



PLANT–MICROBE INTERACTIONS FOR SUSTAINABLE AGRICULTURE: MOLECULAR MECHANISMS, STRESS RESILIENCE, DISEASE SUPPRESSION, AND CROP PRODUCTIVITY

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ABSTRACT

Plant–microbe interaction is now expanding to be a key element of sustainable agriculture as they play a vital role in nutrient acquisition, plant growth, stress response, disease defense and productivity of the crop. The recent progress in the assembly, function and agriculture use of plant-associated microbiomes, especially in the rhizosphere, host genotype, developmental stage, root exudates, microbial interactions, and environmental filtering, was summarized. It also explores the molecular and biochemical mechanisms behind the beneficial plant–microbe interactions such as phytohormone modulation, nutrient mobilization, antioxidant regulation, osmotic adjustment, ion homeostasis and induced systemic resistance. Focus is especially placed on plant growth-promoting rhizobacteria, disease-suppressive microorganisms and functionally complementary combination of microorganisms to improve drought, salinity, nutrient stress and pathogen resistance. Emerging translational strategies such as microbiome manipulation, synthetic microbial communities, biofertilizers, bio stimulants and genotype–microbiome optimization are also reviewed. Significant improvements have been achieved in the lab, but inconsistent colonization, persistence and field performance are areas of challenge. Further studies should focus on selecting microorganisms based on function, validating mechanisms, ensuring ecological compatibility, developing formulations and ensuring compatibility with crop breeding and precision management. These strategies could help to harness the plant microbiomes for resilient, resource efficient and environmentally sustainable crop production.

Keyword: Plant microbiome; Sustainable agriculture; Plant growth-promoting rhizobacteria; Stress resilience; Microbiome engineering

1. Introduction

Biological methods are becoming an increasing part of the transition towards sustainable farming and can help ensure the continuity of crop productivity while limiting the use of intensive chemical interventions. While conventional production systems have largely helped in achieving food security, the overreliance on synthetic fertilizers, pesticides, and resource-intensive management practices has led to worries about soil degradation, biodiversity loss, imbalanced usage of nutrients, and environmental pollution. These challenges are exacerbated by climate variability and increasing need for resilient cropping systems. In this context, there is a great interest in plant-associated microorganisms due to their ability to affect nutrient uptake, plant growth, stress response and plant disease resistance. Plants exist in dynamic biological networks with complex microbial communities present in the rhizosphere, rhizoplane, endosphere and aerial tissues, playing a direct role in plant performance and health (Trivedi et al., 2020).

Plants and microbes (bacteria, fungi, archaea) are in constant exchange with each other via exchange of nutrients, perception of signals and production/modification of metabolites within the physiological processes of plants. Under these interactions, the availability of nutrients, the phytohormonal balance, the root architecture and tolerance to environmental stresses can be improved (Gupta et al., 2021). Recent advances have thus moved the study of the plant microbiome from description to identification of functional relationships that affect the growth, health and productivity of plants. This shift has also sparked an interest in using beneficial microbial communities intentionally in the practice of sustainable crop production (Compant et al., 2025).

The rhizosphere is a critical area for these interactions as it is the area where plant roots, soil characteristics, and microbes all meet. Root exudates form chemically distinct microenvironments which can selectively attract, stimulate or suppress certain populations of microbes. Rhizosphere microorganisms in turn impact nutrient cycling, root growth, signal transduction, and plant reactions to environmental factors. The intricate relationship between plants and insects is growing to be a pivotal area of study for the development of biologically-driven solutions in crop improvement (Shi et al., 2024). Therefore, rhizosphere engineering has been proposed as a potential approach to change the microbial community and its activity to improve nutrient-use efficiency, stress tolerance and plant productivity in different agro-ecological settings (Solanki et al., 2024).

However, several interacting factors shape the assembly of the microbiome and microbiome assembly can not be solely explained by environmental or host determinant. Plant identity, evolutionary history and environmental factors have been shown to affect the diversity of the populations of microbes associated with roots when comparing across different angiosperm species (Fitzpatrick et al. 2018). Field-scale studies also suggest that community patterns are present in the microbiome of plants and that both groups of microorganisms and environmental factors are important for shaping these communities (Hamonts et al., 2018). In addition, plant-associated microorganisms have been shown to have unique structural and

functional features in different geographical and environmental conditions, even in the same region (Xu et al., 2018). Similarly, studies in *A. thaliana* have demonstrated that understanding root microbiome structure by looking at integrated and multi-kingdom bacterial and fungal communities is more comprehensive than understanding it on the basis of just one microbial kingdom (Bergelson et al., 2019).

With the advent of high throughput sequencing, metagenomics, transcriptomics, proteomics and metabolomics, the way plant–microbe interactions are understood has also taken a turn for the better. Postgenomic studies have thus uncovered that beneficial interactions rely on rather than just the presence of specific microbial taxa, but rather are mediated by coordinated molecular communication (Agrahari et al., 2020).

Plant associated microorganisms are also gaining importance as a factor of crop resilience. The protective role of beneficial microbes in plant tolerance to drought, salinity, nutrient deficiency, oxidative stress and other environmental stressors can be attributed to their ability to regulate the plant hormone levels, antioxidant activity, osmotic adaptation, nutrient mobilization, and modulation of plant defense responses (Ali et al., 2024). The plant's phytomicrobiome is therefore a crucial interface that enables plants to adapt to environmental changes (Kumar et al., 2023). Microbial communities also have roles in sustainable crop management beyond stress tolerance, including in biomass accumulation, nutrient-use efficiency, disease suppression, and overall plant productivity (Tiwari et al., 2025).

These functions are now being acknowledged by increasing numbers making the crop microbiomes a major research area in sustainable agriculture (Singh et al., 2020). Yet significant barriers to be overcome are the difficulty of separating correlation from causation, finding consistently positive microbial functions, making inoculants more persistent and ensuring consistent results in the field. This review critically summarizes the existing knowledge on plant–microbe interactions with special focus on microbiome assembly, molecular and biochemical communication among microbes and plant, microbial regulation of plant growth, abiotic stress resistance, disease suppression and crop productivity.

2. Architecture and Assembly of the Plant Microbiome

Plant-associated microbiomes are dynamic and highly organized communities, which change in composition from plant compartment to developmental stage, genotype and environmental factors. The *Populus* holobiont has revealed the influence of plant niche and host genotype on microbial community structure: different microbial communities in different compartments of the plant (Cregger et al., 2018). The results suggest that the assembly of the microbiome is regulated by both the anatomical site and genetically inherited host factors. For example, root-associated environments are exposed to soil-derived microorganisms and root exudates continuously, while aerial tissues experience more fluctuations in nutrient availability, radiation, humidity and temperature.

Genomic adaptations to plant habitats also occur. Comparative studies have indicated that genes linked to the use of plant-derived compounds, to the ability to withstand stress and to adhesion are enriched in bacterial genes associated with plants (Levy et al., 2018). These attributes allow microorganisms to survive in plant-associated niches, and to adapt to selective pressures created by host tissues. The colonization of plants is thus not only contingent upon exposure to microorganisms, but also on the ecological fitness and functionality of the microorganisms that colonize the plants. The principal hosts, environment, and microbial factors that influence plant microbiome assembly are summarized in Table 1.

Table 1. Key Drivers of Plant Microbiome Assembly

Driver	Mechanistic basis	Functional consequence	Representative reference
Plant niche and genotype	Host compartment and genetic filtering shape microbial recruitment	Niche-specific and genotype-dependent microbiome structure	Cregger et al. (2018)
Molecular communication	Plant- and microbe-derived signals regulate recognition and interaction	Coordinates colonization and community function	Leach et al. (2017)
Microbial genomic adaptation	Enrichment of genes for transport, metabolism, adhesion, and stress tolerance	Supports successful plant colonization and persistence	Levy et al. (2018)
Host genetic control	Plant genes influence microbial recruitment and nutrient-associated functions	Links microbiome composition with crop performance	Zhang et al. (2019)
Interkingdom interactions	Bacteria, fungi, and oomycetes form functional networks	Enhances community stability and plant protection	Durán et al. (2018)
Priority effects and keystone taxa	Colonization order and influential strains alter community assembly	Determines microbiome trajectory and stability	Carlström et al. (2019)
Plant developmental stage	Microbial composition shifts across the plant life cycle	Produces stage-specific microbiome structure and function	Edwards et al. (2018)

Host genetics also plays a role in the organization of microbiomes, and can affect agriculturally relevant traits. Differences in the composition of root microbiota and nitrogen-use performance was observed in field-grown rice and correlated with variation in the nitrate transporter gene *NRT1.1B* (Zhang et al., 2019). This offers direct evidence that host genes specific to this function can affect microbial recruitment and at the same time impact nutrient acquisition by the plants. This is significant as it creates a link between plant genotype, microbiome composition, and crop performance that would suggest the use of microbiome-associated traits for future crop development.

Development further adds to the microbiome variability in plants. The bacterial and archaeal communities associated with roots of rice plants were found to significantly change in composition during the plant life cycle, such that development was a major ecological filter (Edwards et al., 2018). The development of roots, their nutrient and exudation needs and immune defence system may change the ecological opportunities for associated microorganisms.

The assembly of the microbiome is also a strong function of intra-microbial relationships. Bacteria, fungi and oomycetes can form cross-kingdom associations, which affect community stability and plant survival. In *Arabidopsis*, community-level, interkingdom interactions were demonstrated to play a role in host protection, and thus, microbial communities in the root microbiome are more important than single microbial taxa within the community (Durán et al., 2018). The observations indicate that beneficial plant responses can occur when coordinated microbial networks are in place with complementary and/or interacting functions.

The order of the microbial colonization of plant tissues also influences the development of the community. Priority effects were observed in experiments with synthetic communities of microorganisms in the phyllosphere of *Arabidopsis* that showed that the condition of the early arriving microorganisms affected the establishment of later ones. Other strains (keystone strains) had disproportionate effects on the overall community organization (Carlström et al., 2019). The results suggest that the composition of the microbiome is also influenced by the microbial community identity, colonization history, and interactions between different microorganisms. Rhizosphere microbiome assembly is a result of interactions between rhizosphere plants, soil properties, and soil microbes, and feedbacks between plants and soil (as shown in Figure 1).

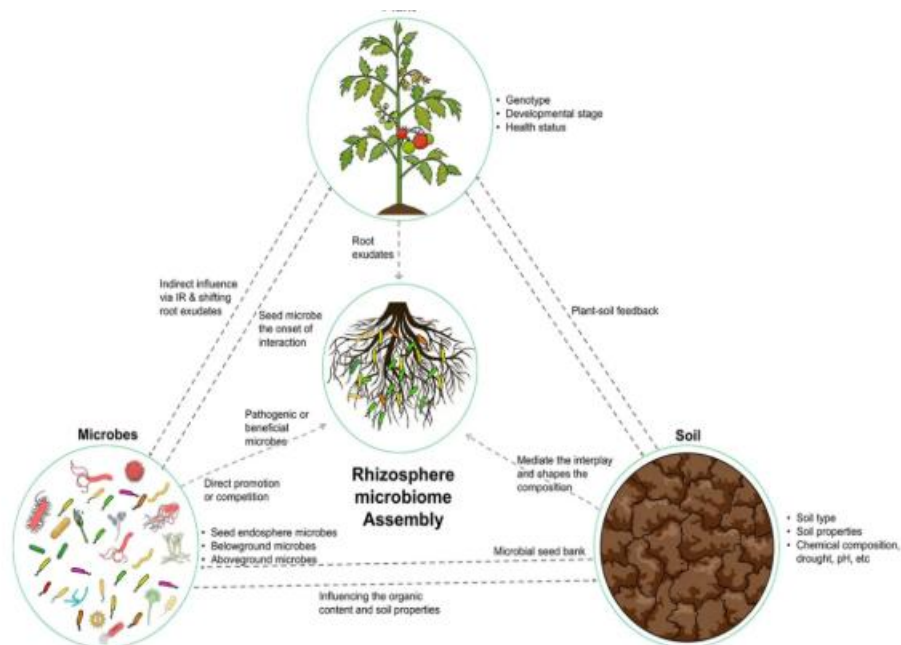


Figure 1. Plant, Soil, and Microbial Determinants Shaping Rhizosphere Microbiome Assembly

Adapted from Park et al. (2023)

Plant microbiome assembly should therefore be viewed as a dynamic process governed by the combined effects of host genotype, plant developmental stage, spatial niche, microbial adaptation, colonization sequence, and intermicrobial interactions. Communication among plants and associated microorganisms further integrates these processes through chemical and biological signaling within the broader phytobiome (Leach et al., 2017).

3. Molecular and Biochemical Basis of Plant–Microbe Crosstalk

The molecular signals, metabolites and ecological feedbacks that regulate plant–microbe interaction are complex and have the capacity to control microbial recruitment, colonization and function to the host. Plants actively manipulate the composition of the microbial community by the release of root metabolites, immune system factors, and selective choice of microbial species based on the plant genotype. Microbial communities also alter the chemical environment around the roots and influence the physiology of the plants. Microbiome composition has been repeatedly found to be filtered by host-specific biological conditions as a result of successive passaging of the microbiome within the host. (Morella et al., 2020)

The early and functional structure of soil microbial communities is also crucial as it may affect the plant's growth and disease. The microbial communities of soil can vary significantly in their pathogen-suppression capacity, nutrient cycling competence and plant root association capacity. Wei et al. (2019) showed that the composition and activity of the soil microbiome prior to host–microbe interactions were sufficient to predict future plant health, indicating the need to consider the context of the microbiome before host–microbe interactions are fully established.

Ecological and evolutionary viewpoints consider plant microbiomes as dynamic communities that are assembled through dynamic interactions among host selection, microbial competition, environmental filtering, and coadaptation. Microorganisms may be selected for abilities to attach to the plant, and plants may select microorganisms that help them acquire more nutrients and/or defend against pathogens. Reciprocal selection pressures have helped to shape the diversification and specialization of microbial communities associated with plants in different environments and host lineages (Cordovez et al., 2019).

One of the most significant molecular mechanisms that plants use to control microbial recruitment is through production of root exudates. These exudates contain sugars, amino acids, organic acids, phenolics, coumarins and other secondary metabolites as food and/or selective chemical signals. The composition and function of microbial communities can be changed by the presence of specific compounds that favour the growth of specific microbial groups and inhibit other groups. Host metabolites can also have a strong selective effect on the structure of a synthetic root microbial community, as was shown to be the case for coumarins in *Arabidopsis* (Voges et al., 2019). As illustrated in Figure 2, the rhizosphere microbial communities can be restructured by metabolites produced by the roots, and these metabolites can have feedback effects on plant growth and defense.

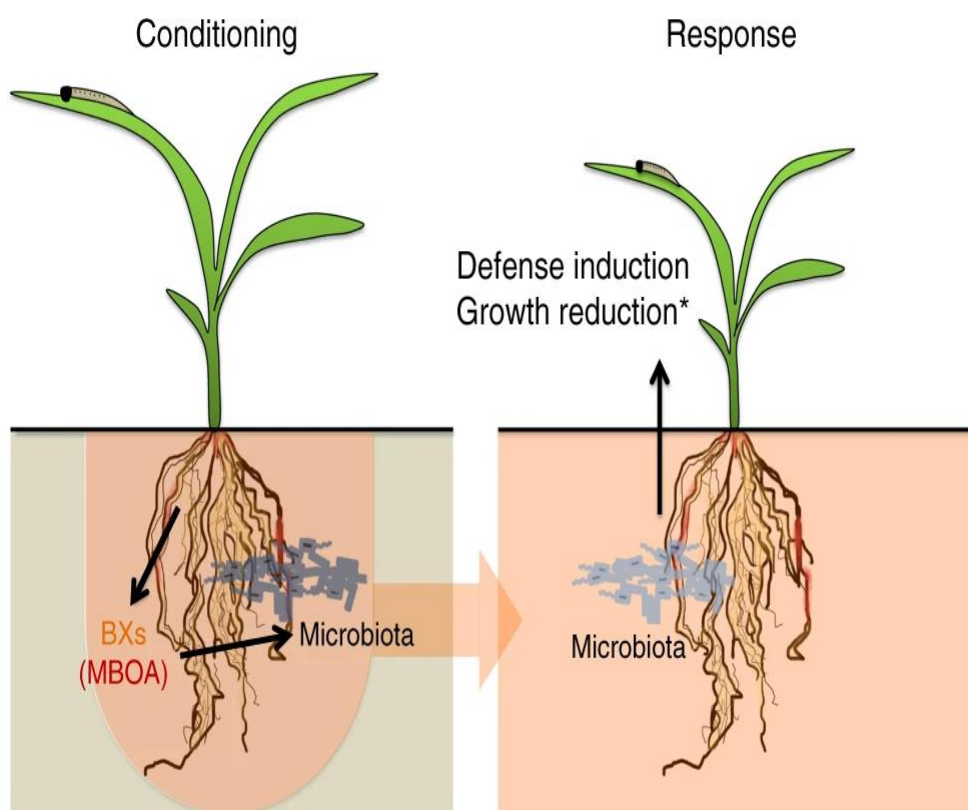


Figure 2. Root Exudate-Mediated Microbiome Conditioning and Its Effects on Plant Growth and Defense

Source: Adapted from Hu et al. (2018)

The regulation of coumarin production further emphasizes the genetic control underlying chemical communication between plants and their microbiomes. MYB72-dependent coumarin exudation has been shown to shape root microbiome assembly while contributing to plant health, linking host transcriptional regulation with microbiome recruitment and functional outcomes (Stringlis et al., 2018). This mechanism illustrates how plant signaling pathways can influence the extracellular chemical environment and selectively favor microbial communities associated with beneficial responses. It also provides a mechanistic bridge between host gene expression, metabolite production, and microbial community organization.

Root exudates additionally mediate feedback between plants and soil microbial communities. Metabolites released from roots can alter microbial composition in ways that subsequently influence plant growth and defense, creating plant–soil feedback loops with lasting ecological consequences. Hu et al. (2018) demonstrated that root exudate metabolites could restructure rhizosphere microbiota and modify subsequent plant growth and defensive responses. Such findings indicate that exudation is not merely a mechanism of nutrient release but an active process through which plants modify their biological environment. Aboveground pathogen infection can alter root exudation patterns and induce changes in soil microbial communities that remain as a biological legacy affecting subsequent plant–soil interactions (Yuan et al., 2018).

4. Microbial Regulation of Plant Growth and Crop Productivity

The plant-associated microorganisms are becoming more and more recognised as functional regulators of crop performance as they affect nutrient acquisition, root architecture, hormonal balance, rhizosphere signalling and tolerance to environmental stress. The importance of these microorganisms for plants cannot be overstated, given how closely they associate with the roots, and the ability to alter plant physiology and soil environment. One of these microorganisms that interacts closely with the plant roots and can alter the physiology of the plants and soil environment is plant growth promoting rhizobacteria (PGPR). Part of these interactions is initiated and maintained by root exudates that include sugars, amino acids, organic acids, phenolics, and other metabolites that serve as nutrient sources and signaling molecules for rhizosphere microorganisms (Baron & Rigobelo 2022). Exudates change the chemistry of and select for microbes around the root, and therefore, can shape the composition and functional properties of the plant's rhizosphere microbiota (Vives-Peris et al., 2020). Plant growth promotion needs to be considered as a two-way process, with plant metabolism influencing the rhizosphere microbial community and microbial activity influencing plant growth and resource acquisition.

This interaction is not limited to plant/microbe interactions, but has a functional complexity. Rhizosphere microorganisms can influence the release of chemicals and metabolite release from roots, affecting plant communication between neighbours. Korenblum et al. (2020) showed that the microbiome can mediate

changes in root exudation that can result in systemic changes to the root, highlighting that microbes play a role as a conduit in root-to-root communication. These interactions could impact microbial recruitment, resource competition, and nutrient cycling among adjacent root systems, indicating that microbiome influence on crop performance can be at both individual-crop and community levels.

PGPR have several complementary mechanisms of plant growth promotion. These include biological nitrogen fixation, phosphate and mineral solubilization, siderophore-mediated iron acquisition, production of phytohormones and modulation of root development. Certain strains also have the ability to produce 1-aminocyclopropane-1-carboxylate deaminase that can decrease the stress-related ethylene accumulation and consequently help maintain root elongation and plant growth during adverse conditions (Hestrin et al. 2019). These mechanisms work synergistically to enhance nutrient-use efficiency, root surface area, biomass production and crop productivity (Backer et al., 2018). The effectiveness of PGPR is not consistent because microbial traits and host genotype, as well as soil and climate conditions, and interactions with resident microbial communities, all influence the performance of PGPR.

The potential of PGPR is especially important for sustainable production of crops, as microbial inoculants could minimize the use of chemically intensive nutrient management. Beneficial rhizobacteria have a stimulating effect on the growth of roots and their functioning (root to soil interaction) as well as on the availability of nutrients and the growth of plants and add to soil biological activity. Biofertilizers and biologically based crop management systems that reduce external inputs to boost productivity are thus interesting candidate applications with which they can be used as multifunctional ingredients (Gouda et al., 2018).

When abiotic stress is limiting the growth of crops, the contribution of PGPR becomes even more important. Water relations, photosynthesis, nutrient uptake, membrane stability and cellular metabolism are affected by drought, salinity, nutrient limitation and oxidative stress. The positive rhizobacteria can help in reducing these effects by regulating phytohormones, improving root system architecture, enhancing antioxidant defenses, and promoting nutrient accessibility (Goswami & Deka, 2020). Such responses may enable plants to continue to grow and acquire resources under circumstances that would otherwise significantly limit their growth and production.

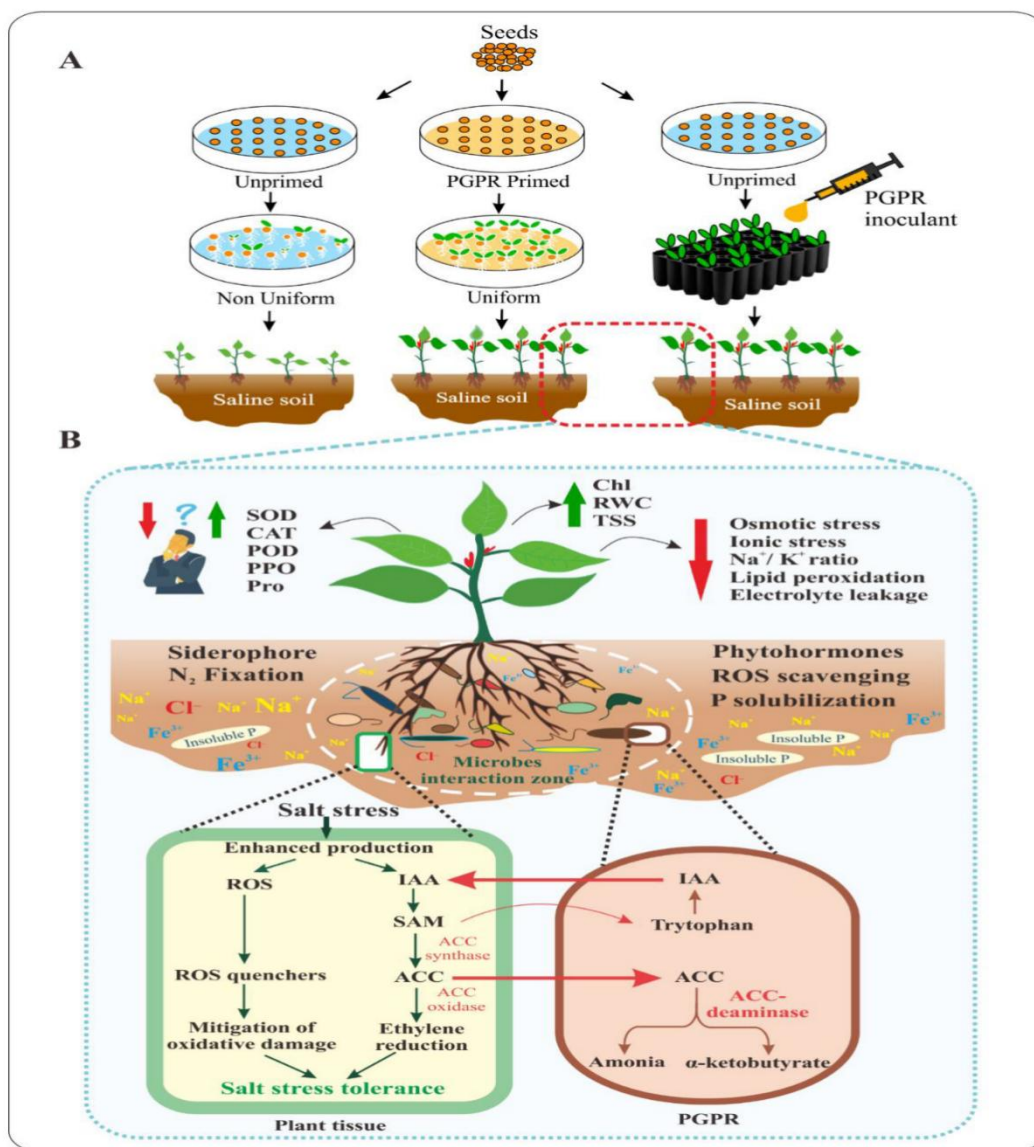


Figure 3. PGPR-Mediated Mechanisms Enhancing Plant Growth and Salinity Stress Tolerance

Source: Adapted from Ha-Tran et al. (2021)

Salinity provides a clear example of this functional integration. Excess salt generates osmotic stress, ion toxicity, nutrient imbalance, and oxidative damage, all of which compromise crop productivity. Salt-tolerant PGPR can improve plant performance by promoting nutrient uptake, regulating ionic balance, producing growth-active metabolites, and enhancing antioxidative and osmoprotective responses (Egamberdieva et al., 2019). At the physiological and molecular levels, PGPR-mediated salinity tolerance involves coordinated regulation of antioxidant metabolism, compatible solute accumulation, hormonal signaling, and ion transport, thereby helping plants maintain cellular homeostasis under saline conditions (Ha-Tran et al., 2021). As illustrated in Figure 3, PGPR enhance salinity tolerance through integrated regulation of nutrient acquisition, phytohormones, antioxidant defenses, ion homeostasis, and ACC deaminase-mediated ethylene reduction.

5. Plant–Microbe Interactions in Abiotic Stress Resilience

Abiotic stresses create multiple constraints on the productivity of crops through effect on water balance, nutrient uptake, photosynthesis, membrane stability, ion balance and redox homeostasis in the cells. Drought and salinity stress are especially harmful and can cause a synergistic impact on the rhizosphere to the whole plant metabolism, and frequently combine with nutrient stress and oxidative stress in the field (Nie et al. 2024). The plant-associated microorganism, and in particular, plant growth-promoting rhizobacteria (PGPR), can reinforce plant resistance by a coordinated regulation of plant root growth, nutrient mobilization, hormonal signaling, osmotic adjustment and antioxidant defense mechanisms. They are multifunctional, which is particularly relevant for sustainable agriculture, where maintaining productivity under environmental stress demands a greater use of internal resources with less reliance on external resources (Wahab et al., 2025).

Microbial regulation of stress adaptation is found to be the major interface in the rhizosphere. The composition of root exudates is affected by the environment and is known to affect microbial recruitment and activity, and includes sugars, amino acids, organic acids, phenolics and other secondary metabolites (Vives-Peris et al., 2020). Such stress-induced exudation may create a selective environment for microorganisms which are beneficial to plant adaptation. Beyond the root-to-root communication, microbiome-mediated root-to-root signaling also highlights that belowground communication can trigger systemic responses in metabolite release, pointing to a coordinated response not just in the root, but in the soil microbial community as well (Korenblum et al., 2020). Such interactions create rhizosphere as a dynamic biological system where chemical signaling and microbial activity interact to affect stress response.

There are multiple links in the chain of effects of PGPR under environmental stress. Resource acquisition is enhanced through biological nitrogen fixation, phosphate solubilization, siderophore production, phytohormone synthesis and modification of root architecture, while excessive stress induced ethylene production is reduced by ACC deaminase activity which also helps to maintain root elongation (Backer et al., 2018). Beneficial rhizobacteria can also help regulate antioxidant metabolism, osmoprotectant accumulation and nutrient availability, which reduces oxidative damage and ensures cell function in adverse conditions (Goswami & Deka, 2020). These mechanisms also enable the use of PGPR as alternatives or supplements to the traditional management, which is based on chemical fertilizers (Gouda et al., 2018). The key microbial processes which have been identified as improving plant drought, salt stress, oxidative stress, nutrient limitation and related abiotic stress tolerance are summarised in Table 2.

Table 2. Microbial Mechanisms Underlying Plant Resilience to Abiotic Stress

Stress/constraint	Key microbial mechanism	Main outcome	Reference
Drought	Root modification, ACC deaminase, osmolytes	Improved water status and biomass	Ahmad et al. (2022); Buragohain et al. (2024)
Drought–soil interaction	EPS production, nutrient mobilization	Better soil moisture and resilience	El-Saadony et al. (2024)
Salinity	Ion regulation, osmotic adjustment, antioxidants	Improved Na ⁺ /K ⁺ balance and reduced injury	Egamberdieva et al. (2019); AbuQamar et al. (2024)
Oxidative stress	ROS scavenging and antioxidant activation	Reduced cellular damage	Ha-Tran et al. (2021)
Stress-induced ethylene	ACC deaminase activity	Sustained root growth	Backer et al. (2018)
Nutrient limitation	N fixation, P solubilization, siderophores	Improved nutrient availability	Gouda et al. (2018)
Rhizosphere adaptation	Stress-responsive exudation and recruitment	Beneficial microbiome restructuring	Vives-Peris et al. (2020)
Belowground signaling	Root-to-root microbial signaling	Coordinated plant responses	Korenblum et al. (2020)
Combined stress	Community restructuring and recruitment	Broader plant resilience	Berendsen et al. (2018); Kwak et al. (2018)

One of these microbial functions is drought resilience, a major application. Water deficit causes stomatal conductance to decrease, photosynthesis to decrease, transport of nutrients to decrease, and growth to decrease, and causes an increase in reactive oxygen species and an increase in damage to membranes. The beneficial effects of PGPR include the promotion of root proliferation, water uptake, control of phytohormones, accumulation of compatible solutes and the activation of enzymatic antioxidant systems, which all contribute to drought tolerance (Ahmad et al., 2022). Sustained plant performance in limited water availability is further enabled by improvements in the relative water content, chlorophyll stability, membrane integrity, and root architecture (Buragohain et al. 2024). Extracellular polymeric substances,

aggregation, nutrient cycling and maintaining the soil microbial environment are additional stress-tolerance-positive soil-health-enhancing benefits of drought adapted PGPR and their potential to improve plant stress tolerance and soil-health (El-Saadony et al., 2024).

The salinity stress is another hurdle as it integrates osmotic stress, ion toxicity, nutritional imbalance and oxidative damage. Salt-tolerant PGPR can enhance plant growth by regulating ion homeostasis, nutrient uptake, root growth and osmotic adjustment, as well as by inducing antioxidant defense mechanisms (Egamberdieva et al., 2019). Extracellular polysaccharides produced by halotolerant microorganisms can also help modify the rhizosphere environment and mitigate the effects of high concentrations of Na⁺ ions on plant physiology (AbuQamar et al., 2024). The cellular mechanisms of salinity tolerance by PGPR include regulation of Na⁺/K⁺ homeostasis, chlorophyll retention, relative water content, accumulation of compatible solutes, antioxidant enzymes and stress-related hormonal pathways. ACC deaminase activity can also mediate ethylene control to ensure growth under situations where root growth is limited by salt stress (Ha-Tran et al., 2021).

More importantly, abiotic stress plant responses cannot be clearly distinguished from the organization of the microbiome community. Environmental stress can cause changes in host physiology and/or microbial recruitment, which may result in changes in subsequent resistance to biological threats. The ability of plant-associated communities to reorganize under stress and affect host resilience is demonstrated in the plant-associated consortiums and microbiome that have been found to be assembled during disease (Berendsen et al., 2018; Kwak et al., 2018). Such a functional overlap suggests that the plant microbiomes are not acting to promote individual traits, but are instead part of an integrated network of resilience.

6. Microbiome-Mediated Disease Suppression and Plant Immunity

Plant associated microbiomes play a significant role in developing resistance to plant diseases, both by direct suppression of pathogens and by stimulation of plant immunity. The rhizosphere, endosphere and phyllosphere are sources of protective microorganisms, which can compete for resources, produce antimicrobial metabolites, alter local resources, and trigger plant defense signals. These functions are particularly relevant to sustainable agriculture as they can help to lower the reliance on chemical pesticides and promote long-term plant and soil health. Host genetics are not the only factors that influence disease resistance; disease resistance is also influenced by the community structure and functionality of associated microbial communities.

The disease-suppressive potential and the structure of the microbiome may be influenced by host breeding. For common bean, resistance was found to modify the microbial community in the rhizosphere, thereby increasing functions related to pathogen suppression, suggesting that indirect selection of microbial communities via resistance may be possible (Mendes et al., 2018). This stems from a greater

understanding of disease resistance being an emergent property of the plant–microbiome system, rather than just the result of the host's genome.

Pathogen attack may also reshape microbial community to a more protective form. Carrión et al. (2019) highlighted the ability of plants to solicit or elicit beneficial microorganisms during invasion by pathogens, for example, in their case pathogen invasion triggered disease-suppressive activity in the endophytic root microbiome. Plant defense goes beyond intrinsic immune pathways with pathogen-responsive restructuring of the microbiome and provides a dynamic ecological element to defense.

Another mechanism of importance is direct microbial antagonism. Plant associated microorganisms can be a source of antibiotics, lytic enzymes, siderophores and volatile compounds that inhibit the growth of pathogens. Microbial interactions and biosynthesis of antibiotics in the *Arabidopsis* leaf microbiome showed remarkable biosynthetic potential to govern community structure and suppress competitors (Helfrich et al., 2018). In the soil, there are several microbial taxa and metabolites that have been associated with disease-suppressive soils, such as Burkholderiaceae and sulfur-containing volatiles, which are associated with the inhibition of pathogens (Carrión et al., 2018). Plant-associated microbiomes have two ways of inhibiting pathogens: through direct antagonistic activity and by activating or priming the plant's immune system, as illustrated in Figure 4.

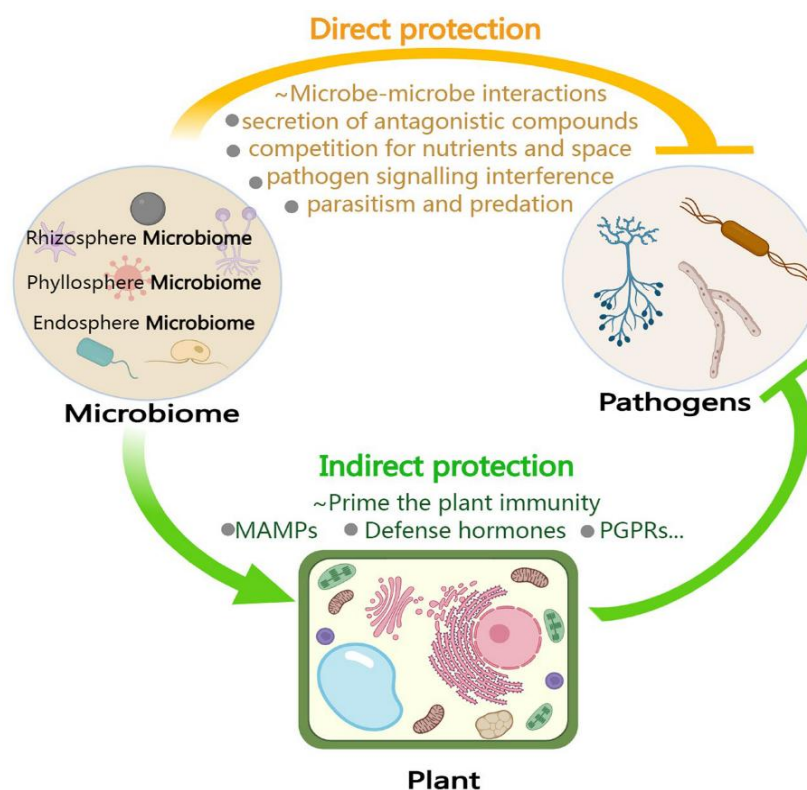


Figure 4. Direct and Indirect Microbiome-Mediated Mechanisms of Plant Disease Suppression

Source: Adapted from Xiong et al. (2023)

Agricultural management can further strengthen microbiome-mediated suppression. Greater crop rotational diversity has been associated with increased disease-suppressive capacity of soil microbiomes, likely through enrichment of functional diversity and disruption of pathogen-favoring ecological conditions (Peralta et al., 2018). This highlights the potential of crop rotation to support biological disease control through microbiome restructuring.

Beneficial microorganisms also enhance immunity through induced systemic resistance. Rhizobacteria-mediated ISR primes plant defense pathways, enabling faster and stronger responses to subsequent pathogen attack while avoiding the continuous metabolic cost of constitutive defense. This process involves coordinated signaling through jasmonic acid, ethylene, salicylic acid, and related regulatory networks (Rabari et al., 2023). Beneficial microbes can therefore function both as direct antagonists and as biological signals that improve host immune readiness (Yu et al., 2022).

7. Translational Strategies for Microbiome-Based Sustainable Agriculture

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Table 3. Microbiome-Based Approaches for Sustainable Crop Productivity and Stress Management

Strategy	Translational role	Key benefit	Representative reference
Root exudate engineering	Selective recruitment of beneficial microbes	Stress resilience and microbiome optimization	Afridi et al. (2024)
Secondary metabolite manipulation	Modulates microbiome structure and function	Improved plant–microbe interactions	Pang et al. (2021)
Synthetic microbial communities	Combines complementary microbial functions	Predictable and multifunctional crop support	Poupin Swinburn (2023)
Genotype–microbiome engineering	Co-selects host and microbial traits	Adaptation to stressed agroecosystems	Vimal et al. (2023)
Microbiome-based biostimulants	Enhances physiological and microbial functions	Improved growth and stress tolerance	Lau et al. (2022)
Microbial consortia	Integrates multiple beneficial strains	Greater functional diversity and stability	Negi et al. (2024)
Biofertilizers	Improves nutrient cycling and availability	Reduced dependence on synthetic fertilizers	Kumar et al. (2022)

Another important translation strategy is the use of synthetic microbial communities. In contrast to naturally-occurring microbiomes, synthetic communities consist of engineered microbial consortia that are composed of microbial strains with complementary functions. Such systems can be designed to deliver nutrient mobilization, production of phytohormones, suppression of pathogens, stress relief and root colonization at the same time (Aloo et al. 2022). They have a significant benefit in being able to establish reproducible microbial communities with known functional roles, but achieving field stability and compatibility is difficult. Laboratory characterization of the dynamics of microbial communities in the rhizosphere indicates that the success of a synthetic community must consider interspecies

competition, cooperation, priority effects and interactions with native microbiota (Poupin Swinburn, 2023).

Plant genotype is also one of the factors that are now recognized as part of microbiome engineering (Ayilara et al. 2023). Root genotype influence on functional outcomes may occur through differences in genotype in root architecture, exudate composition, immune regulation and microbial recruitment that can influence both community composition and functional outcomes. Hence, the possibility of simultaneous selection of plant characteristics and beneficial microorganisms in stressed agricultural systems is provided by genotype–microbiome engineering, which is a nature-based solution. Therefore, joint selection of plant traits and beneficial microorganisms for stressed agriculture is available through the possibilities of genotype–microbiome engineering (Vimal et al., 2023).

Microbiome engineering could also be coupled with plant biostimulants to enhance the resilience of plants. The use of beneficial microorganisms or microbial-derived compounds as biostimulant formulations can increase the use efficiency of nutrients, growth of roots, stress tolerance, plant physiological performance etc. The incorporation of microbiomes could offer a more adaptable approach for improving crop productivity and minimizing the use of chemical fertilizers and pesticides (Lau et al., 2022).

The other benefit of microbial consortia over single strain inoculants is that more than one microorganism can have a complementary function in one formulation. The functional redundancy concept suggests that consortiums could mobilize nutrients better, make them more stress-tolerant, suppress pathogens, and make ecosystems more stable (Negi et al., 2024). However, interactions between consortium members need to be carefully considered as antagonism, competition, or ecological instability could be present that could decrease the field performance. Biofertilizers continue to be one of the most useful uses of beneficial microorganisms in sustainable agriculture. They can enhance the nutrient availability and lower the use of synthetic fertilizers due to their ability to assist in nutrient recycling, biological nitrogen fixation, phosphate solubilization, and soil biological activity (Kumar et al., 2022).

8. Conclusion

Plant–microbe interactions are a core biological element of sustainable agriculture as they encompass nutrient acquisition, plant growth regulation, stress adaptations, disease suppression and crop productivity within a dynamic soil–plant system. The microbiome assemblies are currently known to be influenced by host genotype, developmental stage, exudates from the roots, soil characteristics, microbial competition and the history of the community. Such interactions can be regulated by complex molecular and biochemical signaling pathways which impact both plant physiology and microbial function. The beneficial microorganisms, especially plant growth promoting rhizobacteria and functionally complementary microbial consortia, can help to increase nutrient-use efficiency, control phytohormones,

boost antioxidant capability, balance ions and osmium, boost plant immunity etc. They play a significant role in drought, salinity, nutrient limitation and pathogen pressure. However, it is a significant challenge to utilize the potential in the field, given the inconsistent results achieved. Future advances will require shifting towards function-based and mechanistically validated approaches beyond merely descriptive microbiome profiling. A combination of microbiome engineering, synthetic microbial communities, plant- and soil-genotype selection, biofertilizers and precision rhizosphere management could enhance the reliability of microbiome technologies. Long-term field validation, formulation stability, ecological compatibility and standardized evaluation frameworks will be crucial. These multi-modal strategies may help to leverage plant microbiomes for more resilient, productive and resource efficient agricultural systems.

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