & Han, J. A. (2023). Exploiting Bacterial Genera as Biocontrol Agents: Mechanisms, Interactions and Applications in Sustainable Agriculture.*Journal of Plant Biology*. https://doi.org/10.1007/s12374-023-09404-6

Use of microbial consortia for broad spectrum protection of plant pathogens. (2022). https://doi.org/10.1016/b978-0-12-823355-9.00017-1

Joshi, M., Srivastava, A. K., Ashaq, M., Jaggi, S., Gupta, P., Hasan, W., & Gupta, S. (2024). Biocontrol Agents and Plant Protection.*Uttar Pradesh Journal of Zoology*. https://doi.org/10.56557/upjoz/2024/v45i164292

Beleri, P. S. (2023).*Microbial Solutions to Soil Health: The Role of Biofertilizers in Sustainable Agriculture*. https://doi.org/10.51470/er.2023.5.2.06

Sharma, H. R., Chaudhary, R., Yadav, P., Kalia, M., Nautiyal, S., Rawat, A., Kagday, M., Pal, A. K., Kalia, S., & Rautela, I. (2024). A Sustainable Agriculture Method Using Biofertilizers: An Eco-Friendly Approach.*Plant Science Today*. https://doi.org/10.14719/pst.3094

Chen, L. (2022).*Arbuscular Mycorrhizal Fungi: A Next-Generation Biofertilizer for Sustainable Agriculture*. https://doi.org/10.1007/978-981-19-0733-3_6

Dukare, A., Paul, S., Kumar, R., & Sharma, V. (2021).*Microbial-based inoculants in sustainable agriculture: Current perspectives and future prospects*. https://doi.org/10.1016/B978-0-12-821667-5.00019-1

Giri, B., Prasad, R., Wu, Q.-S., & Varma, A. (2019).*Biofertilizers for sustainable agriculture and environment.*

Nutrient Acquisition and Soil Fertility: Contribution of Rhizosphere Microbiomes in Sustainable Agriculture. (2022).*Microorganisms for Sustainability*. https://doi.org/10.1007/978-981-16-4843-4_1

Biofertilizers for Sustainable Agriculture. (2022). https://doi.org/10.1201/9781003220831-19

Hnini, M., Rabeh, K., & Oubohssaine, M. (2024). Interactions between beneficial soil microorganisms (PGPR and AMF) and host plants for environmental restoration: A systematic review.*Plant Stress*. https://doi.org/10.1016/j.stress.2024.100391

Sorour, A. A., Khairy, H., Zaghloul, E., & Zaghloul, H. A. H. (2022). Microbe- plant interaction as a sustainable tool for mopping up heavy metal contaminated sites.*BMC Microbiology*. https://doi.org/10.1186/s12866-022-02587-x

Arshad, I., Iqbal, H., Iqbal, S. S., Afzaal, M., & Rehman, Y. (2024). A Review on the Synergistic Approaches for Heavy Metals Bioremediation: Harnessing the Power of Plant-Microbe Interactions.*LGU Journal of Life Sciences*. https://doi.org/10.54692/lgujls.2024.0802343

Islam, Md. S., Kormoker, T., Idris, A. M., Idris, A. M., Proshad, R., Kabir, Md. H., & Ustaoğlu, F. (2021). Plant–microbe–metal interactions for heavy metal bioremediation: a review.*Crop & Pasture Science*. https://doi.org/10.1071/CP21322

Khatoon, Z., Orozco-Mosqueda, Ma. del C., & Santoyo, G. (2024). Microbial Contributions to Heavy Metal Phytoremediation in Agricultural Soils: A Review.*Microorganisms*. https://doi.org/10.3390/microorganisms12101945

Plant-microbe association to improve phytoremediation of heavy metal. (2022). https://doi.org/10.1016/b978-0-12-823443-3.00004-1

Upadhyay, N., Vishwakarma, K., Singh, J., Verma, R., Prakash, V., Jain, S., Kumar, V., Rani, R., Tripathi, D. K., & Sharma, S. (2019).*Plant-Microbe-Soil Interactions for Reclamation of Degraded Soils: Potential and Challenges*. https://doi.org/10.1007/978-981-32-9664-0_6

Montreemuk, J., Stewart, T. N., & Prapagdee, B. (2023).*Bacterial-assisted phytoremediation of heavy metals: Concepts, current knowledge, and future directions*. https://doi.org/10.1016/j.eti.2023.103488

Gul, I., Iqrar, I., Manzoor, M., Ali, M. A., Arshad, M., Ahmad, S., Hussain, S., Ahmad, N., & Ilyas, F. (2021).*Molecular Basis of Plant–Microbes Interaction in Remediating Metals and Inorganic Pollutants*. https://doi.org/10.1007/978-981-15-6221-1_19

Carper, D. L., Appidi, M. R., Mudbhari, S., Shrestha, H. K., Hettich, R. L., & Abraham, P. E. (2022). The Promises, Challenges, and Opportunities of Omics for Studying the Plant Holobiont.*Microorganisms*. https://doi.org/10.3390/microorganisms10102013

Tarazona, S., Arzalluz-Luque, Á., Conesa, A., & Conesa, A. (2021).*Undisclosed, unmet and neglected challenges in multi-omics studies*. https://doi.org/10.1038/S43588-021-00086-Z

Jiang, D., Armour, C. R., Hu, C., Mei, M., Tian, C., Sharpton, T. J., & Jiang, Y. (2019). Microbiome Multi-Omics Network Analysis: Statistical Considerations, Limitations, and Opportunities.*Frontiers in Genetics*. https://doi.org/10.3389/FGENE.2019.00995

Mock, T., Daines, S. J., Geider, R. J., Collins, S., Metodiev, M. V., Millar, A. J., Moulton, V., & Lenton, T. M. (2016). Bridging the gap between omics and earth system science to better understand how environmental change impacts marine microbes.*Global Change Biology*. https://doi.org/10.1111/GCB.12983

Rangwala, I., Moss, W., Wolken, J., Rondeau, R., Newlon, K., Guinotte, J., & Travis, W. R. (n.d.).*Uncertainty, Complexity and Constraints: How Do We Robustly Assess Biological Responses under a Rapidly Changing Climate?*https://doi.org/10.3390/cli9120177

Sood, U., Pandey, J., Patel, S. K. S., & Verma, H. (2023). Editorial: Omics techniques in deciphering environmental, industrial and therapeutic applications of microbes.*Frontiers in Microbiology*. https://doi.org/10.3389/fmicb.2023.1327368

Widder, S., Allen, R. J., Pfeiffer, T., Curtis, T. P., Wiuf, C., Sloan, W. T., Cordero, O. X., Brown, S. P., Momeni, B., Shou, W., Kettle, H., Flint, H. J., Haas, A. F., Laroche, B. atrice, Kreft, J.-U., Rainey, P. B., Freilich, S., Schuster, S., Milferstedt, K., … Sanchez, O. X. C. (2016). Challenges in microbial ecology: building predictive understanding of community function and dynamics.*Nature*.

Iram, A., Dong, Y., & Ignea, C. (2024). Synthetic biology advances towards a bio-based society in the era of artificial intelligence.*Current Opinion in Biotechnology*. https://doi.org/10.1016/j.copbio.2024.103143

Singla, P. (2020).*Plant Synthetic Biology: A Paradigm Shift Targeting Stress Mitigation, Reduction of Ecological Footprints and Sustainable Transformation in Agriculture*. https://doi.org/10.1007/978-981-15-9380-2_15

Tan, C., Kalhoro, M. T., Faqir, Y., Ma, J., Osei, M. D., & Khaliq, G. (2022). Climate-Resilient Microbial Biotechnology: A Perspective on Sustainable Agriculture.*Sustainability*. https://doi.org/10.3390/su14095574

Kaul, S., Choudhary, M., Gupta, S. K., & Dhar, M. K. (2021). Engineering Host Microbiome for Crop Improvement and Sustainable Agriculture.*Frontiers in Microbiology*. https://doi.org/10.3389/FMICB.2021.635917

Orukotan, K. E., Elughi, G. N., Abimbola, B. S., Akinyosoye, A. D., Ahuekwe, E. F., & Oziegbe, O. (2023).*Plant Microbiome Engineering: Principles, Methods, and Current Trends*. https://doi.org/10.1007/978-3-031-33370-5_17

Trivedi, P., Mattupalli, C., Eversole, K., & Leach, J. E. (2021). Enabling sustainable agriculture through understanding and enhancement of microbiomes.*New Phytologist*. https://doi.org/10.1111/NPH.17319

Zhang, D., Xu, F., Wang, F., Le, L., & Pu, L. (2024). Synthetic biology and artificial intelligence in crop improvement.*Plant Communications*. https://doi.org/10.1016/j.xplc.2024.101220

Lawson, C. E. (2021).*Retooling Microbiome Engineering for a Sustainable Future*. https://doi.org/10.1128/MSYSTEMS.00925-21

Kozaeva, E., Eida, A. A., Gunady, E. F., Dangl, J. L., Conway, J. M., & Brophy, J. A. N. (2024). Roots of synthetic ecology: microbes that foster plant resilience in the changing climate.*Current Opinion in Biotechnology*. https://doi.org/10.1016/j.copbio.2024.103172