



PLANT-MICROBE INTERACTIONS UNDER ENVIRONMENTAL STRESS: MECHANISMS, ADAPTATION, AND AGRICULTURAL IMPLICATIONS

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ABSTRACT

Plant-associated microorganisms have a key role in controlling plant growth, nutrient uptake, environmental stability, and stress responses. This study aims to summarize the existing information on plant-microbe interactions under drought, salinity, extreme temperature, heavy metal toxicity, nutrient deficiency, and multiple abiotic stresses. Special attention is given to the functional role of plant growth promoting rhizobacteria, arbuscular mycorrhizal fungi, endophytic bacteria and fungi, rhizobia, actinobacteria and microbial consortia. Microbe-mediated stress tolerance mechanisms are mainly phytohormone regulation, ACC deaminase activity, osmolyte production, exopolysaccharide and biofilm formation, antioxidant defense enhancement, nutrient mobilization, and regulation of stress-responsive genes. The interactions lead to better root architecture, photosynthetic activity, water-use efficiency, ion homeostasis, secondary metabolism and systemic tolerance. The study emphasizes the role of genomics, metagenomics, transcriptomics, proteomics, metabolomics, sequencing of microbial communities, and multi-omics integration in the discovery of stress-responsive microbial traits, molecular pathways, and potential microbial biomarkers. Agricultural applications include microbial biofertilizers, biostimulants, stress-tolerant inoculants, and engineered microbial communities for climate-resilient crop production. Yet, field performance, formulation stability, storage, delivery, and host-microbe-environment specificity are limitations. In summary, the strategic management of plant-associated microbiomes has significant potential to create productive, resource-efficient, and climate-smart agriculture systems in a world of increasing environmental stress.

Keyword: Plant–microbe interactions; Abiotic stress; Plant microbiome; Stress tolerance; Climate-smart agriculture

1. Introduction

Plants live with different groups of microorganisms that have a significant impact on plant growth, development, nutrition, immunity and adaptation to environmental stress. These microorganisms comprise the plant microbiome (microbial groups, including bacteria and fungi that reside in plant-associated environments). Beneficial microorganisms have the potential to increase the availability of nutrients, promote root growth, modify plant hormones, reduce disease, and help plants withstand environmental stresses [1]. Plant growth-promoting rhizobacteria (PGPR) are among these microorganisms, which enhance plant growth by fixing nitrogen, solubilizing phosphorus, producing siderophores, synthesizing phytohormones and regulating plant stress pathways [2]. These microbial interactions are now known to be a part of plant fitness and not just surface biological interactions.

Microorganisms that inhabit plants exist in various ecological niches, including the rhizosphere, phyllosphere and plant tissues. The rhizosphere is the region of soil directly affected by the plant's roots, and exuded chemicals from the rhizosphere are one of the most biologically dynamic interfaces between plants and microorganisms. The rhizosphere microorganisms can help alter root architecture, enhance water and nutrient uptake, and affect plant physiology in drought stress situations [3]. Microbial communities colonize aerial plant surfaces, usually in the phyllosphere while endophytic microorganisms penetrate the internal tissues of plants without causing any obvious disease. These compartments make up a dynamic microbiome whose composition and activity are variable based on genotype, plant growth stage, soil properties, climate, and management [4]. Another key part of plant-associated microbial communities is arbuscular mycorrhizal fungi, which have symbiotic associations with the roots and enhance mineral nutrition, water absorption, and stress resistance [5].

The plant's physiology change in response to environmental stresses like drought, salinity, heat, cold, nutrient stress and heavy metals, which also influence the accompanying microbial communities. The decline in soil moisture during drought is especially significant as it impacts microbial abundance, rhizosphere exudation, nutrient diffusion, and rhizosphere signaling. The adverse effects can be mitigated by the beneficial microbiomes that positively influence osmotic adjustment, antioxidant activity, hormonal balance and water-use efficiency [6]. Plant-microbe interactions are thus highly context-dependent, and environmental shifts and shifts in microbial interactions can be beneficial, neutral or even detrimental under certain conditions [7]. However, beneficial microorganisms often play a role in multi-stress tolerance, controlling physiological, biochemical and molecular defense mechanisms [8]. Plant growth-promoting rhizobacteria, for instance, increase the tolerance to abiotic stress by utilizing ACC deaminase activity, production of exopolysaccharides, nutrient uptake and activation of antioxidant defense [9].

The use of beneficial plant-microbe interactions has great potential to create sustainable and climate-resilient agricultural systems. Microbial inoculants can serve as an alternative to agrochemicals such as

synthetic fertilizers and promote nutrient-use efficiency, soil health, crop productivity and environmental stress resistance. As the use of plant microbiomes in agriculture grows, it is moving towards biologically based strategies for crop management, using naturally occurring microbial functions [4]. Improved understanding of microbial establishment, host specificity, environmental compatibility, formulation and persistence is necessary for successful field application, however. The use of microbial biostimulants and beneficial symbionts in crop production is thus considered one of the most promising approaches to ensure productivity in the current climate of environmental variability and stress.

The objective of this study is to summarize the knowledge on the interactions between plants and microbes in environmental stress, focusing on underlying mechanisms, adaptive responses, and applications in sustainable and climate-resistant agriculture.

2. Major Environmental Stresses Affecting Plant–Microbe Associations

2.1 Drought and Water Deficit

Drought/water deficit has a significant impact on plant–microbe relationships through changes in soil moisture, root exudation, microbial activity, nutrient mobility and rhizosphere community structure. Water limitation can affect microbial biomass and disrupt beneficial interactions, however, some plant-associated microorganisms can positively impact plant survival by promoting root growth, osmotic adjustment, antioxidant activity and water-use efficiency. The plant microbiome is thus a key ecological factor in drought adaptation, its efficacy being influenced by host genotype and context [10]. Microbiome-assisted mechanisms are being increasingly taken into account in climate-smart crop development, particularly to enhance resilience to extended periods of water stress [11].

2.2 Salinity Stress

Salinity creates osmotic and ionic stress that results in poor nutrient uptake, decreased photosynthetic activity and oxidative damage. These effects can be reduced by beneficial microbes that can regulate ion homeostasis, phytohormone levels, production of exopolysaccharides, activation of antioxidants and enhance nutrient acquisition. Plant growth promoting rhizobacteria play a special role in improving salt tolerance through regulation of stress-responsive pathways and maintaining physiological balance [12]. Likewise, the endophytic fungi symbionts enhance growth, osmotic adjustment and mineral absorption in the saline conditions [13]. Bacterial inoculants with salt tolerance are also potentially good biological tools for crop production in salt-affected soils [14].

2.3 Heat and Cold Stress

High temperatures can cause instability in membranes, enzyme activity, photosynthetic function and the colonization pattern of microorganisms. Changes in communication between plants and their associated microbiota is another potential effect of heat and cold stress. The beneficial microorganisms can help with

thermal tolerance via stimulating the antioxidant defenses, the modulation of stress hormones, and the accumulation of protective metabolites. These interactions indicate that microbial partnerships play a significant role in plant adaptation to changing climatic conditions [15]. Additionally, within the phytomicrobiome, communication can further regulate stress-responsive signaling networks and enhance plant resilience across different temperature regimes [16].

2.4 Heavy-Metal Toxicity

Cadmium, lead, arsenic, chromium and other heavy metals disrupt the metabolism of plants and cannot be tolerated by soil microorganisms. Some of the beneficial microorganisms lower the toxicity of the metals through biosorption, immobilization, chelation, transformation and enhancement of the plant antioxidant system. These functions aid in the growth of plants and help in the process of phytoremediation in contaminated soil. The broader plant–microbiome interaction is thus considered to be a valuable biological tool in the context of sustaining productivity in chemically degraded conditions [13].

2.5 Nutrient Deficiency and Soil Degradation

Plant productivity is limited by nutrient-poor and degraded soils that limit N, P, Fe, and other plant nutrients. Beneficial microbes can enhance nutrient acquisition through nitrogen fixation, phosphate solubilization, mineralization, siderophore production, and root development. To promote sustainable agriculture, the use of synthetic fertilizers is being reduced, and approaches to enhance nitrogen metabolism through microbiome engineering are being considered [17].

2.6 Combined and Multiple Environmental Stresses

In the natural and agricultural environment, plants are not only subjected to one stress factor but to a combination of stresses. Interacting drought, salinity, nutrient deficiency, temperature extremes and soil degradation may also synergistically affect and place physiological limitations. Microbial communities with the ability to provide multiple stress-response pathways may thus provide greater protection than single-function inoculants. These intricate interactions between plant, microbes, and environment are at the heart of building resilient cropping systems in the face of a more unpredictable environment [10,11]. Table 1 summarizes the major environmental stresses and physiological responses of plant–microbe associations and the microbial responses.

Table 1. Major Environmental Stresses And Microbial-Mediated Responses In Plants

Environmental stress	Principal effects on plants	Effect on plant–microbe association	Beneficial microbial response	Plant benefit	References
Drought/water	Reduced water	Altered root	Improved root	Better water	[10]

deficit	availability, oxidative stress, reduced growth	exudation and rhizosphere structure	growth, osmotic adjustment and antioxidant activity	acquisition and drought tolerance	
Salinity	Osmotic stress, ionic toxicity, nutrient imbalance	Selection of salt- tolerant microbial taxa	Ion regulation, phytohormone modulation, EPS production	Reduced Na ⁺ toxicity and improved growth	[13]
Heat/cold	Membrane instability and impaired photosynthesis	Changes in microbial colonization and communication	Antioxidant activation and stress-signaling regulation	Improved thermal tolerance	[15]
Heavy metals	ROS accumulation and metabolic toxicity	Reduced microbial diversity	Biosorption, immobilization and chelation	Reduced metal toxicity	[13]
Nutrient deficiency	Reduced nutrient availability and biomass	Selection of nutrient- mobilizing microbes	N fixation, P solubilization and siderophore production	Improved nutrition	[12]
Multiple stresses	Combined physiological and metabolic disruption	Complex microbiome restructuring	Multifunctional stress-response mechanisms	Broad- spectrum resilience	[11]

3. Mechanisms of Microbe-Mediated Plant Stress Tolerance

3.1 Phytohormone Production and Regulation

The beneficial microorganisms can increase the stress resistance of plants in part by synthesizing and regulating phytohormones like auxins, cytokinins, gibberellins, abscisic acid, and ethylene. The consequences of these hormonal changes include root development, stomatal control, nutrient uptake, and stress signaling. The plant-associated microbial communities are thus able to remodel host physiology to enhance adaptation to drought, salinity, and other environmental stressors [18]. Biostimulants based on

microbiomes are also gaining momentum as an option to control such hormonal pathways in sustainable crop enhancers [19].

3.2 ACC Deaminase Activity

Producing bacteria that produce ACC deaminases alleviate stress-induced ethylene build-up by breaking down 1-aminocyclopropane-1-carboxylate, the immediate precursor to ethylene. Reduced levels of ethylene would be able to sustain root growth and promote growth of plants in unfavorable conditions. This process is particularly relevant in salty environments, where plant growth-promoting bacteria aid in regaining physiological balance and mitigating stress damage [20]. These microbial activities are significant elements of more extensive interactions between plants and microbiomes affecting plant health [21].

3.3 Osmolyte Production

Compatible osmolytes such as proline, glycine betaine and soluble sugars can be stimulated by or contributed by microbial partners. These compounds assist in preserving cellular water potential, membrane stability, and protein activity in drought and salinity stress. Osmotic balance regulation by the phytomicrobiome is hence a key process of abiotic stress alleviation in crops [22].

3.4 Exopolysaccharides and Biofilm Formation

Numerous beneficial bacteria form biofilms and exopolysaccharides around roots. These structures enhance microbial colonization, soil aggregation, soil moisture and reduce excessive uptake of harmful ions. Microbial consortia with the potential to synthesize protective extracellular matrices can thus enhance plant performance in drought, salinity, and in degraded-soil environments [23].

3.5 Antioxidant Defense Enhancement

Excessive reactive oxygen species production often occurs due to environmental stresses and leads to oxidative damage of membranes, proteins, and nucleic acids. There are beneficial microorganisms that are capable of augmenting antioxidant enzymes like superoxide dismutase, catalase, and peroxidase, and thereby reducing oxidative damage. The same microbial mechanisms play a role in heavy-metal stress, with rhizobacteria aiding in detoxification and phytoremediation of the stressor [24].

3.6 Improved Nutrient Acquisition and Mineral Solubilization

The microorganisms increase the nutritional status of plants by fixing nitrogen, solubilizing phosphates, producing siderophores, mobilizing minerals and developing more root surfaces. These processes are especially useful in nutrient-deficient and degraded soils. Development of plant microbiomes to enhance nutrient-use efficiency is becoming a promising approach towards minimizing fertilizer use and enhancing crop production [25].

3.7 Regulation of Plant Stress-Responsive Genes

The colonization of microorganisms may modify plant gene expression that regulates hormonal signaling, antioxidant, ion transportation, osmotic control, and defense. These transcriptional modifications enhance the ability of the plants to react quickly to environmental stress. The study of this type of molecular communication is gaining significance due to the increasing intensity of climate change, which increases stress factors and pathogen pressures in agricultural environments [26]. The combination of functional microbiomes and crop management thus help to build more climate-adaptive and resilient production systems [22,26]. Figure 1 shows the main physiological, biochemical and molecular processes by which useful microorganisms can increase plant stress tolerance.

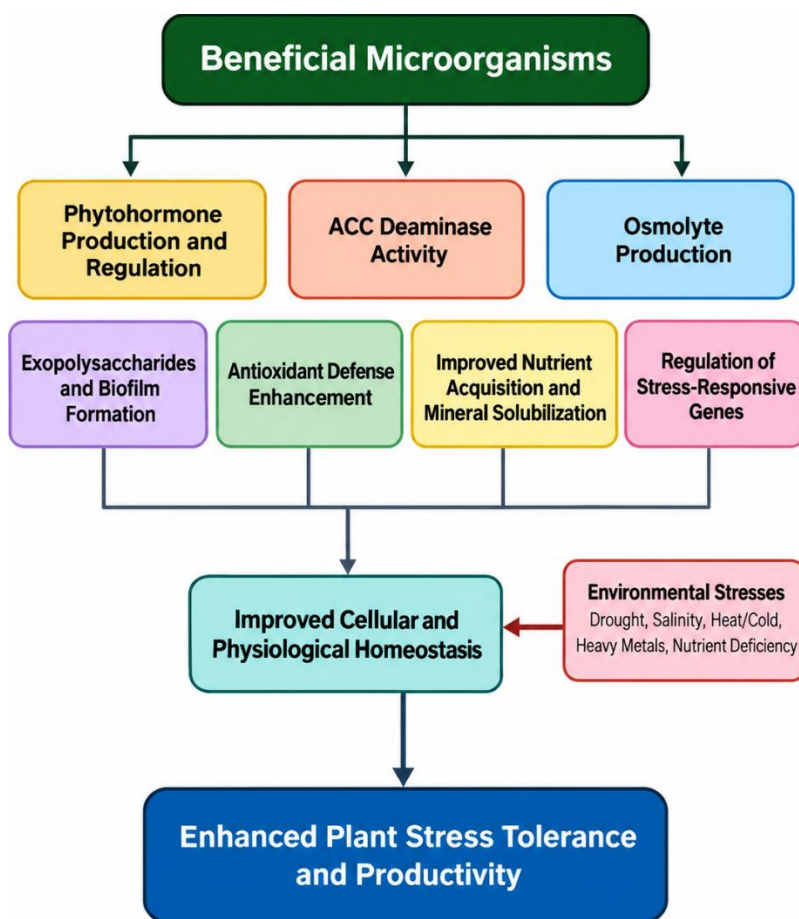


Figure 1 design: Mechanistic framework of microbe-mediated plant stress tolerance

4. Plant Responses and Adaptation Through Microbial Partnerships

4.1 Root Architecture Modification

Positive microorganisms can significantly alter root structure, allowing plants to access a greater volume of soil and access water and nutrients in stressful environments. Growth-promoting rhizobacteria promote lateral root development, root length and root-hair development via the production of phytohormones and other growth-promoting actions. The changes are especially useful in droughty conditions, where a larger

root system would be able to help in the acquisition of water and increase plant survival [27]. Arbuscular mycorrhizal fungi also enhance the effective absorptive area of roots via the fungal hyphae, which enhances water and mineral uptake during drought, salinity, and heavy-metal stress [28].

4.2 Physiological and Biochemical Adaptations

Partnerships of microbes have an effect on various physiological and biochemical processes of plant adaptation. In stressful environments, beneficial microbes have been shown to enhance osmotic adjustments, membrane stability, nutrient balancing, antioxidant activity, and homeostasis in cells. The plant must thus be a dynamic holobiont where the bacteria, fungi and the host co-regulate responses to environmental change [29]. The presence of different microbiomes can have complementary functions that together improve plant performance and help to increase soil and ecosystem stability [30].

4.3 Modulation of Photosynthesis and Water-Use Efficiency

Environmental stress usually decreases the amount of chlorophyll, stomatal conductance, and photosynthetic efficiency. Microbial symbionts have the capacity to sustain photosynthetic activity through enhancement of water uptake, nutrient availability and stomatal control. Recent microbiome-based strategies are more concerned with maintaining carbon assimilation and water-use efficiency in plants in response to climate-related stresses [31]. These reactions play a core role in the creation of climate-resilient crops that can sustain their productivity in a system with fluctuating environmental conditions.

4.4 Induced Systemic Tolerance

Positive microorganisms may be able to prepare plants with faster and more efficient reactions to stress, a process commonly referred to as induced systemic tolerance. Microbial colonization triggers antioxidant defense, hormonal, osmoprotection, and cellular repair signaling pathways. Microbiome engineering provides a means to pick or design microbial communities that can enhance such stress-response reactions in adverse agricultural settings [32]. The efficacy of the microbial inoculants can differ based on the soil type, climate, plant genotype, and microbial development, highlighting the significance of ecology [33].

4.5 Changes in Secondary Metabolites

The formation of phenolics and flavonoids, terpenoids and other secondary metabolites that are used in both stress protection and signaling can be modified by microbial associations. These molecules play a role in antioxidant activity, membrane protection as well as plant-microorganism communication. The development of microbial formulations capable of aiding such biochemical reactions is becoming a crucial topic in climate-smart agriculture [34].

4.6 Plant Immune and Signaling Responses

Plant-associated microorganisms can also modulate immune and signaling pathways of jasmonic acid, salicylic acid, ethylene, abscisic acid, and reactive oxygen species. These pathways are involved in the regulation of responses to abiotic and biotic stress. Combining microbiome engineering with plant physiology thus enhance multi-stress tolerance, due to enhanced interdependent signalling and defence responses [35]. These types of integrated strategies are becoming essential to develop crops that resilient to multiple and interacting environmental stresses. Table 2 summarizes the significant morphological, physiological, biochemical, and molecular changes brought about by positive microbial associations.

Table 2. Plant adaptive responses induced through microbial partnerships

Plant response	Microbial influence	Main mechanism	Adaptive significance	References
Root architecture	Increased root length, lateral roots and absorptive surface	Hormonal regulation and fungal hyphal extension	Improved water and nutrient acquisition	[27]
Osmotic adjustment	Improved cellular hydration	Osmolytes and microbial signaling	Maintenance of cell turgor	[29]
Photosynthesis	Maintenance of chlorophyll and carbon assimilation	Better nutrient and water status	Improved productivity under stress	[31]
Water-use efficiency	Improved water uptake and stomatal regulation	Root–microbe interactions	Greater drought adaptation	[31]
Induced systemic tolerance	Priming of stress pathways	Hormonal and antioxidant signaling	Faster stress response	[32]
Secondary metabolites	Increased phenolics, flavonoids and related compounds	Metabolic reprogramming	Antioxidant and protective effects	[34]
Immune signaling	Modification of JA, SA, ABA and ethylene pathways	Signaling-network regulation	Improved multi-stress tolerance	[35]

5. Role of Different Beneficial Microbial Groups in Stress Mitigation

5.1 Plant Growth-Promoting Rhizobacteria

One of the most significant beneficial microorganisms that are used in stress mitigation is plant growth-promoting rhizobacteria (PGPR). Their presence promotes plant growth by production of phytohormones, solubilization of nutrients, release of siderophores, activity of ACC deaminase, and activation of antioxidant defense. In case of drought, rhizosphere-related bacteria may enhance root growth, water uptake, and physiological stability, which can help to produce drought-resistant crops [36]. The engineering of rhizosphere with beneficial microorganisms is thus becoming a viable strategy to enhance crop performance in unfavorable environmental conditions [37].

5.2 Arbuscular Mycorrhizal Fungi

AMFs are intimate symbionts of plant roots, which develop their effective absorptive surface by elaborating hyphae networks. These fungi enhance phosphorus absorption, water absorption, ion equilibrium and drought and salinity resistance. They also affect plant signaling and rhizosphere microbial assembly proving that beneficial fungal symbionts are significant parts of the larger plant microbiota [38]. Host genotype, soil conditions, and interactions with the other microbial groups, however, determine their ecological effectiveness [39].

5.3 Endophytic Bacteria and Fungi

Endophytic bacteria and fungi inhabit plant tissues as non-pathogenic and some are able to confer tolerance to environmental stresses by modulating hormones, activating antioxidants, accumulating osmolytes, and improving nutrient uptake. Environmental conditions, the stage of plant development, the properties of soil, and the diversity of microbes surrounding them affect their abundance and functional contribution [40]. The advantageous endophytes are then regarded as promising targets for manipulation of plant-associated microbiomes [41].

5.4 Rhizobia and Other Nitrogen-Fixing Microorganisms

Nitrogen-fixing microbes like rhizobia play a part in plant nutrition by fixing nitrogen in the atmosphere into biologically useful forms. Enhanced nitrogen availability helps plants to grow and recover in nutrient limitation and stress. More and more attention is paid to precision microbiome management aimed at using these functional groups and aligning microbial inoculants with specific crops, soils, and agroecosystems [42].

5.5 Actinobacteria

Another functionally important group of plant-associated microorganisms is represented by actinobacteria. Most species secrete antimicrobial compounds, extracellular enzymes, phytohormones and stress-

protective metabolites. They are helpful members of plant stress resilience due to their ability to survive in nutrient-poor, salty, or dry environments. Microbiome-mediated resistance, in general, relies on the interaction of various microbial taxa and not on individual microorganisms [43].

5.6 Microbial Consortia and Synthetic Microbial Communities

The microbial consortia are organisms with complementary functions, such as mobilizing nutrients, maintaining hormonal balance, suppressing pathogens, and withstanding stress. Synthetic microbial communities offer a more tightly controlled method whereby desired microorganisms are compiled to confer plant-beneficial purposes. These may be more stable than single-strain inoculants, but their performance needs to know about community assembly, compatibility, persistence, and ecological context. The focus of research is thus more on how to transfer microbiome knowledge into field-effective applications that can be reproduced and applied in sustainable agriculture [42,44]. Figure 2 shows the complementary functional roles of the key beneficial microbial groups in alleviating environmental stress schematically.

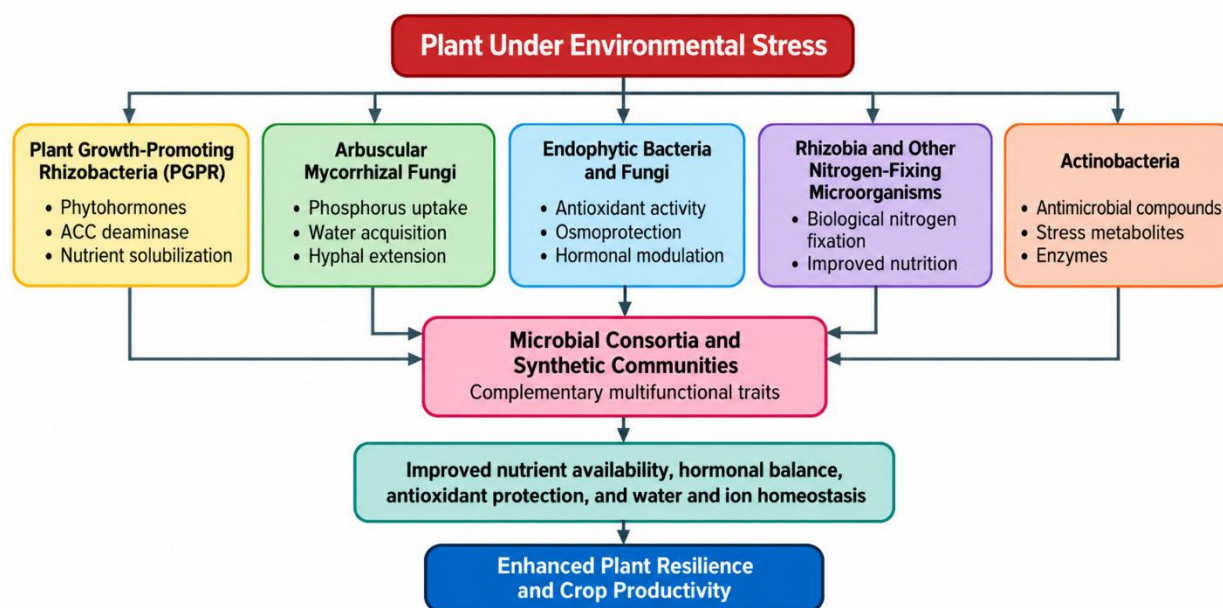


Figure 2 design: Functional roles of beneficial microbial groups

6. Molecular and Omics-Based Insights into Plant–Microbe–Stress Interactions

6.1 Genomics and Metagenomics

Genomics and metagenomics have taken center stage in establishing genes, pathways and functions of microbes involved in stress tolerance of plants. These methods allow describing the plant-associated microbial communities without cultivating them and assist in uncovering genes that act in the production of phytohormones, nutrient uptake, ACC deaminase, and protection against stress. This type of functional

knowledge facilitate microbiome engineering approaches to enhance the growth of plants and biological control in unfavorable environments [45]. Genomic research on PGR can also be helpful in identifying the characteristics of stress adaptation and sustainable crop production [46].

6.2 Transcriptomics

Transcriptomic analysis give an understanding of the gene expression alterations that occur when plants are in contact with useful microorganisms during drought, salinity, or heavy-metal stress. It can show gene activation of antioxidant enzyme-associated genes, osmotic regulation, ion transport, hormone signaling, and defense pathways. Rhizobacteria that produce ACC deaminase, such as, have the ability to affect stress-responsive signaling and enhance drought tolerance by altering plant physiological responses [47]. The transcriptomic methods thus serve to explain how microbial inoculation alters the molecular response of plants in response to environmental stress.

6.3 Proteomics

Proteomics is a complement to transcriptomics that can help recognize stress-responsive proteins and enzymes that are directly involved in plant adaptation. Changes in protein levels can include antioxidant defense, photosynthesis, energy metabolism, membrane stability, and nutrient transportation. Multi-growth-promoting PGPR can activate multiple biochemical pathways at once, and proteomic analysis can be used to learn how they interact in a complex environment (stressful agricultural conditions) [48].

6.4 Metabolomics

Using metabolomics, small molecules that are part of plant-microbe interactions and stress adaptation can be detected, such as amino acids, organic acids, sugars, phenolics, and phytohormones. Alterations in these metabolites have the ability to reflect better osmotic regulation, antioxidant potential, and nutrient conditions. Plant growth regulators and promoters have the potential to provide substantial impacts on the metabolic functions and performance of crops, particularly in rainfed conditions [49]. The complementary contributions of major omics platforms to the investigation of plant–microbe–stress interactions are compared in Table 3.

Table 3. Omics technologies used to investigate plant–microbe–stress interactions

Omics approach	Primary target	Information generated	Application in stress research	References
Genomics	DNA/genes	Functional genes and genetic potential	Identification of stress-tolerance traits	[45]
Metagenomics	Community DNA	Taxonomic and	Identification of stress-	[45]

		functional microbial profiles	associated microbial functions	
Transcriptomics	RNA transcripts	Differential gene expression	Identification of activated stress pathways	[47]
Proteomics	Proteins	Protein abundance and enzyme activity	Antioxidant, metabolic and defense responses	[48]
Metabolomics	Metabolites	Organic acids, sugars, hormones and phenolics	Characterization of metabolic adaptation	[49]
Microbiome sequencing	Microbial markers/community DNA	Microbial community composition	Detection of stress- associated taxa	[50]
Multi-omics	Integrated molecular layers	Systems-level interaction networks	Comprehensive stress- response interpretation	[51]

6.5 Microbiome Sequencing

Massive sequencing of the microbiome assists in the description of changes in the composition and diversity of microbial communities in response to environmental stress. It is especially effective in determining taxa related to drought, salinity and soiled soils. Plant-associated microorganisms have the capacity to modify stress signaling and increase tolerance to toxic metals, and sequencing methods are significant in connecting community structure to functional stress responses [50].

6.6 Multi-Omics Approaches

A combination of genomics, transcriptomics, proteomics, and metabolomics can give a systems-level perspective on the interaction between plants and microbes. Multi-omics methods can be used to relate the composition of microbial communities to host gene expression, protein activity, and alterations in metabolites. This applies particularly to complex symbioses, including arbuscular mycorrhizal associations, which enhance biomass, root development, and nutrient uptake in drought stress situations [52]. Figure 3 depicts the combination of various omics layers into a systems-level understanding of plant-microbe interactions to environmental stress.

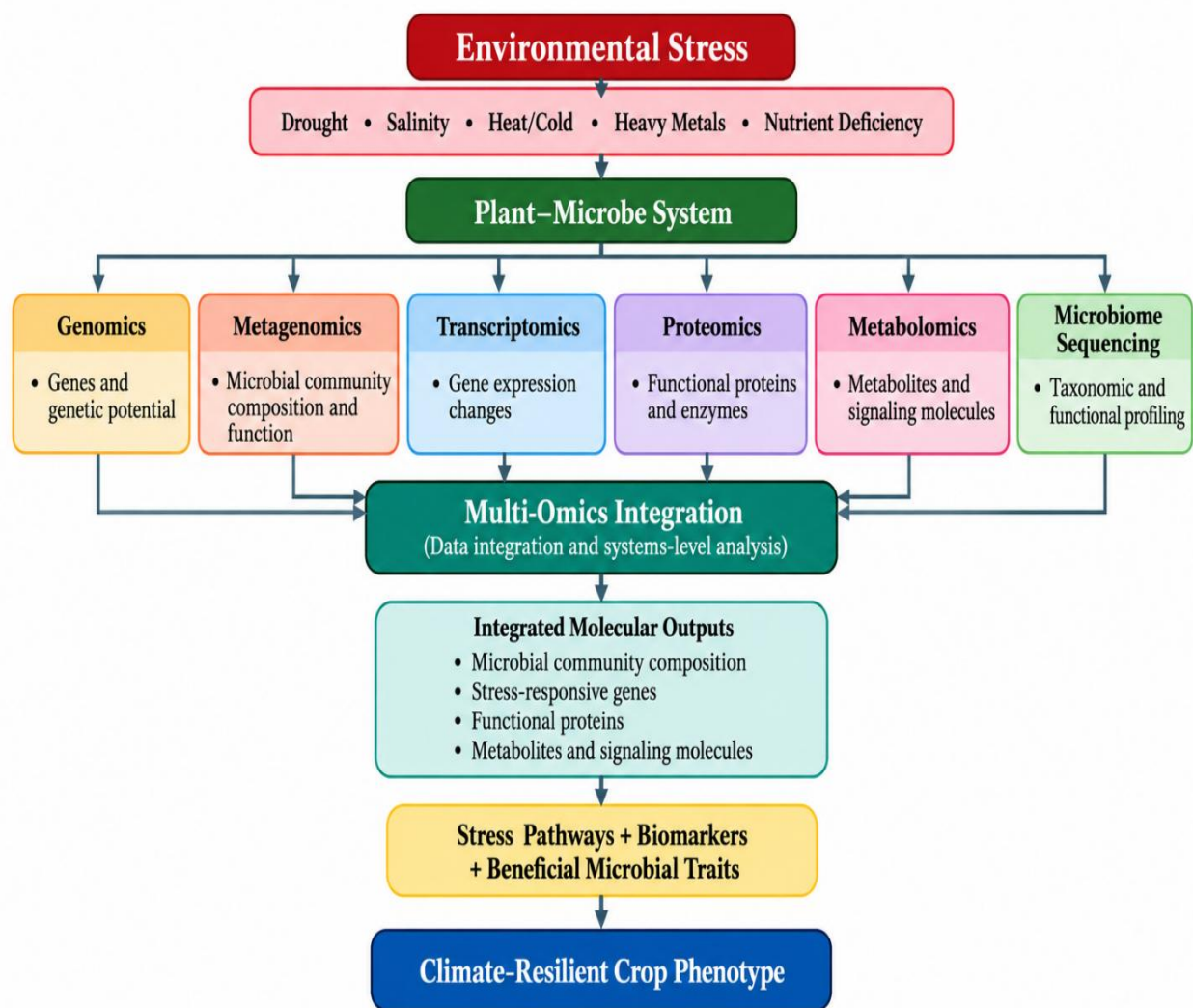


Figure 3 design: Multi-omics integration framework

6.7 Identification of Stress-Responsive Microbial and Plant Genes

The candidate genes that are implicated in stress tolerance, microbial colonization, ion homeostasis, antioxidant activity, and symbiosis signaling can also be identified using omics technologies. Arbuscular mycorrhizal fungi may also mediate salty habitats, modulating plant molecular and physiological processes that enhance stress tolerance and ionic homeostasis [51]. The discovery of these stress-responsive genes can aid in breeding in the future, engineering microbiomes, and tailored microbial interventions to climate-tolerant agriculture. Figure 4 outlines the steps involved in the evolution of the perception of environmental stress to the molecular characterization and identification of microbial-assisted stress-resilience characteristics.

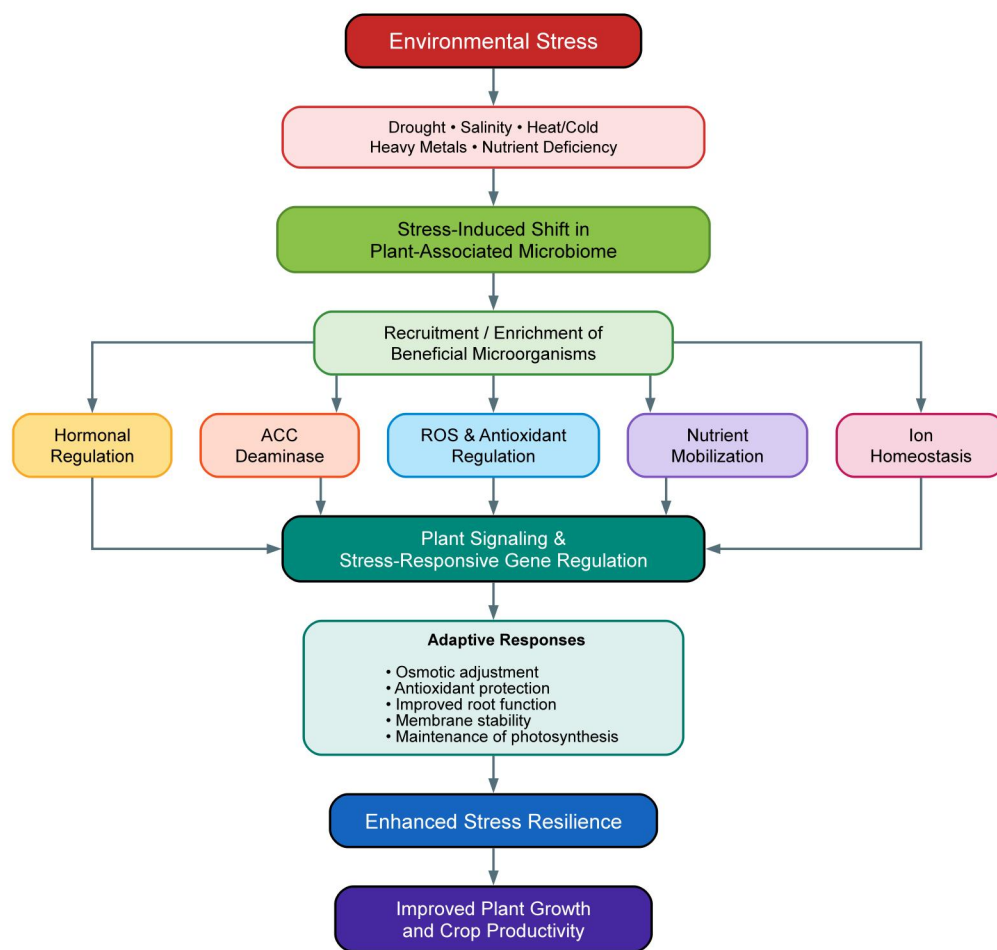


Figure 4 design: Molecular pathway from stress exposure to resilient phenotype

7. Agricultural Applications, Challenges, and Future Perspectives

Microbial biofertilizers, biostimulants and stress-tolerant inoculants are potential solutions to enhancing crop output in drought, salty, and degraded-soil environments. The beneficial microbes would be able to increase nutrient uptake, stabilize stress-related pathways, and support physiological adaptation, and halotolerant bacteria reduce the harm caused by salinity through the regulation of secondary metabolites and molecular responses [53]. Such applications are especially pertinent since salt stress affects ion balance, signaling, and plant growth at a variety of molecular scales [54].

The activity of microbial inoculants in the field, however, is less predictable than that in controlled laboratory conditions due to variation in soil properties, climate, crop genotype and native microbial communities. The difficulties associated with formulation, shelf life, storage, delivery, and host-microbe-environment specificity need to be tackled, however. Future studies must concentrate on strong microbial consortia, microbiome engineering and synthetic communities which work reliably in a variety of agroecosystems and can be used in sustainable and climate-smart agriculture.

8. Conclusion

Plant–microbe interactions are one of the basic biological strategies by which plants cope with the environment and continue to grow under adverse conditions. Plant growth-promoting rhizobacteria, arbuscular mycorrhizal fungi, endophytes, rhizobia, actinobacteria and microbial consortia improve plant resistance by several complementary mechanisms. These include phytohormone regulation, ACC deaminase activity, osmolyte accumulation, exopolysaccharide production, antioxidant defense, nutrient mobilization and modulation of stress-responsive genes. These interactions help to improve root architecture, photosynthesis, water-use efficiency, ion balance, and systemic drought, salt, temperature, heavy metals, and nutrient-deficient soil. The molecular interactions between plants and microbes and plant–stress interactions are also being further understood with the advancement of genomics, transcriptomics, proteomics, metabolomics, microbiome sequencing and integrated multi-omics approaches. On an agricultural level, microbial biofertilizers, biostimulants and designed microbial communities have potential in lowering inputs of chemicals and boosting climate resilience. But field performance, formulation stability, storage, delivery and specificity of host–microbe–environment are still big issues. Future studies should thus focus on field scale validation, stabilization of synthetic communities, precision microbiome engineering, and linking with crop breeding and soil management. This use of plant-associated microbiomes can lead to more productive, resource efficient and climate-friendly agri-systems.

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