



Plant–microbe interactions for climate-resilient agriculture: Mechanisms, stress signaling and microbiome engineering

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Abstract

Plant–microbe interactions play a fundamental role in regulating plant growth, nutrient acquisition, stress adaptation, and overall ecosystem stability, making them increasingly important in the development of climate-resilient agricultural systems. Beneficial microorganisms, including plant growth-promoting rhizobacteria (PGPR), arbuscular mycorrhizal fungi (AMF), endophytes, and other rhizospheric microbes, enhance plant productivity through diverse mechanisms such as biological nitrogen fixation, phosphate solubilization, phytohormone production, and pathogen suppression. This review provides a comprehensive overview of the ecological, physiological, and molecular foundations of plant–microbe interactions, emphasizing their role in improving plant tolerance against major abiotic stresses such as drought, salinity, temperature extremes, oxidative stress, heavy metal toxicity, and nutrient deficiency, as well as resistance against biotic stresses. Particular attention is given to stress signaling pathways involving reactive oxygen species, calcium signaling, phytohormonal crosstalk, pattern-triggered immunity, and effector-triggered immunity that mediate adaptive plant responses. The review further examines recent advances in microbiomebased technologies, including multi-omics approaches, systems biology, artificial intelligence, synthetic biology, and phytomicrobiome engineering, which are transforming plant–microbe research from descriptive to predictive and engineering-driven frameworks. Although microbial interventions offer promising alternatives to chemical-intensive agriculture, challenges related to field-level consistency, microbial establishment, biosafety, and largescale adoption remain significant. Integrating mechanistic insights with advanced computational and bio-digital technologies offers substantial potential for designing nextgeneration microbial solutions that enhance crop resilience, improve resource-use efficiency, and support sustainable agriculture under changing climatic conditions.

Keywords: Plant–microbe interactions, climate resilience, rhizosphere microbiome, plant growth-promoting microorganisms (PGPM), stress signalling, microbiome engineering, sustainable agriculture

Introduction

Agriculture today faces major challenges from climate change, soil degradation, biodiversity loss and the excessive use of chemical fertilizers and pesticides, all of which threaten longterm crop productivity and global food security (Vishwakarma *et al.*, 2020; Muhammad *et al.*, 2024) ^[30, 46]. These growing concerns have increased interest in sustainable approaches that can improve crop performance while minimizing environmental damage. Among such approaches, plant–microbe interactions have gained considerable attention because of their important roles in improving plant growth, maintaining soil health and enhancing plant resilience under stressful environmental conditions.

The rhizosphere, defined as the narrow zone of soil directly influenced by plant roots, represents a critical interface where intense interactions occur between plants and soil microorganisms. This region harbors a highly diverse and dynamic microbial community, collectively known as the rhizosphere microbiota, comprising bacteria, fungi, archaea, protozoa, oomycetes, viruses and other microorganisms. These microbial communities play essential roles in regulating plant growth, health and overall ecosystem functioning through a wide range of biological processes.

Rhizosphere microorganisms contribute significantly to plant productivity by enhancing nutrient acquisition, improving soil fertility, suppressing soil-borne pathogens and increasing plant tolerance to both biotic and abiotic stresses. Many beneficial microorganisms facilitate nutrient cycling and mineral solubilization, thereby improving the availability of essential nutrients to plants. In addition, they synthesize plant growth-promoting substances such as auxins, gibberellins and cytokinins, which regulate root development and overall plant growth. These microorganisms also produce extracellular enzymes including cellulases, chitinases, phosphatases and lignin-degrading enzymes that decompose complex organic matter into simpler compounds, making nutrients more accessible for plant uptake (Tharanath *et al.*, 2024) ^[44].

Plants and their associated microbial communities are increasingly recognized as integrated biological units known as holobionts, in which the host plant and its microbiome collectively influence growth, development, adaptation and survival. The rhizosphere typically contains microbial populations five to ten times higher than those found in bulk soil due to the continuous release of root exudates that serve as both nutrient sources and signaling molecules for microbial growth and colonization (Korenblum *et al.*, 2022)

[25]. This dynamic exchange of metabolites creates a highly interconnected system in which plants and microorganisms continuously influence each other's physiology and metabolic activities, contributing to nutrient cycling, plant health and ecosystem stability. Plant–microbe interactions encompass a broad spectrum of ecological relationships, including mutualism, commensalism, competition, amensalism and parasitism. Mutualistic interactions, such as those involving nitrogen-fixing bacteria and mycorrhizal fungi, provide reciprocal benefits to both partners, whereas pathogenic microorganisms negatively affect plant health and productivity. The balance among these interactions is strongly influenced by environmental conditions, host genotype and microbial community composition. Understanding the complexity of these relationships is essential for elucidating the mechanisms that govern plant growth, nutrient acquisition, stress resilience and ecosystem sustainability (Yang *et al.*, 2024) [47].

Recent advances in microbiome research, multi-omics technologies and systems biology have significantly expanded our understanding of plant-associated microbial communities and their functional roles in nutrient cycling, disease suppression and adaptation to environmental stresses. These developments have opened new opportunities for microbiome-based agricultural interventions, including microbial inoculants, synthetic microbial communities and precision microbiome engineering, aimed at reducing dependence on chemical inputs while improving agricultural sustainability. Although substantial progress has been made in understanding plant–microbe interactions, existing reviews often focus on specific aspects such as rhizosphere ecology, plant growth-promoting microorganisms, or stress physiology in isolation. A comprehensive synthesis integrating ecological interactions, molecular signaling mechanisms, stress adaptation and emerging microbiome engineering technologies remains limited. Therefore, this review aims to provide an integrated overview of plant–microbe interactions, highlighting their ecological significance, mechanistic basis, roles in stress resilience and future applications in sustainable agriculture. This review is

organized into sections covering ecological interactions, molecular signaling pathways, plant growth-promoting microorganisms, stress adaptation mechanisms, emerging technologies and future perspectives in microbiome-assisted agriculture.

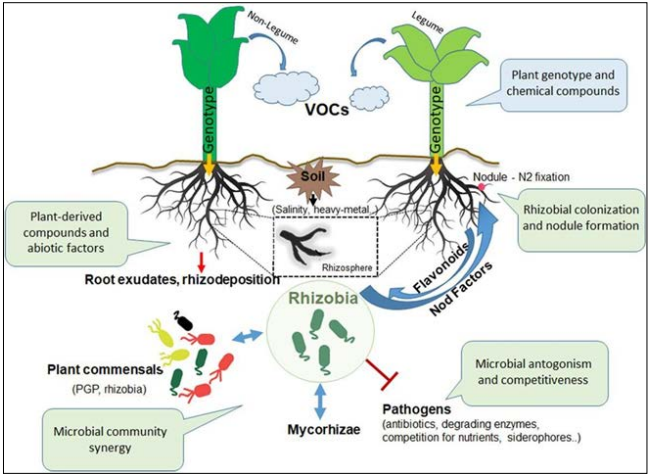


Fig 1: Integrated overview of plant–microbe interactions in the rhizosphere showing beneficial and detrimental microbial associations, signaling through root exudates, and their collective effects on plant growth, nutrient acquisition, stress tolerance, and disease resistance.

Ecological Framework of Plant–Microbe Interactions

Plant–microbe interactions can be broadly classified as positive (beneficial), neutral, or negative (harmful) based on their effects on plant growth, fitness and survival. These interactions are commonly represented as positive–positive (+/+), positive–neutral (+/0), negative–neutral (–/0), positive–negative (+/–), or negative–negative (–/–) ecological relationships. However, these categories are not strictly fixed and instead exist along a dynamic continuum shaped by environmental conditions, host genotype, nutrient availability and microbial community structure. Together, these interactions influence plant health, productivity and ecosystem stability.

Table 1: Major Types of Plant–Microbe Interactions and Their Ecological Significance

Interaction Type	Ecological Effect	Description	Example
Mutualism	+/+	Both partners benefit	Rhizobium–legume symbiosis
Protocooperation	+/+	Mutual benefit, non-obligatory	PGPR–root association
Commensalism	+/0	One benefits, other unaffected	Root colonization
Facilitation	+/+ or +/0	Indirect environmental modification	Microbial nutrient mobilization
Competition	–/–	Competition for limited resources	Iron competition
Amensalism	–/0	One inhibited, other unaffected	Antibiotic secretion
Parasitism	+/–	One benefits at host expense	Fusarium infection

Positive Plant–Microbe Interactions

Positive interactions include mutualism, protocooperation, facilitation and commensalism, where one or both partners benefit without causing significant harm to the host. These beneficial associations play central roles in nutrient acquisition, stress adaptation and plant health.

Mutualism

Mutualism represents one of the most extensively studied and ecologically significant plant–microbe interactions, in which both plant and microorganism derive benefits.

Classical examples include symbiosis between legumes and nitrogen-fixing bacteria such as *Rhizobium* and associations between plants and arbuscular mycorrhizal fungi (AMF). In these systems, microorganisms enhance plant nutrient acquisition, particularly nitrogen and phosphorus, while receiving photosynthetically derived carbon and a protected ecological niche from the host. These associations are regulated through highly specific chemical signaling pathways. For instance, legume roots secrete flavonoids that induce bacterial production of Nod factors, which initiate

nodule formation. Similarly, plant-derived strigolactones stimulate AMF spore germination and hyphal branching, whereas fungal signaling molecules activate conserved symbiotic pathways in plants. Such coordinated signaling enables successful colonization, nutrient exchange and improved tolerance to abiotic stress (Dolatabadian, 2021).

Protocooperation

Protocooperation is a non-obligatory beneficial interaction in which both partners benefit but can survive independently. Many plant growth-promoting rhizobacteria (PGPR) exhibit protocooperative relationships with plants by enhancing nutrient availability, producing phytohormones, or suppressing pathogens without forming highly specialized symbiotic structures. These associations are often flexible and strongly influenced by environmental conditions.

Commensalism

Commensalism is a (+/0) interaction in which microorganisms benefit from plant-derived resources without significantly affecting plant fitness. Commensals utilize root exudates, plant metabolites and ecological niches such as the rhizosphere, phyllosphere and endosphere. Although traditionally regarded as neutral, commensal interactions are increasingly recognized as context-dependent and capable of shifting toward mutualism or antagonism under changes in nutrient availability, abiotic stress, or microbial competition. These interactions contribute to microbial diversity, community stability and functional redundancy within the plant microbiome (Mathis and Bronstein, 2020) [27].

Facilitation

Facilitation refers to indirect positive interactions in which one organism enhances the growth or survival of another by modifying the surrounding environment rather than through direct resource exchange. In the rhizosphere, plants release root exudates such as sugars, amino acids, flavonoids and organic acids that recruit beneficial microorganisms and stimulate nutrient cycling. Microorganisms, in turn, improve nutrient availability, produce phytohormones and enhance tolerance to biotic and abiotic stress. Facilitative interactions are especially important in intercropping systems and complex microbial communities, where synergistic relationships improve nutrient-use efficiency and ecosystem productivity (Stachowicz, 2001) [41].

Syntrophy is an obligate mutualistic metabolic interaction in which two or more microbial partners depend on one another to carry out essential biochemical reactions. Such tightly coupled interactions commonly occur in nutrient-limited or anaerobic environments, where individual microorganisms combine complementary metabolic capabilities to degrade substrates that neither could efficiently utilize alone. This cooperative metabolism enables energetically unfavorable reactions to proceed because one partner continuously consumes inhibitory metabolic by-products, such as hydrogen or formate, thereby maintaining favorable thermodynamic conditions. Through this metabolic interdependence, syntrophic microbial communities enhance nutrient cycling, organic matter decomposition, and ecosystem stability, ultimately contributing to soil fertility and sustainable agricultural productivity (Morris *et al.*, 2013) [29].

Negative Plant–Microbe Interactions

Negative interactions include competition, amensalism, parasitism and antagonism, all of which can reduce plant growth, health, or productivity.

Competition

Competition occurs when microorganisms compete for limited resources such as nutrients, iron, ecological niches and root colonization sites. Microbes employ various competitive strategies including rapid nutrient uptake, antimicrobial metabolite production, secretion of volatile organic compounds (VOCs) and contact-dependent inhibition systems. For example, *Pseudomonas* species produce siderophores that sequester iron, restricting pathogen growth and contributing to disease suppression. Such interactions are central to disease-suppressive soils, where beneficial microbes limit pathogen establishment through resource competition and antagonism (Hassani *et al.*, 2018) [16].

Amensalism

Amensalism is a (−/0) interaction in which one organism is inhibited while the other remains unaffected. In plant-associated ecosystems, this often occurs through the release of allelochemicals, phenolic compounds, antibiotics and other secondary metabolites into the rhizosphere. These compounds suppress competing or harmful microorganisms and influence microbial community composition, niche exclusion and disease suppression (Lin *et al.*, 2022) [25].

Parasitism and Pathogenesis

Parasitic interactions involve one organism benefiting at the expense of the host. Phytopathogens such as *Fusarium*, *Phytophthora*, *Pseudomonas syringae* and *Xanthomonas* cause major agricultural losses by infecting plant tissues and disrupting physiological functions. Plants recognize pathogens through pathogen-associated molecular patterns (PAMPs) detected by pattern recognition receptors (PRRs), triggering PAMP-triggered immunity (PTI). To overcome this defense, pathogens secrete effector molecules that suppress host immunity. Plants may subsequently activate effector-triggered immunity (ETI) through resistance proteins, generating a stronger and more specific defense response (Dolatabadian, 2021) [7].

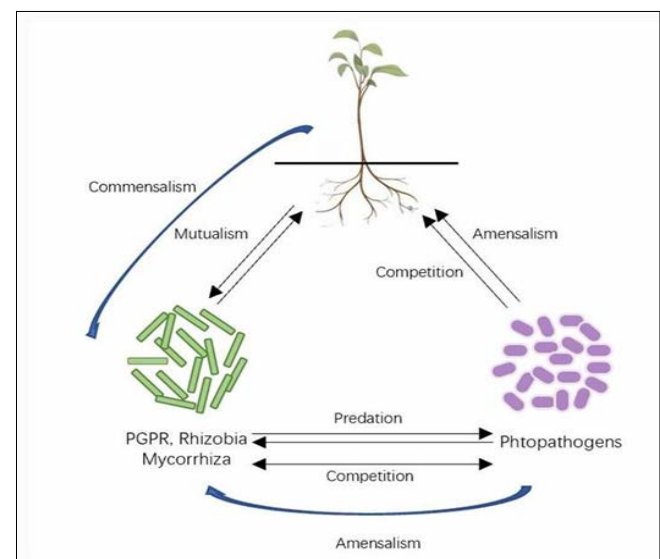


Fig 2: Types of Plant–Microbe Interactions

Ecological Perspective

Plant–microbe interactions should not be viewed as isolated categories but as components of a dynamic ecological network. Mutualistic, neutral and antagonistic interactions frequently coexist and may shift depending on environmental conditions, host physiology and microbial community structure. This interaction network forms the basis of the plant holobiont, where microbial assemblages collectively regulate plant health, stress resilience and productivity. Understanding these ecological relationships is essential for developing sustainable agricultural strategies, including enhanced biological nitrogen fixation, microbiome-based disease suppression and reduced dependence on chemical fertilizers. Emerging approaches such as genome-wide association studies (GWAS), synthetic microbial communities and CRISPR-based microbiome engineering are further expanding opportunities to design stable and beneficial plant–microbe partnerships for future agricultural systems (Goyal *et al.*, 2021) ^[15].

Despite the usefulness of classifying plant–microbe interactions into discrete ecological categories, such classifications often oversimplify the highly dynamic nature of these relationships. In natural ecosystems, interactions are rarely fixed and the same microorganism may shift from beneficial to neutral or even pathogenic depending on host genotype, developmental stage, nutrient availability, environmental stress and interactions with other microbes. For example, certain strains of *Pseudomonas* can function as plant growth-promoting rhizobacteria under favorable conditions, while others behave as opportunistic pathogens. Similarly, some *Fusarium* species are well-known pathogens, whereas non-pathogenic endophytic strains may enhance plant growth and stress tolerance. These observations highlight that plant–microbe relationships exist along a fluid ecological continuum rather than as rigid categories. A major challenge in plant microbiome research therefore lies in predicting how environmental perturbations and microbial community dynamics influence interaction outcomes under field conditions.

Plant Growth-Promoting Microorganisms (PGPM)

Plant growth-promoting microorganisms (PGPM) represent a major group of beneficial microbes involved in plant–microbe interactions that enhance plant growth, nutrient acquisition and overall crop productivity. These microorganisms inhabit the rhizosphere, phyllosphere, or internal plant tissues and include bacteria, fungi, actinomycetes, cyanobacteria and arbuscular mycorrhizal fungi (AMF). Among them, plant growth-promoting rhizobacteria (PGPR) are among the most extensively studied, with important genera including *Pseudomonas*, *Bacillus*, *Azospirillum*, *Azotobacter*, *Klebsiella*, *Burkholderia* and *Enterobacter*. PGPM contribute significantly to sustainable agriculture by improving soil fertility, enhancing nutrient-use efficiency and reducing dependence on synthetic fertilizers and pesticides (Jha & Saraf, 2015; Goswami *et al.*, 2016; Basu *et al.*, 2021) ^[5, 14, 19].

The beneficial effects of PGPM are mediated through both direct and indirect mechanisms. Direct mechanisms include biological nitrogen fixation, phosphate solubilization, mobilization of potassium and micronutrients such as zinc and silicon and production of phytohormones including auxins, cytokinins and gibberellins. These activities improve

nutrient availability, stimulate root growth and enhance plant biomass accumulation. Certain PGPM also produce 1-aminocyclopropane-1-carboxylate (ACC) deaminase, an enzyme that reduces stress-induced ethylene accumulation and supports root elongation under adverse environmental conditions (Bharti & Barnawal, 2019; Timofeeva *et al.*, 2023) ^[6, 45].

Indirectly, PGPM protect plants by suppressing phytopathogens and stimulating host defense responses. They produce siderophores, antibiotics, hydrogen cyanide, lytic enzymes and other antimicrobial metabolites that inhibit pathogen proliferation through nutrient competition and antagonism. Additionally, many PGPM trigger induced systemic resistance (ISR), priming plant defense pathways for faster and stronger responses against pathogen invasion (Pieterse *et al.*, 2014; Singh *et al.*, 2022; Mehmood *et al.*, 2023) ^[20, 33, 40].

Important PGPM include diazotrophic bacteria such as *Azospirillum*, *Azotobacter* and *Rhizobium*, which improve nitrogen availability through biological nitrogen fixation. Species such as *Azospirillum brasilense* and *Azospirillum lipoferum* are particularly recognized for enhancing root architecture, nutrient absorption and crop productivity in cereals and grasses (Cassán & Diaz-Zorita, 2016; Cassán *et al.*, 2020; Pedraza *et al.*, 2020). *Azotobacter* species improve soil fertility not only through nitrogen fixation but also via synthesis of phytohormones, vitamins and exopolysaccharides that improve soil aggregation and water retention (Jnawali *et al.*, 2015; Hindersah *et al.*, 2020; Aasfar *et al.*, 2021) ^[49]. In leguminous crops, *Rhizobium* establishes one of the most specialized mutualistic plant–microbe interactions, inducing root nodule formation where symbiotic nitrogen fixation occurs through highly coordinated molecular signaling between plant flavonoids and bacterial Nod factors (Shamseldin *et al.*, 2017; Mathesius *et al.*, 2021; Singh & Verma, 2023) ^[26, 38, 39].

Endophytic diazotrophs such as *Gluconacetobacter diazotrophicus* further enhance nutrient acquisition and plant vigor through internal colonization of plant tissues. These microorganisms contribute to nitrogen fixation, phytohormone production and nutrient solubilization while improving stress resilience (Chawla *et al.*, 2014; Reis & Teixeira, 2015^[19]; Silva *et al.*, 2020). Non-diazotrophic PGPR such as *Pseudomonas fluorescens* and *Pseudomonas putida* are widely recognized for strong rhizosphere colonization, phosphate solubilization, siderophore secretion and biocontrol activity against soil-borne pathogens (Singh *et al.*, 2022; Mehmood *et al.*, 2023) ^[20, 40].

Arbuscular mycorrhizal fungi (AMF) constitute another important group of PGPM, forming mutualistic associations with plant roots. Through extensive extraradical hyphal networks, AMF significantly increase nutrient and water uptake, particularly phosphorus acquisition, while improving soil structure and root development. AMF frequently act synergistically with beneficial microorganisms such as *Trichoderma* and *Bacillus subtilis*, forming microbial consortia that enhance nutrient cycling, microbial activity and plant performance under diverse agroecosystems (Yang *et al.*, 2022; Gebreslassie *et al.*, 2024; Rotoni *et al.*, 2025) ^[3, 13, 36].

Beyond growth promotion and nutrient mobilization, PGPM also play crucial roles in plant stress adaptation by modulating osmotic balance, antioxidant defense systems, hormonal signaling and induced resistance. Their

contribution to abiotic and biotic stress tolerance highlights their importance as central components of sustainable and climate-resilient agricultural systems. The specific mechanisms through which plant–microbe interactions confer stress tolerance are discussed in the following subsection (Basu *et al.*, 2021; Timofeeva *et al.*, 2023) ^[5, 45]. Despite substantial evidence supporting the beneficial effects of plant growth-promoting microorganisms, their field-level performance often remains inconsistent. Many PGPM strains demonstrate promising results under controlled

Laboratory or greenhouse conditions but fail to maintain similar efficacy under diverse field environments due to variations in soil physicochemical properties, climatic conditions, indigenous microbial competition, and host specificity. Poor survival, limited rhizosphere colonization, and reduced shelf stability of microbial formulations further constrain commercial adoption. These limitations highlight the need for crop-specific strain selection, improved bioformulation technologies, and long-term field validation before large-scale agricultural implementation.

Table 2: Major plant growth-promoting microorganisms (PGPM), their mechanisms and agricultural benefits in sustainable crop production.

Microorganism	Group	Major Mechanisms	Agricultural Benefits
<i>Rhizobium</i>	Symbiotic diazotrophic bacteria	Biological nitrogen fixation, root nodulation	Improved nitrogen availability in legumes
<i>Azospirillum</i>	Associative diazotrophic bacteria	Nitrogen fixation, IAA production, root stimulation	Enhanced root growth and nutrient uptake
<i>Azotobacter</i>	Free-living diazotrophic bacteria	Nitrogen fixation, phytohormone production, EPS secretion	Improved soil fertility and water retention
<i>Gluconacetobacter diazotrophicus</i>	Endophytic diazotroph	Nitrogen fixation, IAA production, nutrient solubilization	Increased nutrient use efficiency
<i>Pseudomonas fluorescens</i>	PGPR	Phosphate solubilization, siderophore production, ISR	Disease suppression and growth promotion
<i>Bacillus subtilis</i>	PGPR Biocontrol bacteria	Antibiotic production, ISR, nutrient mobilization	Improved disease resistance
AMF	Fungal symbionts	Phosphorus uptake, water absorption, hyphal extension	Improved drought tolerance and nutrient uptake
<i>Trichoderma</i> spp.	Root stimulation, antagonism, ISR	Enhanced stress tolerance and pathogen suppression	

Molecular Basis of Plant–Microbe Interactions

At the molecular level, plant–microbe interactions involve highly coordinated signaling networks that enable plants to recognize, communicate with and respond to diverse microorganisms present in their environment. Plants possess specialized pattern recognition receptors (PRRs), primarily receptor-like kinases and receptor-like proteins located on the plasma membrane, which detect conserved microbial-associated molecular patterns (MAMPs) or pathogen-associated molecular patterns (PAMPs). Recognition of these molecular signatures initiates complex signaling cascades that determine whether the interaction leads to defense activation or symbiotic association. Key molecular components involved in these interactions include receptor kinases, Nod and Myc factors, nitrogen fixation (*nif*) genes, resistance (R) genes, transcription factors and quorum sensing molecules. These signaling networks regulate extensive transcriptional reprogramming and downstream physiological responses, enabling plants to distinguish beneficial microbes from pathogenic organisms and establish appropriate outcomes (Chiquito-Contreras *et al.*, 2024) ^[9].

In beneficial plant–microbe associations such as rhizobial symbiosis and arbuscular mycorrhizal interactions, specific microbial signaling molecules play a central role in symbiotic establishment. Rhizobia produce lipochitooligosaccharides known as Nod factors, while mycorrhizal fungi release Myc factors, which are recognized by LysM receptor-like kinases on root cells. This recognition activates the common symbiosis signaling pathway (CSSP), involving SYMRK, nuclear calcium oscillations, calcium/calmodulin-dependent protein kinase (CCaMK) and downstream transcriptional regulators such as CYCLOPS. Activation of this pathway induces

symbiosis-related gene expression, promotes nodule organogenesis, facilitates root colonization and enhances nutrient exchange, particularly nitrogen and phosphorus acquisition, thereby improving plant productivity under low-input agricultural systems.

Plants employ a multilayered immune system composed primarily of pattern-triggered immunity (PTI) and effector-triggered immunity (ETI). PTI constitutes the first layer of defense through PRR-mediated recognition of conserved microbial molecules, leading to calcium influx, mitogen-activated protein kinase (MAPK) activation, callose deposition and defense gene expression. However, many pathogenic bacteria and fungi deploy effector proteins to suppress PTI and manipulate host cellular processes. In bacterial pathogens, these effectors are commonly delivered through the type III secretion system (T3SS). Intracellular resistance proteins, particularly nucleotide-binding leucine-rich repeat (NLR) proteins, detect these pathogen-derived effectors and activate ETI, resulting in stronger and faster defense responses, including hypersensitive response and systemic acquired resistance (SAR) (Saijo *et al.* 2018) ^[37].

Reactive oxygen species (ROS) play central roles in plant–microbe interactions as both signaling molecules and defense mediators. Although historically considered harmful byproducts of aerobic metabolism, ROS are now recognized as crucial secondary messengers involved in plant immunity, stress signaling, programmed cell death and stomatal regulation. During microbial recognition, rapid oxidative bursts are primarily mediated by respiratory burst oxidase homologs (RBOHs), generating superoxide and hydrogen peroxide at infection sites. Controlled ROS accumulation contributes to pathogen restriction and signal amplification, while antioxidant enzymes such as superoxide dismutase, catalase and peroxidases maintain

redox homeostasis to prevent excessive cellular damage. Thus, the balance between ROS production and scavenging determines the intensity and duration of ROS-mediated responses during plant–microbe interactions (Khan *et al.*, 2023) ^[22].

Intracellular calcium signaling serves as another important secondary messenger system during both defense and symbiotic interactions. Recognition of microbial signals induces characteristic transient calcium signatures in plant cells, which are decoded by calcium-binding proteins including calmodulins, calcineurin B-like proteins and calcium-dependent protein kinases (CDPKs). These calcium signatures regulate downstream pathways associated with ROS production, defense gene activation, hormone signaling and immune modulation. In beneficial interactions such as rhizobial and mycorrhizal symbioses, distinct calcium spiking patterns function as molecular signatures that activate symbiotic signaling and facilitate microbial colonization (Negi *et al.*, 2023) ^[43].

Phytohormones such as salicylic acid, jasmonic acid, ethylene, auxins, abscisic acid and gibberellins also play essential roles in regulating plant responses to microorganisms. These hormones operate through interconnected signaling networks that coordinate immune activation, stress adaptation, growth regulation and symbiotic establishment. Hormonal crosstalk enables plants to fine-tune defense responses according to microbial lifestyle and environmental conditions, thereby balancing resource allocation between growth and immunity. For instance, the transcription factor WRKY30 enhances jasmonic acid-mediated defense signaling during fungal infection, illustrating the close integration between hormone signaling and transcriptional regulation in plant immunity (Zhao and Li, 2021) ^[51].

Transcription factors and small non-coding RNAs provide additional regulatory layers controlling gene expression during plant–microbe interactions. Major transcription factor families such as WRKY, MYB, NAC and bZIP regulate defense-related genes, secondary metabolite biosynthesis and stress-responsive pathways. Meanwhile, microRNAs (miRNAs) and small interfering RNAs (siRNAs) contribute to post-transcriptional regulation by modulating genes associated with resistance signaling, hormone pathways and immune responses. Differential expression of miRNAs, including miR482 and related families, has been associated with enhanced resistance against microbial pathogens, highlighting the importance of RNA-mediated regulatory networks in plant defense (Kajla *et al.*, 2023) ^[20].

Epigenetic regulation has emerged as an additional layer of molecular control in plant–microbe interactions, particularly under recurring stress conditions. DNA methylation, histone modifications and chromatin remodeling influence gene accessibility and transcriptional responsiveness during microbial challenge. Such epigenetic modifications can establish stress memory, enabling plants to mount faster and stronger responses upon subsequent pathogen exposure. This molecular memory contributes significantly to long-term stress adaptation and resilience in sustainable agricultural systems.

Microbial signaling and bidirectional chemical communication further shape plant responses within the rhizosphere. Root exudates released by plants function as chemical cues that attract beneficial microorganisms and influence microbial community assembly. In response, microbes produce signaling compounds such as auxins, cytokinins, siderophores, volatile organic compounds and quorum sensing molecules that modulate plant growth, nutrient acquisition and defense responses. These reciprocal signaling mechanisms establish dynamic communication networks that regulate colonization, symbiosis and plant immunity (ChiquitoContreras *et al.*, 2024) ^[1].

Specialized secondary metabolites secreted through root exudates act as selective chemical filters that recruit beneficial microbes or suppress harmful organisms. Recent studies demonstrate that maize (*Zea mays* L.) utilizes benzoxazinoids to influence microbial recruitment, while tomato (*Solanum lycopersicum*) secretes α -tomatine to enrich beneficial microbial taxa. Under nutrient stress, maize roots additionally exude flavones such as apigenin and luteolin, which attract beneficial bacteria that improve nutrient acquisition and stimulate root development. These findings illustrate the dynamic feedback between plant metabolism and rhizosphere microbial community assembly (Cadot *et al.*, 2021; Nakayasu *et al.*, 2021; Yu *et al.*, 2021) ^[7, 31].

Recent advances in multi-omics technologies have greatly expanded understanding of plant–microbe interactions by revealing complex regulatory networks involving genomics, metagenomics, transcriptomics, proteomics, metabolomics and epigenomics. These approaches provide systems-level insights into how plants integrate microbial signals with environmental cues to coordinate adaptive responses. Emerging technologies such as synthetic microbial consortia, microbiome engineering, CRISPR-based genome editing and artificial intelligence-assisted microbial screening are now enabling targeted manipulation of plant-associated microbial communities to improve crop productivity, nutrient use efficiency, stress tolerance and agricultural sustainability. These advances offer promising opportunities for the development of next-generation microbiome-based strategies for climate-resilient agriculture.

Although significant progress has been made in understanding molecular signaling pathways such as pattern-triggered immunity, effector-triggered immunity, calcium signaling, and hormone-mediated communication, many mechanistic details remain unresolved. Most molecular studies are derived from model plant systems such as *Arabidopsis thaliana*, which may not fully represent complex crop-specific interactions in agricultural settings. Furthermore, signaling networks involving phytohormones, reactive oxygen species, and secondary metabolites exhibit extensive crosstalk, making it difficult to establish linear cause–effect relationships. Future studies integrating multi-omics and real-time imaging are essential for unraveling these highly dynamic molecular networks under natural conditions.

Table 3: Key Molecular Components Involved in Plant–Microbe Interactions

Molecular Component	Examples / Key Molecules	Primary Function	Role in Interaction
Pattern Recognition Receptors (PRRs)	FLS2, EFR, CERK1	Recognize MAMPs/PAMPs and initiate signaling	Early microbial recognition
Symbiotic Signal Receptors	LysM-RLKs, NFR1, NFR5	Detect Nod/Myc factors	Establish rhizobial and mycorrhizal symbiosis
Nod / Myc Factors	Lipochitooligosaccharides	Trigger symbiosis signaling	Nodule formation and colonization
Resistance (R) Proteins / NLRs	NLR proteins, R genes	Recognize pathogen effectors	Activate ETI
Pathogen Effectors	Avr proteins, T3SS effectors	Suppress host immunity	Promote infection
MAPK Cascades	MPK3, MPK6	Signal amplification	Defense signaling
Calcium Signaling Components	Ca ²⁺ , CDPKs, Calmodulin, CCaMK	Decode microbial signals	Defense and symbiosis
Reactive Oxygen Species (ROS)	H ₂ O ₂ , O ₂ ⁻ , RBOH	Oxidative burst and signaling	Defense activation
Phytohormones	SA, JA, ET, ABA, Auxin	Coordinate immune and growth responses	Stress adaptation
Transcription Factors	WRKY, MYB, NAC, bZIP	Regulate gene expression	Defense and stress tolerance
Small RNAs	miR482, siRNAs	Post-transcriptional regulation	Fine-tuning immunity
Epigenetic Regulators	DNA methylation, histone modifiers	Stress memory and gene accessibility	Long-term adaptation
Root Exudates	Flavonoids, benzoxazinoids, organic acids	Recruit/select microbes	Rhizosphere shaping
Microbial Signaling Molecules	Quorum sensing molecules, VOCs, siderophores	Microbe-to-plant communication	Growth promotion and defense
Omics / Emerging Tools	Metagenomics, CRISPR, AI	Microbiome engineering	Sustainable agriculture

Plant–Microbe Interactions in Stress Tolerance

Plant–microbe interactions play a central role in enhancing plant resilience under environmental stress conditions and constitute an important adaptive framework for sustainable agriculture. Under adverse environmental conditions, plants activate a specialized signaling strategy often described as the “cry for help” response, in which roots secrete diverse metabolites such as amino acids, organic acids, sugars, flavonoids and phenolic compounds into the rhizosphere. These root-derived signals selectively recruit beneficial microorganisms, including plant growth-promoting bacteria (PGPB) and arbuscular mycorrhizal fungi (AMF), thereby restructuring the surrounding microbial community and establishing a functional plant holobiont that collectively improves plant fitness and stress tolerance (Rodriguez and Durán, 2020) ^[35].

Under abiotic stress conditions such as drought, salinity, temperature extremes and nutrient deficiency, beneficial microorganisms enhance plant survival through multiple physiological and biochemical mechanisms. One important mechanism involves the production of extracellular polymeric substances (EPS), which improve soil aggregation, increase water retention and immobilize toxic ions such as sodium, thereby reducing their bioavailability in the rhizosphere. Beneficial microbes also stimulate the accumulation of compatible osmolytes such as proline, glycine betaine and soluble sugars, which maintain osmotic balance and preserve cellular integrity under dehydration and salinity stress (Acharya *et al.*, 2024; Teiba *et al.*, 2023; Ahmad *et al.*, 2022) ^[1, 3, 43].

A major component of microbial-mediated stress tolerance is the reinforcement of the plant antioxidant defense system. Environmental stress often induces excessive accumulation of reactive oxygen species (ROS), leading to oxidative damage of lipids, proteins and nucleic acids. Plant-

associated microorganisms enhance the activity of ROS-scavenging enzymes such as superoxide dismutase, catalase, ascorbate peroxidase and peroxidases, thereby minimizing oxidative damage and preserving cellular homeostasis (Singh *et al.*, 2022) ^[40].

Hormonal regulation further integrates plant adaptation to stress. Microbially produced auxins improve root branching and root hair development, enhancing water and nutrient uptake. Absciscic acid contributes to stomatal regulation and water conservation during drought, while ACC deaminase-producing microorganisms reduce stress-induced ethylene accumulation by degrading 1-aminocyclopropane-1-carboxylate (ACC), thereby preventing premature senescence and growth inhibition. In addition, AMF extend the functional root system through extraradical hyphal networks and glomalin production, improving water uptake efficiency and nutrient acquisition under water-limited conditions (Bharti & Barnawal, 2019) ^[6].

Plant–microbe interactions also provide strong protection against biotic stress caused by phytopathogens. Beneficial microbes suppress pathogens through competition for nutrients and ecological niches, siderophore-mediated iron sequestration, secretion of antibiotics and volatile organic compounds and production of lytic enzymes such as chitinases, glucanases and proteases. In addition to direct antagonism, microbial elicitors activate induced systemic resistance (ISR), priming plant immune systems through signaling pathways involving calcium flux, mitogen-activated protein kinase (MAPK) cascades, salicylic acid, jasmonates and reactive oxygen species. This priming enables faster and stronger defense responses against future pathogen invasion (Pieterse *et al.*, 2014; Singh *et al.*, 2022; Mehmood *et al.*, 2023) ^[20, 33, 40].

Microbial-mediated stress alleviation also involves several biochemical mechanisms that improve plant resilience under

adverse environmental conditions. Plant growth-promoting microorganisms enhance nutrient availability through phosphorus solubilization and siderophore production, thereby improving iron uptake and reducing nutrient-related stress. Many beneficial microbes also produce ACC deaminase, which lowers plant ethylene levels and mitigates stress-induced growth inhibition. Additionally, microbial inoculation often stimulates antioxidant defense systems, including superoxide dismutase, catalase and peroxidases, thereby reducing reactive oxygen species accumulation and oxidative damage under stress conditions (Tariq and Farhat, 2025) ^[42].

Heavy metal contamination represents a severe abiotic stress that disrupts plant metabolism, nutrient uptake and cellular redox balance. Beneficial microorganisms mitigate heavy metal toxicity through biosorption, biofilm formation, metal precipitation, organic acid-mediated chelation and efflux-based detoxification. Extracellular polymeric substances bind toxic metals through negatively charged functional groups, while phosphate-solubilizing microbes may precipitate metals into insoluble complexes, reducing plant uptake. These microbial processes alleviate oxidative stress and help sustain root growth and nutrient acquisition in

contaminated soils (Muhammad *et al.*, 2025).

Plant responses to abiotic and biotic stresses do not operate independently but form interconnected regulatory networks. Shared signaling molecules such as reactive oxygen species, nitric oxide, calcium ions, salicylic acid and jasmonates act as central hubs linking stress adaptation and immune responses. Through this signaling crosstalk, beneficial microorganisms enhance cross-tolerance, enabling plants to better withstand multiple simultaneous stresses under fluctuating environmental conditions (Bakker *et al.*, 2018) ^[4].

Overall, plant–microbe interactions function as dynamic regulators of plant resilience by integrating nutrient acquisition, hormonal modulation, antioxidant defense, pathogen suppression and soil stabilization. Rather than acting as isolated inoculants, beneficial microorganisms operate as components of a co-evolved plant holobiont capable of sensing environmental changes, restructuring microbial communities and reprogramming host physiology to withstand diverse stresses. These adaptive interactions highlight the importance of microbiome-based strategies in developing climate-resilient and sustainable agricultural systems (Basu *et al.*, 2021; Muhammad *et al.*, 2025) ^[5, 34].

Table 4: Mechanisms of plant–microbe-mediated stress tolerance in sustainable agricultural systems

Stress Type	Representative Microorganisms	Key Problem in Plants	Major Microbial Mechanisms	Physiological Outcome
Drought Stress	<i>Azospirillum</i> , AMF, <i>Bacillus</i>	Loss of turgor, reduced water uptake, stomatal closure	EPS production, AMF hyphal association, osmolyte induction (proline, glycine betaine)	Improved water retention, enhanced drought tolerance, sustained growth
Salinity Stress	<i>Pseudomonas</i> , <i>Bacillus</i> , AMF	Na ⁺ toxicity, ionic imbalance, osmotic stress	EPS-mediated Na ⁺ sequestration, ion homeostasis regulation, ACC deaminase activity	Reduced salt toxicity, improved K ⁺ /Na ⁺ balance, better nutrient uptake
Temperature Stress (Heat/Cold)	<i>Bacillus</i> , <i>Pseudomonas</i> , <i>Trichoderma</i>	Protein denaturation, membrane instability, oxidative stress	Antioxidant activation, heat shock protein regulation, phytohormone modulation	Enhanced thermotolerance and metabolic stability
Oxidative Stress (ROS)	<i>Pseudomonas</i> , <i>Azotobacter</i> , AMF	Lipid peroxidation, protein and DNA damage	Induction of antioxidant enzymes (SOD, CAT, APX, POD)	Reduced oxidative damage and improved cellular protection
Biotic Stress / Pathogen Attack	<i>Trichoderma</i> , <i>Bacillus subtilis</i> , <i>Pseudomonas fluorescens</i>	Infection, tissue damage, reduced yield	Induced systemic resistance (ISR), siderophore production, VOCs, antibiotics, lytic enzymes	Enhanced systemic immunity and pathogen suppression
Heavy Metal Stress	<i>Pseudomonas</i> , <i>Rhizobium</i> , <i>Enterobacter</i>	Metal toxicity, oxidative stress, growth inhibition	EPS biosorption, organic acid chelation, metal precipitation, biofilm formation, efflux pumps	Reduced metal bioavailability, improved detoxification and plant growth
Nutrient Deficiency Stress	<i>Rhizobium</i> , <i>Azotobacter</i> , Phosphatesolubilizing bacteria	Limited N, P, K and micronutrient availability	Nitrogen fixation, phosphate solubilization, potassium mobilization, micronutrient solubilization	Improved nutrient uptake, enhanced growth and productivity
Root Growth Inhibition /	ACC deaminase-producing PGPR	Excess ethylene causing	ACC deaminase-mediated	Enhanced root elongation and
Ethylene Stress	(<i>Pseudomonas</i> , <i>Enterobacter</i>)	inhibited root growth	degradation of ACC into ammonia and acetobutyrate	biomass accumulation
Combined Abiotic + Biotic Stress	Microbial consortia (PGPR+ AMF + <i>Trichoderma</i>)	Multiple simultaneous stress effects	Holobiont regulation, hormonal crosstalk, ROS–MAPK–SA signaling integration	Cross-tolerance, improved resilience and adaptive capacity

Microbial-mediated stress tolerance offers significant promise for improving crop resilience under climate change; however, its practical application faces several limitations.

Plant responses to microbial inoculation under abiotic and biotic stresses are often highly variable and influenced by stress intensity, duration, crop genotype, and environmental

heterogeneity. In many cases, microbial consortia that perform effectively under single-stress laboratory experiments exhibit reduced stability under combined or field-scale stresses. Additionally, the mechanisms underlying stress cross-tolerance remain incompletely understood, particularly under simultaneous abiotic and biotic stress exposure. Addressing these knowledge gaps is essential for developing reliable microbial interventions for climate-resilient agriculture.

Emerging Technologies

Emerging technologies are transforming the study and application of plant–microbe interactions by enabling deeper insights into microbial diversity, molecular communication and functional mechanisms involved in plant growth, stress adaptation and sustainable agriculture. Advanced analytical, computational and digital tools now allow researchers to investigate plant–microbe interactions at multiple biological levels, from genes and proteins to metabolites and ecological networks, thereby accelerating the development of targeted microbiome-based agricultural solutions.

Multi-Omics Approaches

Multi-omics approaches have emerged as powerful tools for deciphering the complexity of plant–microbe interactions at cellular and molecular levels. Individual omics approaches such as metagenomics, transcriptomics, proteomics, metabolomics and epigenomics generate largescale datasets describing microbial diversity, gene expression, protein function, metabolic responses and epigenetic regulation. When integrated, these datasets provide systems-level insights into microbial community structure, functional genes, signaling pathways and stressresponsive networks. These approaches enable the identification of key microbial taxa, stressresponsive biomarkers and host regulatory pathways involved in nutrient acquisition, stress mitigation and disease resistance. Such integrated analyses facilitate precise understanding of rhizosphere dynamics and provide opportunities for developing targeted microbiome-based interventions for sustainable agriculture (Tariq and Farhat, 2025)^[42]. Advanced transcriptomic approaches such as dual RNA sequencing (dual RNA-seq) further enable simultaneous analysis of gene expression in both host plants and associated microbes during interaction, providing detailed insights into bidirectional molecular communication during symbiosis or pathogenesis (Imam *et al.*, 2016)^[18].

Systems Biology and Computational Modeling

Systems biology has emerged as an integrative framework that bridges multi-omics data generation and predictive computational analysis. By combining genomic, transcriptomic, proteomic and metabolomic datasets, systems biology enables the construction of comprehensive interaction networks describing plant–microbe communication. Such integrative analyses help identify regulatory hubs, signaling bottlenecks and emergent biological properties that are difficult to detect using single-omics approaches alone. Computational biology and genome-scale metabolic modeling further strengthen predictive understanding by reconstructing metabolic pathways and simulating nutrient exchange, carbon allocation and stress-responsive metabolic fluxes between

plants and associated microorganisms. Computational tools such as flux balance analysis (FBA) support prediction of microbial behavior under varying environmental conditions and facilitate the design of efficient microbial consortia for agricultural applications (Imam *et al.*, 2016)^[18].

Artificial Intelligence, Machine Learning and Deep Learning

Artificial intelligence (AI), machine learning (ML) and deep learning (DL) are increasingly revolutionizing plant–microbe research by enabling efficient analysis of complex, highdimensional and compositional microbiome datasets. Traditional bioinformatics approaches often struggle to interpret large multi-omics datasets due to their complexity, sparsity and nonlinear relationships. In contrast, AI-based analytical frameworks can identify hidden biological patterns and extract meaningful insights without extensive manual feature engineering, thereby improving understanding of plant-associated microbial communities and their functional roles in sustainable agriculture (Hernández Medina *et al.*, 2022; Zhao *et al.*, 2023)^[17, 52].

Advanced computational methods, including dimensionality reduction and visualization techniques such as Principal Coordinate Analysis (PCoA), t-distributed stochastic neighbor embedding (t-SNE) and Uniform Manifold Approximation and Projection (UMAP), facilitate interpretation of complex microbiome datasets by compressing multi-dimensional data into biologically meaningful representations. Machine learning algorithms such as Random Forests, Support Vector Machines and Artificial Neural Networks have demonstrated significant potential in microbial classification, functional gene annotation and prediction of plant performance under diverse environmental conditions. AI-driven predictive modeling also supports the rational design of synthetic microbial communities (SynComs) and enables realtime monitoring of crop health, disease outbreaks and environmental stress when integrated with remote sensing and imaging technologies.

Synthetic Biology and Phytomicrobiome Engineering

Synthetic biology and phytomicrobiome engineering are increasingly being applied to develop next-generation bioinoculants with enhanced functional traits. Conventional application of beneficial microorganisms often faces limitations such as poor root colonization, limited persistence and competition from native soil microbiota. To overcome these challenges, advanced engineering strategies are being developed to design stable and functionally enhanced microbial communities capable of improving crop productivity under diverse environmental conditions (Foo *et al.*, 2017^[11]; Ke *et al.*, 2021).

Two major strategies are employed in phytomicrobiome engineering: bottom-up and top-down approaches. In bottom-up engineering, beneficial microbial strains are isolated, genetically modified and assembled into synthetic microbial communities with desirable traits such as enhanced nitrogen fixation, phosphate solubilization, phytohormone production, stress tolerance and pathogen suppression. In contrast, top-down approaches focus on direct modification of native rhizosphere microbial communities to enhance beneficial functions while preserving ecosystem complexity. Genome editing tools such as CRISPR-Cas systems and advanced validation

platforms further improve the precision of microbial engineering. However, biosafety measures remain essential for safe field deployment. Overall, phytomicrobiome engineering offers significant potential for improving crop resilience, reducing chemical inputs and supporting sustainable agriculture.

Precision Agriculture and Bio-Digital Integration

Precision agriculture technologies, including biosensors, remote sensing, Internet of Things (IoT)-based monitoring systems and smart delivery platforms, are emerging as valuable tools for real-time assessment of soil health, plant physiological status and rhizosphere activity. These technologies enable site-specific microbial management, optimize bioinoculant application and improve resource-use efficiency under field conditions. Bio-digital integration and proximal sensing further strengthen precision agriculture by enabling continuous monitoring of both physical and biological indicators such as soil moisture, temperature, pH, nutrient availability, microbial respiration and rhizosphere activity. The integration of biological and digital datasets supports closed-loop decision systems in which real-time sensor data optimize the timing, dosage and delivery of plant growth-promoting microorganisms such as arbuscular mycorrhizal fungi and phosphate-solubilizing bacteria. When combined with satellite imaging, machine learning and predictive analytics, these technologies enable proactive management of crop health, disease outbreaks and environmental stress. Despite challenges related to cost, sensor calibration, data interoperability and regulatory constraints, continued advances in digital infrastructure are expected to accelerate adoption of bio-digital systems in sustainable agriculture (Adamchuk *et al.*, 2017; Rezaee Danesh, 2025; Yin *et al.*, 2021) [2, 34, 49].

Although emerging technologies such as multi-omics, artificial intelligence, synthetic biology, and precision agriculture are transforming plant–microbe research, several practical and technical limitations remain. High-throughput omics platforms generate massive datasets that often require complex computational pipelines, advanced infrastructure, and interdisciplinary expertise for meaningful interpretation. AI-based predictive models may also suffer from data bias, limited training datasets, and poor generalizability across agroecosystems. In synthetic biology, biosafety concerns, ecological risks, and regulatory restrictions continue to limit field deployment of engineered microbial systems. Furthermore, the high cost of advanced sensing and digital agriculture technologies may restrict adoption in resource-limited agricultural settings, particularly in developing countries.

Collectively, emerging technologies such as multi-omics, systems biology, artificial intelligence, synthetic biology and precision agriculture are shifting plant–microbe interaction research from descriptive studies toward predictive and engineering-driven approaches. The integration of biological knowledge with computational and digital innovations enables precise manipulation of phytomicrobiomes for improved crop productivity, enhanced stress resilience and reduced dependence on chemical inputs. These technological advances are expected to play a crucial role in developing climate-smart and sustainable agricultural systems.

Future Scopes

Despite significant advances in understanding plant–microbe interactions, several challenges remain in

translating laboratory findings into large-scale agricultural applications. Future research should focus on improving mechanistic understanding of plant–microbiome assembly, microbial colonization dynamics and long-term stability of beneficial microbial communities under diverse agroecological conditions. Since microbial performance often varies across soil types, climatic regions and cropping systems, there is a critical need for field-based validation to ensure consistent efficacy of microbial inoculants.

Emerging omics technologies, systems biology and advanced computational approaches are expected to further revolutionize plant–microbe research. Future studies should emphasize integration of multi-omics datasets with artificial intelligence and machine learning to enable predictive modeling of microbial community behavior, stress responses and plant performance under dynamic environmental conditions. Such integrative frameworks may facilitate identification of key microbial biomarkers and improve precision selection of beneficial microbial consortia for crop-specific applications.

Synthetic biology and microbiome engineering offer promising opportunities for designing next-generation bioinoculants with enhanced functional stability, stress resilience and improved colonization efficiency. Future efforts should focus on developing robust synthetic microbial communities tailored to specific crops and environmental conditions while ensuring biosafety, ecological compatibility and regulatory compliance. Advances in genome editing and engineered signaling pathways may further enable precise manipulation of plant–microbe communication for targeted agricultural benefits.

The integration of bio-digital technologies, including biosensors, remote sensing, Internet of Things (IoT) and precision agriculture platforms, is expected to play a crucial role in real-time monitoring and management of soil–plant–microbe interactions. Future smart farming systems may utilize continuous sensor feedback and predictive analytics to optimize microbial inoculant application, nutrient delivery and stress management, thereby improving resource efficiency and minimizing environmental impact.

In addition to technological advancement, future progress will depend on interdisciplinary collaboration among microbiologists, plant scientists, agronomists, computational biologists, engineers, policymakers and industry stakeholders. Supportive regulatory frameworks, standardized evaluation protocols and farmer-centered extension programs will be essential for accelerating adoption of microbial technologies. Overall, future developments in plant–microbe interaction research are expected to enable climate-resilient, resource-efficient and sustainable agricultural systems capable of meeting global food security demands under changing environmental conditions.

Conclusion

Plant–microbe interactions play a crucial role in plant growth, nutrient acquisition, stress adaptation, and overall ecosystem stability, making them vital for climate-resilient agriculture. Beneficial microorganisms such as plant growth-promoting rhizobacteria, arbuscular mycorrhizal fungi, and endophytes enhance plant productivity through mechanisms including nutrient mobilization, phytohormone regulation, pathogen suppression, and improved stress

tolerance. These beneficial effects are mediated by complex molecular signaling networks involving reactive oxygen species, calcium signaling, phytohormonal crosstalk, and immune responses.

Microbial-assisted stress mitigation has emerged as a promising strategy to enhance crop resilience against major abiotic and biotic stresses such as drought, salinity, temperature extremes, heavy metal toxicity, and pathogen attack. However, despite encouraging laboratory findings, field-level application remains challenged by environmental variability, microbial establishment, and formulation limitations.

Recent advances in multi-omics, artificial intelligence, synthetic biology, and microbiome engineering are shifting plant–microbe research toward predictive and application-driven approaches. Integrating mechanistic understanding with advanced bio-digital technologies offers significant potential for developing targeted microbial solutions for sustainable agriculture. Overall, harnessing plant–microbe interactions will be essential for improving crop productivity, strengthening climate resilience, and ensuring global food security in the face of changing environmental conditions.

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