

## Exploring ecotypic plant adaptations and the influence of microbiota on mitigating environmental challenges

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### Abstract

The idea of ecotypes, which refer to unique groups of plants that have evolved to flourish in specific habitats, is gaining attention owing to climate fluctuations and changes in the associated microbiota. The term "ecotype" described plant populations that are specially adapted to particular environments, as revealed by common garden experiments showcasing genetically distinct characteristics. This concept remains relevant in modern plant science, where garden experiments continue to uncover how natural selection promotes species diversity, underscoring the crucial role of the plant microbiota in adaptation. Recent research has highlighted the microbial interactions that aid plants in adapting to environmental stress. Plants that shape soil microbial communities exhibit differential responses along ecological gradients owing to environmental stressors that influence interactions with soil microorganisms. Understanding the differentiation within plant populations and the emergence of new species is vital for discerning natural selection patterns. Environmental stressors profoundly impact global crop production, whereas plant-microbiota symbioses significantly influence plant growth and defense through nutrient acquisition and metabolite synthesis. Plant adaptation mechanisms include enzymatic antioxidant production and osmolyte accumulation, which are regulated by phytohormones that orchestrate responses to biotic and abiotic stressors, respectively. Despite breeding and genetic engineering efforts, progress in enhancing plant tolerance to extreme conditions remains limited, necessitating the development of sustainable agricultural alternatives. This study offers a comprehensive overview of recent advances in plant ecotype research, particularly focusing on symbiotic relationships with the microbiota and traits that contribute to improved nutrient uptake and plant health.

**Keywords:** ecotypic plant; influence; microbiota; mitigating environmental

### Introduction

An ecotype is a unique cluster of plants that has adapted to flourish in specific habitats, a concept that has garnered growing interest given climate variability and its associated microbiota. The distinction between the genetic and environmental effects within the domain of plant evolutionary ecology has prompted the development of robust experimental approaches. The term "ecotype" was originally introduced by Turesson in 1922 to characterize plant populations exceptionally suited to distinct environments. These distinctions were

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established through common garden experiments, wherein observable traits, apart from the genetic basis set ecotypes, were used (van Wallendael *et al.*, 2022). Plants play a pivotal role in the composition of soil microbial communities. These interactions can be both beneficial and detrimental, because microbes may either cooperate or compete with each other. Environmental factors coupled with natural selection contribute to phenotypic diversity observed along ecological gradients. As plants face various environmental stresses, they undergo adaptation mechanisms that are unique to individual species. For example, different ecotypes of a species may exhibit distinct responses to environmental changes, thereby influencing its interactions with soil microorganisms. Notably, low-elevation ecotypes tend to exhibit higher chemical defenses even as elevation increases (Bakhtiari *et al.*, 2019). Plant species frequently form symbiotic relationships with microorganisms to obtain nutrients, with minimal energy expenditure. The distribution of these plants is influenced by various factors such as root exudates, crop species, and cultivar. To adapt to environmental conditions and activate defense mechanisms, plants produce antioxidant enzymes and accumulate osmolytes such as proteins, proline, glycine betaine, phenolic compounds, and soluble sugars, thereby adjusting their cellular osmotic and water potential. Phytohormones play a crucial role in regulating developmental processes and signaling networks, allowing plants to respond effectively to both biotic and abiotic stresses for survival. Significant progress has been made in understanding the roles of ethylene, salicylic acid, and jasmonates in plant responses to abiotic stresses. Additionally, other hormones, such as auxin, gibberellic acid, brassinosteroids, abscisic acid, and peptide hormones, are involved in various plant defense signaling pathways. Ongoing interactions between plant-associated microbes and their hosts may lead to the production of biologically active secondary metabolites. Advances in molecular, analytical, and next-generation sequencing technologies have enabled the examination and characterization of the microbial communities inhabiting plants. Cutting-edge sequencing methodologies such as genomics, metabolomics, metagenomics, and proteomics generate extensive datasets that offer valuable insights into cultivated accessions across different ecotypes (Egamberdieva *et al.*, 2017). Turesson's enduring influence resonates with modern plant science as researchers continue to employ garden experiments to decipher how natural selection promotes diversity within plant species. Central to this understanding is the recognition of the pivotal role of the plant microbiota in facilitating adaptation. A healthy plant harbors a diverse array of microbiota that contribute to its well-being and resilience against pathogens. However, the intricacies of the interaction between ecotype-driven local adaptability and the rhizosphere microbiota remain largely unexplored. It is essential to address this knowledge gap to propel the development of climate-smart agriculture and to promote sustainable crop production. Recognizing the significance of the plant microbiota in fostering plant growth and defense underscores the need to unravel the complexities of multipartite interactions that shape plant phenotypes. Recent studies have emphasized that microbial interactions aid plants in learning and adapting to edaphic stress (Santoyo *et al.*, 2021). Understanding the variance within plant populations and the evolution of new species is essential for uncovering the nuances of natural selection in plant ecotypes. Environmental stressors such as land degradation, water scarcity, climate fluctuations, pests, diseases, heavy metal contamination, and salinity have significantly affected crop production worldwide. Microbiomes, which comprise various microorganisms in the soil, contribute significantly to plant growth through diverse activities, such as nutrient fixation, mineralization, and solubilization. They also produce compounds, such as siderophores and antibiotics, while interacting with plant roots and releasing growth-stimulating substances, such as auxins and gibberellins (Egamberdieva *et al.*, 2017). For example, genomic data from barley and avocado have provided significant insight into the effects of their ecotypes. Despite efforts in breeding and genetic manipulation to enhance plant resilience under extreme conditions, the progress remains limited. Therefore, there is an urgent need to explore sustainable alternatives for agricultural production, particularly under adverse environmental conditions.

In this study, we provide a comprehensive overview of the latest advancements in plant ecotype research focusing on the symbiotic relationships between plants and their associated microbiota. We explored the traits that contribute to enhanced nutrient uptake and overall plant.

## **Role of ecotypes and soil microbiota**

In living systems, plants coexist with a diverse range of microorganisms, collectively known as microbiota. These microbes inhabit the internal tissues of plants (endosphere) and the external surfaces (episphere). The presence of bacteria, viruses, and fungi in microbiota significantly influences the ecology and physiology of plants. Various factors, including those associated with the host, microorganisms, and environment, play crucial roles in shaping the structure and diversity of the plant microbiota (Dastogeer *et al.*, 2020). Ecotypes, also known as ecosystems, are unique variations within species adapted to specific environments. Despite displaying phenotypic diversity due to environmental differences, ecotypes typically maintain their fertility and vigor, even when interbreeding with neighboring ecotypes (Sher and Molles, 2015). Multi-cellular species maintain various microbial associations that can be commensal, symbiotic, or parasitic (De Sordi *et al.*, 2019). Plants exhibit remarkable adaptability to environmental challenges through ecotypic modifications that are facilitated by both internal and external factors (Young *et al.*, 2018). The ability of plants to adapt allows them to effectively manage a range of challenges, including nutrient deficiency and toxicity. Importantly, plants form symbiotic connections with nearby soil microbes, which greatly affects their robustness and resistance to environmental stressors (Cavicchioli *et al.*, 2019). The composition and dynamics of soil microbial communities are intricately shaped by factors, such as pH, moisture levels, temperature, root exudates, and anthropogenic activities (Daniel, 2005). Within this intricate microbial milieu, two main categories of microorganisms thrive: endophytes and epiphytes, each playing distinct roles in plant-microbe interactions (Whipps *et al.*, 2008). Plants serve as the primary carbon source for soil microbes through leaf litter and root exudates, thereby fostering a symbiotic exchange that is crucial for plant adaptability. Soil microbes further augment plant resilience by releasing growth regulators and enhancing phytohormone production, thereby promoting adaptive responses (Gouda *et al.*, 2018). In mutualistic relationships, plants reciprocate by exchanging hexose sugars with fungal symbionts for inorganic phosphate (Chibucos and Tyler, 2009). Moreover, certain beneficial bacteria, known as growth-promoting bacteria (GPB), play pivotal roles in facilitating plant growth and defense mechanisms. The functions of GPBs include nitrogen fixation, mineral solubilization, hormone synthesis, and pathogen suppression (Bloemberg and Lugtenberg, 2001). Root-associated microorganisms are pivotal for improving plant resilience to drought, through their effects on plant physiology and biochemistry. Studies have demonstrated that the interactions between plants and rhizosphere microbes bolster stress resistance and promote plant growth. These microbial activities encompass diverse processes including biofilm formation, hormone level regulation, osmotic adjustment, enhancement of antioxidative enzymes, facilitation of water and nutrient uptake, and regulation of gas exchange (Soumyadev *et al.*, 2022). Furthermore, that fungal communities undergo more significant alterations than bacterial populations during drought stress.

## **Ecotypic adaptations and microbial dynamics in plant communities**

Numerous studies have emphasized the unique adaptations of various plant ecotypes to environmental stress. For instance, in Kerala, India, two coconut ecotypes, Bedakam and Annur, demonstrated remarkable resilience to drought and salinity (Rajesh *et al.*, 2014). Similarly, in the Mediterranean region, four ecotypes of *Crocus sativus* have been examined for their capacity to thrive under challenging conditions (Cardone *et al.*, 2021). Furthermore, the importance of ecotypic adaptations extends to pH tolerance, as evidenced by the significant lignin production observed in limestone ecotypes of the wild grass *Holcus lanatus*. This adaptation, along with the involvement of non-arbuscular mycorrhiza, has been confirmed using transcriptome analysis (Young *et al.*, 2018). The development of plant ecotypes is intricately linked to their environment, as exemplified by the locally adapted *Mimulus guttatus* ecotypes, which display genetic variations that affect

rhizosphere ecosystems (Bowsher *et al.*, 2020). In *Arabidopsis thaliana* leaves, 19 microbiota have been identified as crucial components of microbial communities, highlighting the importance of these microorganisms in plant health (Almario Juliana *et al.*, 2022). Further insights into the dynamics of microbial communities within plant ecotypes were gained through studies on the major prairie grass, *Andropogon gerardii*. Investigations into the rhizospheres of the three *A. gerardii* ecotypes revealed variations in bacterial populations but not in overall microbial communities (Sarkar Soumyadev *et al.*, 2022). Over time, the processes of domestication and selective breeding have led to discernible differences in the microbiota of current crop varieties compared with their wild progenitors. A study assessing the rhizosphere of 20 wild barley (*Hordeum vulgare*) genotypes along four domesticated barley cultivars highlighted the distinct ecological and geographical constraints imposed by their respective host plants (Alegria Terrazas *et al.*, 2020). Remarkably, bacterial communities exhibit specific colonization patterns even among plant species that share the same habitat. For instance, research involving *Lotus japonicus* and *A. thaliana* grown together revealed indications of preferential colonization by certain commensal bacteria, emphasizing the influence of host preference within a community setting (Wippel *et al.*, 2021).

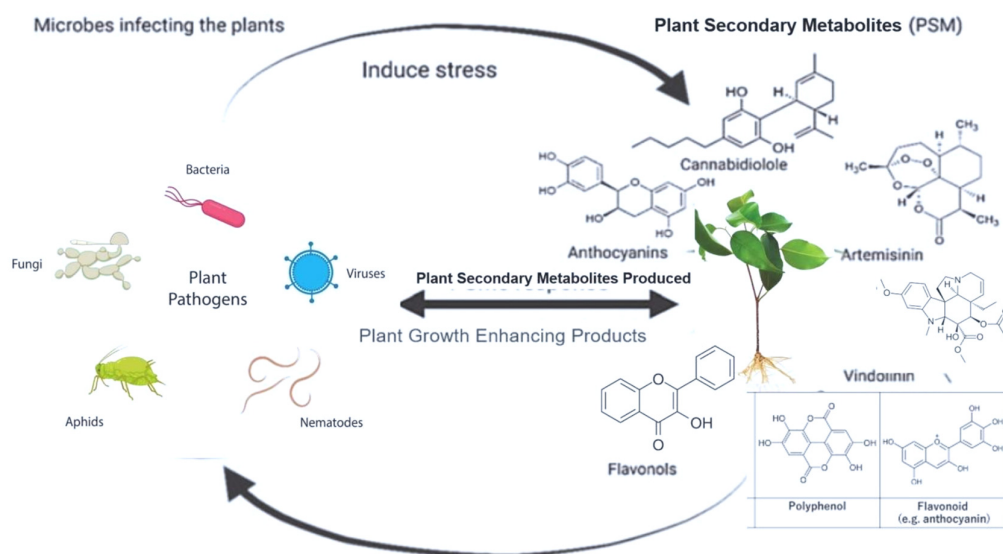
### **Diverse microbial interactions in plant stress responses**

Research on *Arabidopsis* ecotypes has revealed the positive effects of microbes during periods of cold stress (Etemadi *et al.*, 2018). After experiencing drought stress, the soil surrounding the rhizosheath exhibited a notable increase in *Acinetobacter* and *Citrobacter* populations, indicating that drought stress promotes microbial aggregation in this area. Furthermore, investigations of ecotype-specific rhizospheric microbiomes have underscored the variability in the responses to drought stress among switchgrass plants (Liu *et al.*, 2021). In karst environments, the Donggang Pasque flower (DPF) exhibits a wider array of microbial species in its natural habitat than in its cultivation. Despite notable distinctions, both wild and cultivated DPF plants commonly harbor a fundamental bacterial community as endophytes. These bacterial strains play a pivotal role in promoting plant growth through nitrification, nutrient absorption, and phytohormone synthesis, resulting in discernible variations in the growth patterns of *A. thaliana* (Dutta *et al.*, 2021). Gupta *et al.* (2020) investigated the efficacy of two strains of *Pseudomonas fluorescens*, cultivated in the rhizosphere, in combatting mustard blight caused by *Alternaria brassicae*. Singer *et al.* (2019) observed that switchgrass (*Panicum virgatum*) harbors diverse microbiota that is particularly rich in *Alphaproteobacteria* and *Actinobacteria*. Luo *et al.* (2022) identified common microbiota cores within *Burkholderiaceae* and *Sphingomonas* families. Additionally, Pang *et al.* (2020) emphasized the prevalence of the *Enterobacteriaceae* family among root microbes in rice ecotypes, particularly in response to highland climate.

### **Roles and regulation of plant secondary metabolites (PSMs)**

Plant secondary metabolites (PSMs) are comprised of a diverse range of chemical compounds that originate from various biosynthetic pathways. This expansive category encompasses approximately 100,000 distinct compounds, with ongoing discoveries continually broadening this diversity. Classified into groups such as flavonoids, alkaloids, steroids, terpenes, and phenolics (Kessler and Kalske, 2018), these secondary metabolites are generated by plants in response to environmental cues and interactions with microbes, serving diverse functions, including defense against pathogens. The presence of microbial colonies can induce changes in the plant biosynthetic pathways, potentially leading to the synthesis of new metabolites (Huang *et al.*, 2014). Endophytes, microorganisms residing within plant tissues, are increasingly being acknowledged for their

influence on plant metabolism and production of various secondary metabolites. Studies have shown that Poplar plants inoculated with *Paenibacillus* spp. exhibit elevated levels of asparagine, urea, and threitol. Similarly, inoculation with *Enterobacter ludwigii* resulted in a significant increase in vanillic acid levels, along with decreased concentrations of catechin, esculin, arbutin, astringin, pallidol, ampelopsin, D-quadrangularin, and isohopeaphenol. Specific secondary metabolites (Figure 1), such as calexin and glucosinolates, have been shown to increase in response to encounters with pathogenic microbes such as *Pseudomonas syringae* pv. tomato (Pst) (Brotman *et al.*, 2012). These plant secondary metabolites, summarized in Table 1, play vital roles as mediators of abiotic stress response. They facilitate improved nutrient and water absorption while reducing the generation of reactive oxygen species (ROS) by enhancing root peroxidase production (Naylor and Coleman-Derr, 2018).



**Figure 1.** Plants produce secondary metabolites as a defense mechanism against stress and pathogens. Specific beneficial microbes stimulate plants to boost secondary metabolite production, thus increasing the overall value of the plant

**Table 1.** Plants interact with various microorganisms resulting in the production of secondary metabolites

Serial No	Microorganism	Plant spp.	Secondary metabolite	References
1	<i>Pseudonocardia</i> sp.	<i>Artemisia annua</i>	Artemisinin	(Li <i>et al.</i> , 2012)
2	<i>Curvularia</i> sp. and <i>choanephora infundibulifera</i>	Bookoo kush, Burmese, maui wowie, white widow, and sour diesel	Cannabidiol	(Pandey <i>et al.</i> , 2016)
3	<i>Azospirillum</i> sp. B510	Rice plant	p-Coumaric and ferulic acid	(Yasuda <i>et al.</i> , 2009)
4	<i>A. Brasilense</i> CFN-535, <i>Az. Lipoferum</i> CRT1 and <i>A. brasilense</i> UAP-154	Maize cultivars (PR37Y15 and DK315)	Zoxazinoids	(Walker <i>et al.</i> , 2011)
5	<i>Azospirillum lipoferum</i>	Rice cultivars (cigaron and nipponbare)	Cigaron	(Chamam <i>et al.</i> , 2013)
6	<i>Pseudomonas syringae</i>	Taxane	<i>Taxus globosa</i> and <i>Taxus media</i>	(Ramirez-Estrada <i>et al.</i> , 2015)

7	<i>Protomyces gravidus</i>	<i>Ambrosia artemisiifolia</i>	Thiarubrine A	(Bhagwath and Hjortsø, 2000)
8	<i>Rhizoctonia solani</i>	<i>Hyoscyamus muticus</i>	Sesquiterpenes	(Singh <i>et al.</i> , 2014)
9	<i>Phytophthora parasitica</i>	<i>Cichorium intybus</i>	Coumarin	(Bais <i>et al.</i> , 2000)

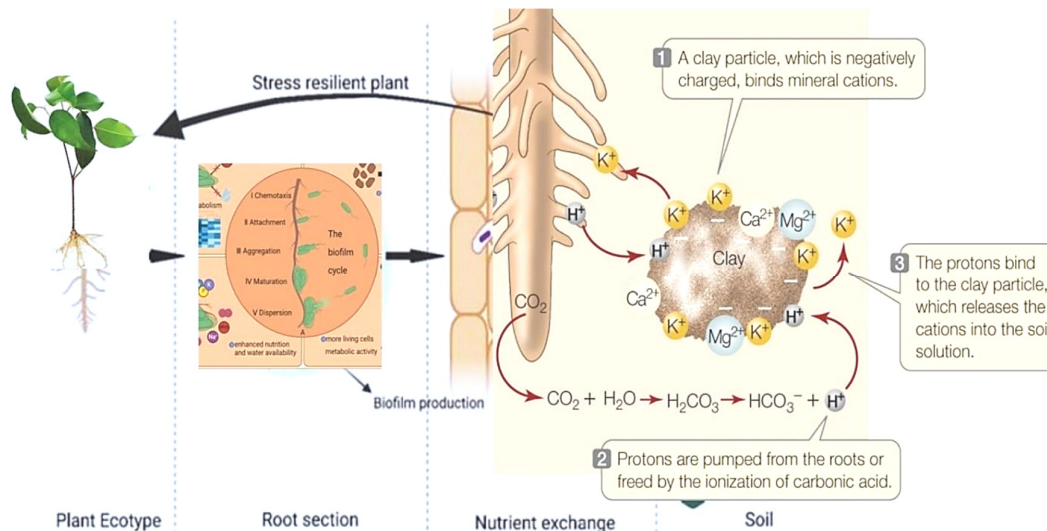
### Interactions between plant ecotypes and rhizosphere microbiota

Different plant ecotypes, shaped by genetic adaptations to specific local conditions, uniquely engage with their environments. Recent studies have revealed the ever-changing composition of the microbiota surrounding the plant roots in response to various environmental factors (Liu *et al.*, 2021). Microorganisms, including bacteria, viruses, fungi, algae, and archaea, form intricate communities in the soil, and are primarily sustained by nutrients released by plant roots, such as root exudates and secondary metabolites (Subrahmanyam *et al.*, 2020). Compounds, such as flavonoids, strigolactones, and terpenoids, present in root exudates facilitate underground chemical communication. Investigations into ecotypic plant pathogens, such as switchgrass (*Panicum virgatum*), have revealed that symbiotic microbes play a role in nutrient absorption, enhance leaf stress tolerance, and exhibit specific distributions across root zones (van Wallendael *et al.*, 2022). Plant growth-promoting rhizobacterial strains exist in various taxonomic groups that coexist in the soil environment (Al-Khayri and Khan, 2024). Despite the wide array of microbiomes associated with different plant species and varieties, evidence indicates that plants actively attract beneficial microbial partners via root-derived signals (Jacoby *et al.*, 2017). Microorganisms in the soil are essential for supporting the health and productivity of switchgrass plants while also governing soil fertility and nutrient cycling (Wagg *et al.*, 2014). In a reciprocal transplant study involving two *Mimulus guttatus* ecotypes adapted to distinct environments, researchers found that the interaction between plant roots and soil microorganisms significantly influences plant well-being and productivity. This highlights the capacity of various *M. guttatus* ecotypes to flourish in novel habitats and to engage with phylogenetically linked rhizosphere communities. Nonetheless, disparities in rhizosphere communities were noted between the ecotypes at both locations, partly due to variations in the presence or absence of microbial taxa, particularly less common taxa (Bowsher *et al.*, 2020). Understanding and assessing the mutualistic relationships between plants and microbes is crucial for ecotypic plant production systems, because they can enhance yields, aid in nutrient uptake and stress resilience, and contribute to ecological health, such as carbon sequestration and soil biodiversity enhancement (Hestrin *et al.*, 2021). Rhizosphere microbiome plays a pivotal role in abiotic stress tolerance, nutrient acquisition, and defense against plant pathogens. Consequently, researchers require a thorough understanding of the molecular mechanisms and dynamics of the rhizosphere microbiome, which can be categorized as direct and indirect mechanisms (Subrahmanyam *et al.*, 2020). Direct mechanisms involve the production of phytohormones, ACC deaminase, nitrite synthesis, sulfide oxidation, organic phosphate mineralization, and inorganic phosphorus solubilization. In contrast, indirect mechanisms include interference with quorum sensing signaling, induced systemic resistance, biofilm formation, competition for nutrients and space, synthesis of antibiotics, antimicrobial compounds, or lytic enzymes, and inhibition of quorum sensing signaling (Díaz-Rodríguez *et al.*, 2021). The enhanced plant development observed in plants inoculated with plant growth-promoting rhizobacteria (PGPR) may be partly attributed to improved nutrient absorption resulting from growth-promoting activities (Calvo *et al.*, 2019).

### Role of bacterial chemical synthesis in plant growth and nutrition

Bacterial chemical synthesis enhances the absorption of essential nutrients and micronutrients from the soil while also playing a crucial role in producing plant growth regulators like IAA (indole-3-acetic acid),

deaminase, and ACC. These growth-promoting substances not only accelerate growth, but also counteract the inhibitory effects of stress-induced ethylene on plant development. Moreover, these bacteria contribute to essential processes, such as iron and zinc adsorption, phosphorus and potassium solubilization, atmospheric nitrogen fixation, and the synthesis of plant hormones (Munir *et al.*, 2022). Plant growth-promoting rhizobacteria (PGPR), along with other beneficial bacteria, such as actinomycetes, are key components of bacteria-based plant biostimulants (BSs), including *Acetobacter*, *Agrobacterium*, *Azospirillum*, *Azotobacter*, *Bacillus*, *Burkholderia*, *Enterobacter*, *Frankia*, *Pseudomonas*, *Rhizobia*, *Serratia*, and *Streptomyces*. These biostimulants enhance root formation, growth, and stress tolerance of plants. Diazotrophs, particularly nitrogen-fixing bacteria, play crucial roles in maintaining plant nutrition, particularly during periods of resource scarcity. Symbiotic rhizobia, (Figure 2) which utilize nitrogenase, can fulfill up to 90% of the nitrogen needs of host legumes by converting atmospheric elemental nitrogen into ammonia. Moreover, non-symbiotic diazotrophic and N<sub>2</sub>-fixing bacterial species have been shown to enhance plant nitrogen uptake. Nitrogen levels influence cellular nitrate concentrations, affecting root cell membrane hydrodynamic characteristics, and facilitating water movement from the soil into root cells. Aquaporin expression, which is responsible for regulating water transport, varies depending on nitrogen availability, and potentially links nitrogen levels to aquaporin activity (Bardi and Malusa, 2012). Nitrogen input may upregulate the expression of root-specific aquaporin genes associated with root hydraulic conductivity such as OsPIPs and OsTIPs. The nitrate transporter NRT2.1 may contribute to this process by influencing the transcript levels of PIP aquaporins in *Arabidopsis*, subsequently affecting root hydraulic conductivity. Additionally, research has suggested that ammonium, unlike nitrate, may enhance the drought resilience of certain ecotypic plants. Certain Gram-positive microorganisms such as *Thermoleophilum* and *Actinobacteria* have been shown to facilitate the transition of lowland rice ecotypes from paddy fields to upland conditions (Xiong *et al.*, 2021).



**Figure 2.** Plants and soil participate in the exchange of various nutrients through their roots

### Role of fungi chemical synthesis in plant growth and nutrition

Inoculating seedlings with rhizosphere microflora derived from mature switchgrass stands led to notable enhancements in both shoot and root weights along with increased nitrogen and phosphorus uptake (Brejda *et al.*, 1998). For instance, *Trichoderma* species have been shown to amplify root-to-shoot signaling by stimulating the synthesis of various hormones that are crucial for enhancing nutrient solubility, uptake, and assimilation

processes. Studies have suggested that Arbuscular Mycorrhizal (AM) fungi can bolster salt tolerance through diverse mechanisms, such as regulating the  $K^+/Na^+$  ratio within plant cells, facilitating ion salt transport to vacuoles, promoting growth hormone production, and ameliorating soil and rhizospheric conditions. Moreover, AM fungi contribute to osmoregulation by increasing the sugar and electrolyte concentrations, thereby mitigating the adverse effects of salt stress. A series of investigations has shown that AM fungi can enhance antioxidant capacity by activating the plant glutathione ascorbate cycle, leading to increased resistance to salt stress (Koza *et al.*, 2022). Under drought stress conditions, the effect of arbuscular mycorrhizal fungi (AMF) on root morphology is significantly amplified, underscoring the heightened significance of AMF in root adaptation. Of the three examined nutrient uptakes, mycorrhizal involvement in phosphorus (P) absorption surpassed that in nitrogen (N) and potassium (K) uptake. Phosphorus and nitrogen play pivotal roles in influencing plant cell structure and function, governing growth patterns, while potassium levels regulate the upregulation of plant defense mechanisms, accumulation of osmolytes, antioxidant profiles, and enzymatic regulation of plant metabolism. Transcriptome responses observed in *Holcus lanatus* (L.) suggest that both AM and non-AM fungi, particularly certain genera of Ascomycota, contribute to P and Fe nutrition in limestone soils. Conversely, non-AM Ascomycota, notably those associated with *Phialocephala*, may enhance N and K nutrition, reinforce tolerance to metal(loid) ions in acidic bog soils and facilitate ecotype adaptation (Young *et al.*, 2018). Investigation of three sorghum (*Sorghum bicolor*) ecotypes revealed heightened glutamine synthetase (GS) activity in the roots and leaves, along with increased glutamate dehydrogenase (GDH) activity in the roots, indicating that nitrate assimilated by AMF can be directly transported to root cells for utilization and integration into organic structures. These enzymatic modifications might enhance plant development and overall health (Anass *et al.*, 2021).

### **Microbiota's contribution to mitigating environmental challenges**

Plant-associated microbiota is pivotal for mitigating various environmental challenges, including diseases, pests, and other stressors.

### **Soil microbial diversity and agricultural sustainability**

The endeavor to enhance agricultural productivity faces a significant challenge owing to the depletion and degradation of land resources, which disrupts the delicate equilibrium in global agroecosystems. Soil microbial diversity is critical for ensuring the sustainability of agricultural systems and is intricately linked to ecosystem processes. Microorganisms play vital roles in augmenting plant development, productivity, and adaptability (Yadav *et al.*, 2018). These microbes, pertaining to crops, can be categorized into three main types: rhizospheric, phyllospheric, and endophytic. The rhizosphere, which is influenced by plant roots releasing various substances that affect microbial activity, is a prominent example of this interaction. Numerous microbial species from the genera *Azospirillum*, *Alcaligenes*, *Arthrobacter*, *Acinetobacter*, *Bacillus*, *Paenibacillus*, *Burkholderia*, *Enterobacter*, *Erwinia*, *Flavobacterium*, *Methylobacterium*, *Pseudomonas*, *Rhizobium*, and *Serratia* have been identified (Shah *et al.*, 2017). Various bacterial species are commonly associated with plant rhizosphere. For instance, endophytic bacteria inhabit plant tissues without harming their hosts, localize at the point of entry, or spread widely throughout the plant, residing in circulatory systems, cellular compartments, or intercellular spaces (Jacobs *et al.*, 1985; Patriquin and Dobereiner, 1978). A diverse range of endophytic bacteria genera, including *Achromobacter*, *Azoarcus*, *Burkholderia*, *Enterobacter*, *Gluconacetobacter*, *Herbaspirillum*, *Klebsiella*, *Microbiospora*, *Micromonospora*, *Nocardioides*, *Pantoea*, *Planomonospora*, *Pseudomonas*, *Serratia*, *Streptomyces*, and *Thermomonospora*, have been identified across various host plants



such as wheat, chickpea, pea, maize, rice, common bean, and soybean (Yadav *et al.*, 2018). The leaf surface, referred to as the phyllosphere, provides a conducive setting for mutually beneficial relationships between the bacteria and plants. Certain bacteria are specially adapted to thrive on leaf surfaces, enduring harsh conditions, such as temperatures ranging from 40 °C to 55 °C and intense UV radiation. Various bacteria, including *Agrobacterium*, *Methylobacterium*, *Pantoea*, and *Pseudomonas* have been identified within the phyllosphere. These microorganisms associated with crops play vital roles in promoting plant growth. The microbiomes found in epiphytic, endophytic, and rhizospheric habitats have been observed to directly enhance plant growth through processes such as nitrogen fixation, mineral solubilization (e.g., phosphorus, potassium, and zinc), and the synthesis of siderophores and plant growth hormones such as cytokinins, auxins, and gibberellins. In addition, the microbiome significantly affects the occurrence and spread of plant diseases (Erlacher *et al.*, 2014). Fungi and bacteria are the main classes of plant pathogens responsible for plant diseases. The prevailing belief is that the severity of a disease diminishes as host fitness increases. Furthermore, interactions between plant and fungal pathogens fall into two categories: race specific and race specific. For instance, race-specific interactions are well documented in leaf infections, such as rust or powdery mildew fungus (Sacristán and García-arenal, 2008), whereas race-nonspecific interactions occur in various soil-borne pathogens. Infections can spread across plant surfaces or reside internally within the plant tissues. However, our understanding of the factors influencing the ecology of plant pathogens remains limited, primarily because studies of plant infections typically focus on already damaged plants. Despite the availability of specific methods for cultivating and diagnosing plant pathogens, some obligate pathogens cannot be cultured. Despite advancements in cultivation-dependent techniques, there are still microorganisms that can resist cultivation in natural environments (Bai *et al.*, 2015). Imbalances in the soil microbiota, referred to as dysbiosis, may contribute to various diseases such as plant diseases, in which the causative pathogen remains unidentified. Pathogens exhibit versatility in their interactions with plants, adopting various modes such as biotrophs, necrotrophs, obligates, or facultative. For example, fungal pathogens can transition from a non-pathogenic lifestyle to a non-host plant species to an endophytic pathogenic role within the host plant. *Verticillium dahliae*, a fungal pathogen, is often found in the endosphere of numerous plant species (Götz *et al.*, 2006). Various organisms, such as Rhizoctonia, demonstrate biological control efficacy, significantly impacting diverse crops while showing partial host specificity. Investigations into whether microbial diversity consistently underlies the emergence of specific "microbiome ailments" arise from the prevalence of potential pathogens in plants. Microbial invasion can induce shifts in the microbiome, with endophytes potentially aiding in disease control. For instance, Mendes (Rodrigo *et al.*, 2007) The genus *Burkholderia* has proven potential in improving plant performance. In recent decades, a huge diversity of *Burkholderia* spp. have been reported with diverse capabilities of plant symbiosis which could be harnessed to enhance plant growth and development. Colonization of endophytic *Burkholderia* spp. have been extensively studied through techniques like advanced microscopy, fluorescent labelling, PCR based assays, etc., and found to be systemically distributed in plants. (Pal *et al.*, 2022). Notably, pathogens often originate from the Enterobacteriaceae family, which is known for its ability to degrade plant tissues (Erlacher *et al.*, 2014). Crop rotation, dating back to biblical scriptures, was one of the earliest plant protection techniques in history. Its enduring effectiveness in preventing numerous ailments lies in its ability to enhance microbial diversity in the soil through the specificity of the plant microbiome.

### **Impact of water stress on root microbiome**

The increase in abiotic stress, attributed to changing precipitation patterns resulting from climate change, disrupts the supply of the vital nutrients necessary for plant growth. This occurrence is mainly linked to intensified land use and increased fertilizer application (Trenberth, 2011). Understanding how the root microbiome responds to environmental changes is crucial for the development of strategies to enhance plant

stress resilience. These strategies may involve the identification and selective introduction of new plant growth-promoting (PGP) microbes into agricultural areas or the active management of soil communities through farming practices conducive to strengthening plant tolerance to abiotic stress (Schlaeppli and Bulgarelli, 2015). However, scientists still struggle to fully understand the relative influences and complex interactions between soil and plant factors that shape root microbial communities, adding layers of complexity to this pursuit (Naylor and Coleman-Derr, 2018). In this study, we explored how water stress, including flooding and drought, affects plants and subsequently influences their root microbiomes. Land plants, especially crops, face significant challenges when submerged for extended periods, owing to the increasing frequency and severity of floods. Prolonged submersion, particularly affecting non-photosynthetic plant parts, such as roots, leads to reduced oxygen levels, hindering cellular respiration (Voesenek *et al.*, 2006). Understanding how microbial populations respond to flooding is crucial for identifying beneficial bacteria or fungi that are capable of enhancing stress tolerance in plants experiencing hypoxic or anoxic conditions. For example, certain bacteria produce ACC deaminase, which regulates ethylene levels in plants, which is a crucial stress hormone. Bacteria possessing ACC deaminase can alleviate plant stress by breaking down ACC, thereby reducing the ethylene levels. This phenomenon was observed in basil (*Ocimum sanctum*) plants inoculated with ACC deaminase-producing bacteria, demonstrating improved growth and reduced ethylene levels compared with non-inoculated plants (Barnawal *et al.*, 2012). Similarly, in cucumber (*Cucumis sativus*) plants inoculated with *Pseudomonas putida* UW4, which synthesizes ACC deaminase and is subjected to hypoxic conditions, proteomic analysis revealed a shift in protein expression towards those involved in nutrient metabolism, defense stress, and antioxidant activity. This suggests potential mechanisms through which bacteria promote plant growth under stress conditions (Li *et al.*, 2013). Although plant-beneficial microbes have shown resilience in flooded environments, studies focusing on bacterial communities that specifically investigate how non-wetland plant species respond to flooding are lacking. For instance, investigations into root-associated microbial communities in poplar (*Populus* sp.) seedlings subjected to experimental flooding have revealed significant shifts in bacterial composition within the rhizosphere and whole root compartments compared with bulk soil (Graff and Conrad, 2005). Similarly, a study on wheat (*Triticum aestivum*) demonstrated that flooding and nitrogen restriction altered the abundance of certain denitrifying bacteria and reshaped their community structure in the rhizosphere compared with bulk soil samples distant from root influence (Hamonts *et al.*, 2013). The transition from aerobic to facultative anaerobes to strict anaerobes reflects the changes in oxygen availability. This shift towards anaerobic bacteria may contribute to the increased relative abundance of *Aquaspirillum* in flooded poplar rhizosphere and root samples (Whitman *et al.*, 2015). Numerous plants adapt to flooding by forming specialized, gas-filled tissues termed aerenchyma, which aids in oxygen transfer from oxygen-rich shoots to oxygen-deprived roots. Although these tissues are common in aquatic and wetland flora, non-wetland species typically produce them in response to stressors such as flooding (Hartman and Tringe, 2019). When confronted with flooding-induced cell damage, plants activate a defense mechanism involving the release of phytotoxic compounds such as ethanol, lactic acid, and alanine. These substances accumulate in the root tissues of plants such as tomatoes, peas, and maize when exposed to low oxygen levels during aerobic respiration (Badri and Vivanco, 2009).

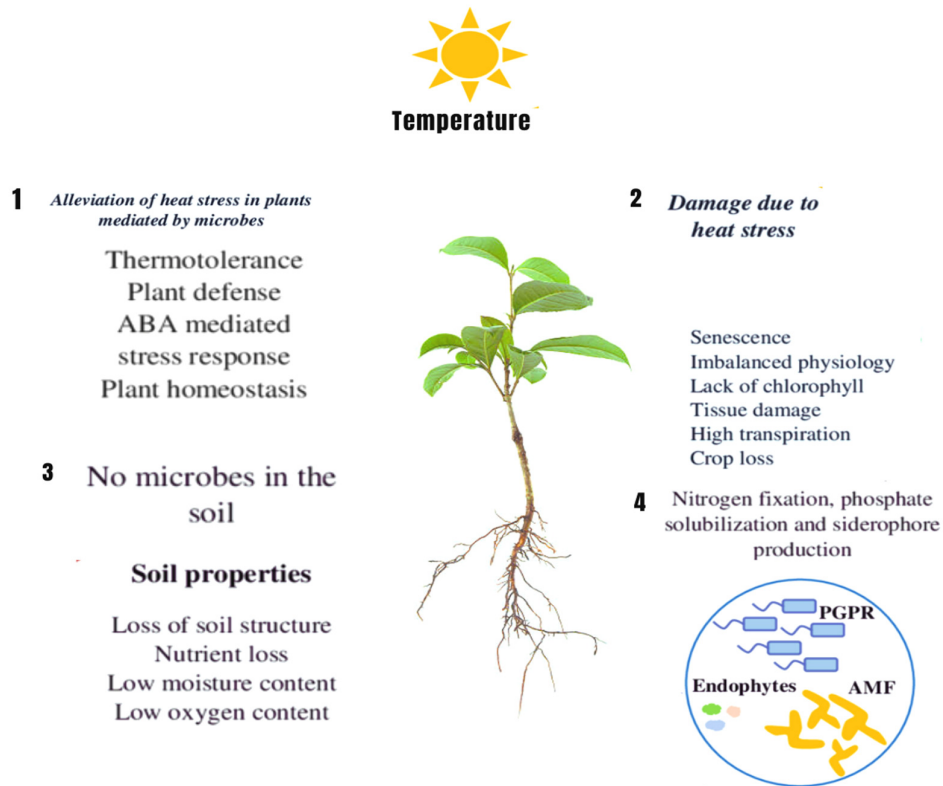
### **Interactions of soil microorganisms with plants under drought stress**

In arid regions, arbuscular mycorrhizal fungi (AMF) play a vital role in enhancing plant resilience to drought by improving nutrient absorption and controlling stomatal conductance, thereby boosting water-use efficiency. However, it is crucial to acknowledge that the effect of AMF on drought resistance varies depending on the species (Auge, 2001). Limited research has been conducted on the responses of non-mycorrhizal root-associated fungi to drought. Existing studies suggest that these fungi generally exhibit minimal or no reaction

to drought, possibly because of the overall resilience of bulk soil fungi under arid conditions. However, deviations from this pattern underscore the sensitivity of certain fungal communities to drought, indicating that factors other than soil moisture levels influence their behavior. For instance, recent research conducted by Santos-Medelln (Christian *et al.*, 2017) demonstrated significant changes in fungal communities associated with the roots of drought-stressed rice plants. Nevertheless, the lack of precise taxonomic identification hampers our understanding of the specific fungal taxa that are responsive to drought. Therefore, further investigation is crucial to uncover the nuanced reactions of different fungal taxa to dry conditions in both the bulk soil and plant roots. In addition to fungi, recent studies of the root bacterial microbiomes of various plant species under drought stress have revealed a remarkable increase in the number of bacteria belonging to the phylum *Actinobacteria*, particularly *Streptomyces*. These bacteria exhibited a six-fold increase in relative abundance within root endosphere communities under drought conditions across diverse plant species (Fitzpatrick *et al.*, 2018). As soils become drier, channels facilitating the diffusion of water-soluble substances between soil particles and bacteria diminish, leading to a decrease in water potential and subjecting microbes to osmotic stress (Schimel, 2018). Bacteria store osmolytes within their cells to reduce their internal solute potential and to prevent water loss. Gram-positive bacteria, which naturally accumulate osmolytes and respond to drought, enhance their tolerance to osmotic stress (Harris, 1981). Additionally, their cell wall structure is thought to bolster their resistance to desiccation, thereby improving their drought tolerance (Schimel *et al.*, 2007). These physiological adaptations make *Actinobacteria* well suited for thriving in drought environments, giving them a competitive advantage in the droughted root microbiome. Interestingly, the current data highlight the role of plants in shaping the drought response of root-associated microbial populations. Specifically, drought significantly altered the bacterial community composition only in soils with grassland plant communities, which were characterized by an increased relative abundance of *Actinobacteria*. These changes in the root microbiome may be attributed to alterations in root metabolites induced by drought. For example, shifts in sorghum root metabolomic profiles under drought conditions are correlated with a transition towards *Actinobacteria* dominated communities. Drought-affected roots exhibited substantial increases in various carbohydrates and amino acids, with glycerol-3-phosphate (G3P), a crucial precursor for peptidoglycan production, exhibiting the most significant enrichment. Furthermore, it has been demonstrated that members of the root microbiome, including recognized plant growth-promoting (PGP) bacteria, actively respond to plant stress conditions at the transcriptional level. (Sheibani-Tezerji *et al.*, 2015) discovered that *Burkholderia phytofirmans*, an endophytic bacterium that colonizes potato plants exposed to drought, upregulates genes that are likely involved in reactive oxygen species (ROS) detoxification. During periods of drought, changes in the photosynthetic pathways can lead to increased ROS generation, resulting in oxidative damage and cell death (Cruz de Carvalho, 2008). Hence, the activation of these bacterial genes might be a common strategy for mitigating oxidative stress in host plants (Sheibani-Tezerji *et al.*, 2015). Hence, it is crucial to advance the genomic characterization of crop species to facilitate a deeper understanding of the intricate interactions between hosts and microbes. This understanding is pivotal for deciphering the mechanisms through which bacteria and fungi promote plant growth (PGP), particularly in regulating root microbiome assembly and function during drought stress. Such insights will pave the way for the development of novel crop cultivars tailored to harnessing specific microbial inoculants.

### **Impact of temperature on root microbiome in agriculture**

Climate change-induced global temperature rise is increasing the occurrence and severity of extreme heat and cold events worldwide, posing a significant threat to plant health and crop productivity. The microbiome is a pivotal element in assisting plants in navigating both biotic and abiotic challenges (Figure 3).



**Figure 3.** Different microorganism protects plants from water-logging and salinity stress by regulating osmotic pressure  
*Arbuscular mycorrhizal* (AM) fungi, in conjunction with specific PGPR bacteria, aid the degradation of heavy metals. They also function as protective barriers or immune enhancers against pathogens, thereby providing a shield for plants.

However, climate change-induced alterations in the composition and function of plant microbiota can disrupt host functions. With the mounting pressure to sustainably enhance crop yields and mitigate losses from environmental stresses by increasing food demands and population growth, understanding how to harness the plant microbiome has become imperative. Environmental temperature directly affects soil characteristics, such as moisture levels, aggregation, pH, and nutrient diffusion, thereby affecting plants and microorganisms (Onwuka and Mang, 2018). Heat stress induces various metabolic disruptions in plants, including the generation of reactive oxygen species (ROS), modulation of phytohormone signaling, decreased photosynthetic and respiratory rates, protein inactivation, and alterations in cellular membrane fluidity and permeability. Similarly, cold stress affects plants by modifying the composition and structure of nucleic acids, proteins, and membranes in the microbiota, thereby influencing microbial physiological functions (Fortunato *et al.*, 2023). A recent study conducted (Wipf *et al.*, 2021) explored the combined effects of heat and drought stress on bacterial populations in sorghum roots. They noted that distinct Actinobacteria were more prevalent under drought and heat conditions, indicating the selective recruitment of microbiota members by sorghum plants in response to these stresses. Although individual heat and drought stresses amplified the abundance of *Actinobacteria* while diminishing the prevalence of Proteobacteria in the roots and soil, further investigations are warranted to elucidate the mechanisms underlying plant recruitment of diverse bacteria and their roles in bolstering plant heat stress tolerance. Emerging studies suggest that microbiota play a pivotal role in aiding plants in withstanding heat stress by fostering enhanced growth, nutrient uptake, and detoxification of reactive oxygen species, thereby mitigating cellular damage (Shekhawat *et al.*, 2021). In regions with moderate to hot climates, *B. cereus* promotes soybean growth and elevates chlorophyll levels. Additionally, introduction of *B.*

*cereus* mitigated the heat stress-induced increase in ABA levels. Another study demonstrated that plants inoculated with the AM fungus *Glomus fasciculatum* exhibited heightened heat tolerance, which correlated with increased antioxidative activity (Maya and Matsubara, 2013). These findings suggest a potential role for bacteria in enhancing plant heat tolerance, although the precise mechanisms remain largely unexplored. Further investigation revealed that both laboratory- and field-grown wheat plants displayed enhanced heat tolerance following inoculation with the root endophyte *Enterobacter* sp. SA187. This enhancement was associated with alterations in the trimethylation of lysine 4 on histone H3 (H3K4me3), a constitutive change in the promoters of the heat-stress genes APX2 and HSP18.2. SA187-induced thermotolerance in *A. thaliana* was found to be mediated by ethylene signaling, which primes a heat stress response beneficial to plant growth without necessarily activating it. These findings highlight the potential of root endophytes in improving the resilience of agricultural crops to heat stress. Moreover, ethylene signaling has been identified as a contributing factor to the ability of tomatoes and rice to withstand heat stress (Pan *et al.*, 2019). Similarly, *Arbuscular mycorrhizal* (AM) fungi have been found to fortify plants against cold stress. In one study, tomato plants inoculated with *Glomus mosseae* exhibited improved growth, chlorophyll content, and antioxidant enzyme activity under both normal and cold stress conditions (Caradonia *et al.*, 2019). *Arbuscular mycorrhizal* (AM) fungus (*Rhizophagus intraradices*) mitigates the adverse effects of water deficit on the growth, photosynthesis, and antioxidant system of *Euonymus maackii* Rupr. Seedlings of *E. maackii* were exposed to five levels of water deficit, corresponding to soil water contents of 20%, 40%, 60%, 80%, and 100% field capacity (Wu *et al.*, 2021). Capitalizing symbiotic interactions between plants and their environments for agricultural management holds promise for enhancing crop yield and performance. Therefore, prioritizing symbiosis and implementing strategic agricultural practices are crucial for optimizing crop tolerance and productivity.

## Conclusions

Plants serve as key players in shaping soil microbial communities, with interactions ranging from cooperation to competition. Environmental stresses drive adaptation mechanisms unique to each species, leading to varied responses among ecotypes. For instance, elevation-associated differences in chemical defenses highlight the role of ecotypes in shaping plant-microbe interactions. Symbiotic relationships between plants and microorganisms facilitate nutrient acquisition with minimal energy expenditure. Plants adapt to environmental challenges by producing antioxidant enzymes and osmolytes, modulating cellular osmotic balance. Phytohormones orchestrate plant responses to both biotic and abiotic stresses, further enhancing resilience. Cutting-edge technologies such as genomics and metagenomics offer insights into microbial communities associated with different ecotypes. Understanding these interactions is crucial for developing climate-resilient agricultural practices and ensuring sustainable crop production. The study underscores the need to explore the complexities of plant-microbe interactions to harness their potential for enhancing plant growth and defense. Addressing knowledge gaps in ecotype-driven adaptability and rhizosphere microbiota dynamics is essential for advancing climate-smart agriculture. As environmental stressors continue to impact crop production, there is an urgent call for sustainable alternatives. Despite breeding efforts, genetic manipulation alone may not suffice. Therefore, a holistic approach that integrates ecological principles with cutting-edge technologies is imperative for future agricultural sustainability.

## Authors' Contributions

Both authors read and approved the final manuscript.

### **Ethical approval** (for researches involving animals or humans)

Not applicable.

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### **Conflict of Interests**

The authors declare that there are no conflicts of interest related to this article.

### **References**

- Alegria Terrazas R, Balbirnie-Cumming K, Morris J, Hedley PE, Russell J, Paterson E, Baggs EM, Fridman E, Bulgarelli D (2020). A footprint of plant eco-geographic adaptation on the composition of the barley rhizosphere bacterial microbiota. *Scientific Reports* 10(1):12916. <https://doi.org/10.1038/s41598-020-69672-x>
- Almario J, Mahmoudi M, Kroll S, Agler M, Placzek A, Mari A, Kemen E (2022). The leaf microbiome of *Arabidopsis* displays reproducible dynamics and patterns throughout the growing season. *MBio* 13(3):0282521. <https://doi.org/10.1128/mbio.02825-21>
- Anass K, Reda BM, Imad K, Redouane EO, Youssef B, Amina A, Mohamed N (2021). Effect of mycorrhization on growth and enzymes involved in carbon/nitrogen interaction in sorghum plants. *Research Journal of Biotechnology* 16:1. <https://doi.org/10.1007/s005720100097>
- Auge' RM (2001). Water relations, drought and vesicular-arbuscular mycorrhizal symbiosis. *Mycorrhiza* 11(1):342. <https://doi.org/10.1007/s005720100097>
- Badri D, Vivanco J (2009). Regulation and function of root exudates. *Plant, Cell and Environment* 32:666-681. <https://doi.org/10.1111/j.1365-3040.2008.01926.x>
- Bai Y, Muller DB, Srinivas G, Garrido-Oter R, Potthoff E, Rott M, ... Schulze-Lefert P (2015). Functional overlap of the *Arabidopsis* leaf and root microbiota. *Nature* 528(7582):364-369. <https://doi.org/10.1038/nature16192>
- Bais HP, Govindaswamy S, Ravishankar GA (2000). Enhancement of growth and coumarin production in hairy root cultures of witloof chicory (*Cichorium intybus* L. cv. Lucknow local) under the influence of fungal elicitors. *Journal of Bioscience and Bioengineering* 90(6):648-653. [https://doi.org/10.1016/S1389-1723\(00\)90011-2](https://doi.org/10.1016/S1389-1723(00)90011-2)
- Bakhtiari M, Formenti L, Caggi' a V, Glauser G, Rasmann S (2019). Variable effects on growth and defense traits for plant ecotypic differentiation and phenotypic plasticity along elevation gradients. *Ecology and Evolution* 9(7):3740-3755. <https://doi.org/10.1002/ece3.4999>
- Bardi L, Malusa', E (2012). Drought and nutritional stresses in plant: Alleviating role of rhizospheric microorganisms. *Abiotic Stress: New Research* 1-57. <https://www.researchgate.net/publication/260902565>

- Barnawal D, Bharti N, Maji D, Chanotiya CS, Kalra A (2012). 1-Aminocyclopropane-1-carboxylic acid (ACC) deaminase-containing rhizobacteria protect *Ocimum sanctum* plants during waterlogging stress via reduced ethylene generation. *Plant Physiology and Biochemistry* 58:227-235. <https://doi.org/10.1016/j.plaphy.2012.07.008>
- Bedada G, Westerbergh A, Muller T, Galkin E, Bdolach E, Moshelion M, Fridman E, Schmid KJ (2014). Transcriptome sequencing of two wild barley (*Hordeum spontaneum* L.) ecotypes differentially adapted to drought stress reveals ecotype-specific transcripts. *BMC Genomics* 15(1):995. <https://doi.org/10.1186/1471-2164-15-995>
- Bhagwath SG, Hjortso MA (2000). Statistical analysis of elicitation strategies for thiarubrine A production in hairy root cultures of *Ambrosia artemisiifolia*. *Journal of Biotechnology* 80(2):159-167. [https://doi.org/10.1016/S0168-1656\(00\)00256-X](https://doi.org/10.1016/S0168-1656(00)00256-X)
- Bloemberg GV, Lugtenberg B. JJ (2001). Molecular basis of plant growth promotion and biocontrol by rhizobacteria. *Current Opinion in Plant Biology* 4(4):343-350. [https://doi.org/10.1016/S1369-5266\(00\)00183-7](https://doi.org/10.1016/S1369-5266(00)00183-7)
- Bowsher AW, Kearns PJ, Popovic D, Lowry DB, Shade A (2020). Locally adapted *Mimulus* ecotypes differentially impact rhizosphere bacterial and archaeal communities in an environment-dependent manner. *Phytobiomes Journal* 4(1):53-63. <https://doi.org/10.1094/PBIOMES-05-19-0026-R>
- Brejda JJ, Moser LE, Vogel KP (1998). Evaluation of switchgrass rhizosphere microflora for enhancing seedling yield and nutrient uptake. *Agronomy Journal* 90(6):753-758. <https://doi.org/10.2134/agronj1998.00021962009000060006x>
- Brotman Y, Lisek J, Me'ret M, Chet I, Willmitzer L, Viterbo A (2012). Transcript and metabolite analysis of the trichoderma-induced systemic resistance response to *Pseudomonas syringae* in *Arabidopsis thaliana*. *Microbiology* 158(1):139-146. <https://doi.org/10.1099/mic.0.052621-0>
- Calvo P, Zebelo S, McNear D, Kloeppe J, Fadamiro H (2019). Plant growth-promoting rhizobacteria induce changes in *Arabidopsis thaliana* gene expression of nitrate and ammonium uptake genes. *Journal of Plant Interactions* 14(1):224-231. <https://doi.org/10.1080/17429145.2019.1602887>
- Caradonia F, Francia E, Morcia C, Ghizzoni R, Moulin L, Terzi V, Ronga D (2019). Arbuscular mycorrhizal fungi and plant growth promoting rhizobacteria avoid processing tomato leaf damage during chilling stress. *Agronomy* 9(6). <https://doi.org/10.3390/agronomy9060299>
- Cardone L, Castronuovo D, Perniola M, Cicco N, Molina RV, Renau-Morata B, Nebauer SG, Candido V (2021). *Crocus sativus* L. Ecotypes from mediterranean countries: Phenological, morpho-productive, qualitative and genetic traits. *Agronomy* 11(3). <https://doi.org/10.3390/agronomy11030551>
- Cavicchioli R, Ripple WJ, Timmis KN, Azam F, Bakken LR, Baylis M, ... Webster NS (2019). Scientists' warning to humanity: Microorganisms and climate change. *Nature Reviews Microbiology* 17(9):569-586. <https://doi.org/10.1038/s41579-019-0222-5>
- Chamam A, Sanguin H, Bellvert F, Meiffren G, Comte G, Wisniewski-Dye' F, Bertrand C, Prigent-Combaret C (2013). Plant secondary metabolite profiling evidences strain-dependent effect in the *Azospirillum Oryza sativa* association. *Phytochemistry* 87:65-77. <https://doi.org/10.1016/j.phytochem.2012.11.009>
- Chibucos MC, Tyler BM (2009). Common themes in nutrient acquisition by plant symbiotic microbes, described by the gene ontology. *BMC Microbiology* 9(1):1-8.
- Cruz de Carvalho MH (2008). Drought stress and reactive oxygen species. *Plant Signaling and Behavior* 3(3):156-165. <https://doi.org/10.4161/psb.3.3.5536>
- Daniel R (2005) The metagenomics of soil. *Nature Reviews Microbiology* 3(6):470-478. <https://doi.org/10.1038/nrmicro1160>
- Dastogeer KMG, Tumpa FH, Sultana A, Akter MA, Chakraborty A (2020). Plant microbiome: an account of the factors that shape community composition and diversity. *Plant Interactions with Microbes and Environment* 23: 100161. <https://doi.org/10.1016/j.cpb.2020.100161>
- De Sordi L, Lourenc, M, Debarbieux L (2019). The battle within: Interactions of bacteriophages and bacteria in the gastrointestinal tract. *Cell Host and Microbe* 25(2):210-218. <https://doi.org/10.1016/j.chom.2019.01.018>
- Díaz-Rodríguez AM, Salcedo Gastelum LA, Fe'lix Pablos CM, Parra-Cota FI, Santoyo G, Puente ML, Bhattacharya D, Mukherjee J, de los Santos Villalobos S (2021a). The current and future role of microbial culture collections in food security worldwide. *Frontiers in Sustainable Food Systems* 4: 614739. <https://doi.org/10.3389/fsufs.2020.614739>



- Ding Y, Shi Y, Yang S (2019). Advances and challenges in uncovering cold tolerance regulatory mechanisms in plants. *New Phytologist* 222(4):1690-1704. <https://doi.org/10.1111/nph.15696>
- Dutta S, Na CS, Lee YH (2021). Features of bacterial microbiota in the wild habitat of *Pulsatilla tongkangensis*, the endangered “long-sepal *Donggang pasque*-flower plant,” endemic to karst topography of Korea. *Frontiers in Microbiology* 12:1873. <https://doi.org/10.3389/fmicb.2021.656105>
- Egamberdieva D, Wirth SJ, Alqarawi AA, Abd\_Allah EF, Hashem A (2017). Phytohormones and beneficial microbes: Essential components for plants to balance stress and fitness. *Frontiers in Microbiology* 8:2104. <https://doi.org/10.3389/fmicb.2017.02104>
- Erlacher A, Cardinale M, Grosch R, Grube M, Berg G (2014). The impact of the pathogen *Rhizoctonia solani* and its beneficial counterpart *Bacillus amyloliquefaciens* on the indigenous lettuce microbiome. *Frontiers in Microbiology* 5:175. <https://doi.org/10.3389/fmicb.2014.00175>
- Etemadi M, Zuther E, Müller H, Hincha DK, Berg G (2018). Ecotype-dependent response of bacterial communities associated with *Arabidopsis* to cold acclimation. *Phytobiomes Journal* 2(1):3-13. <https://doi.org/10.1094/PBIOMES-04-17-0015-R>
- Fitzpatrick CR, Copeland J, Wang PW, Guttman DS, Kotanen PM, Johnson MTJ (2018). Assembly and ecological function of the root microbiome across angiosperm plant species. *Proceedings of the National Academy of Sciences* 115(6):E1157-E1165. <https://doi.org/10.1073/pnas.1717617115>
- Fortunato S, Lasorella C, Dipierro N, Vita F, de Pinto MC (2023). Redox signaling in plant heat stress response. *Antioxidants* 12:605. <https://doi.org/10.1146/annurev.py.26.090188.000451>
- Ge Y, Tan L, Wu B, Wang T, Zhang T, Chen H, Zou M, Ma F, Xu Z, Zhan R (2019). Transcriptome sequencing of different Avocado ecotypes: De novo transcriptome assembly, annotation, identification and validation of EST-SSR markers. *Forests* 10(5). <https://doi.org/10.3390/f10050411>
- Gilbert JA, Quinn RA, Debelius J, Xu ZZ, Morton J, Garg N, Jansson JK, Dorrestein PC, Knight R (2016). Microbiome-wide association studies link dynamic microbial consortia to disease. *Nature* 535(7610):94-103. <https://doi.org/10.1038/nature18850>
- Gotz M, Nirenberg H, Krause S, Wolters H, Draeger S, Buchner A, Lottmann J, Berg G, Smalla K (2006). Fungal endophytes in potato roots studied by traditional isolation and cultivation-independent DNA-based methods. *FEMS Microbiology Ecology* 58(3):404-413. <https://doi.org/10.1111/j.1574-6941.2006.00169.x>
- Gouda S, Kerry RG, Das G, Paramithiotis S, Shin HS, Patra JK (2018). Revitalization of plant growth promoting rhizobacteria for sustainable development in agriculture. *Microbiological Research* 206:131-140. <https://doi.org/10.1016/j.micres.2017.08.016>
- Graff A, Conrad R (2005). Impact of flooding on soil bacterial communities associated with poplar (*Populus* sp.) trees. *FEMS Microbiology Ecology* 53(3):401e415. <https://doi.org/10.1016/j.femsec.2005.01.009>
- Gupta S, Didwania N, Singh D (2020). Biological control of mustard blight caused by *Alternaria brassicae* using plant growth promoting bacteria. *Plant Interactions with Microbes and Environment* 23:100166. <https://doi.org/10.1016/j.cpb.2020.100166>
- Hamonts K, Clough TJ, Stewart A, Clinton PW, Richardson AE, Wakelin SA, O'Callaghan M, Condon LM (2013). Effect of nitrogen and waterlogging on denitrifier gene abundance, community structure and activity in the rhizosphere of wheat. *FEMS Microbiology Ecology* 83(3):568-584. <https://doi.org/10.1111/1574-6941.12015>
- Harris RF (1981). Effect of water potential on microbial growth and activity. In: *Water potential relations in soil microbiology*. Soil Science Society of America, Madison, pp 23-95. <https://doi.org/10.2136/sssaspepub9.c2>
- Hartman K, Tringe SG (2019). Interactions between plants and soil shaping the root microbiome under abiotic stress. *Biochemical Journal* 476(19):2705-2724. <https://doi.org/10.1042/BCJ20180615>
- Hestrin R, Lee MR, Whitaker BK, Pett-Ridge J (2021a). The switchgrass microbiome: A review of structure, function, and taxonomic distribution. *Phytobiomes Journal* 5(1):14-28. <https://doi.org/10.1094/PBIOMES-04-20-0029-FI>
- Huang S, Zhang J, Tao Z, Lei L, Yu Y, Huang L (2014). Enzymatic conversion from pyridoxal to pyridoxine caused by microorganisms within tobacco phyllosphere. *Plant Physiology and Biochemistry* 85:9-13. <https://doi.org/10.1016/j.plaphy.2014.10.006Hestr>
- Jacobs MJ, Bugbee WM, Gabrielson DA. (1985). Enumeration, location, and characterization of endophytic bacteria within sugar beet roots. *Canadian Journal of Botany* 63(7):1262-1265. <https://doi.org/10.1139/b85-174>



- Jacoby R, Peukert M, Succurro A, Koprivova A, Kopriva S (2017). The role of soil microorganisms in plant mineral nutrition current knowledge and future directions. *Frontiers of Plant Science* 8:1617. <https://doi.org/10.3389/fpls.2017.01617>
- Kang J, Peng Y, Xu W (2022). Crop root responses to drought stress: Molecular mechanisms, nutrient regulations, and interactions with microorganisms in the rhizosphere. *International Journal of Molecular Sciences* 23(16). <https://doi.org/10.3390/ijms23169310>
- Kessler A, Kalske A (2018). Plant secondary metabolite diversity and species interactions. *Annual Review of Ecology Evolution and Systematics* 49(1):115-138. <https://doi.org/10.1146/annurev-ecolsys-110617-062406>
- Koza NA, Adedayo AA, Babalola OO, Kappo AP (2022). Microorganisms in plant growth and development: Roles in abiotic stress tolerance and secondary metabolites secretion. *Microorganisms* 10(8). <https://doi.org/10.3390/microorganisms10081528>
- Li J, McConkey BJ, Cheng Z, Guo S, Glick BR (2013). Identification of plant growth-promoting bacteria-responsive proteins in cucumber roots under hypoxic stress using a proteomic approach. *Journal of Proteomics* 84:119-131. <https://doi.org/10.1016/j.jprot.2013.03.011>
- Liu TY, Ye N, Wang X, Das D, Tan Y, You X, Long M, Hu T, Dai L, Zhang J, Chen MX (2021). Drought stress and plant ecotype drive microbiome recruitment in switchgrass rhizosphere. *Journal of Integrative Plant Biology* 63(10):1753-1774. <https://doi.org/10.1111/jipb.13154>
- Li J, Zhao GZ, Varma A, Qin S, Xiong Z, Huang HY, Zhu WY, Zhao LX, Xu LH, Zhang S, Li WJ (2012). An endophytic pseudonocardia species induces the production of artemisinin in *Artemisia annua*. *PLoS One* 7(12):e51410. <https://doi.org/10.1371/journal.pone.0051410>
- Liu Y, Wang H, Peng Z, Li D, Chen W, Jiao S, Wei G (2021). Regulation of root secondary metabolites by partial root-associated microbiotas under the shaping of licorice ecotypic differentiation in northwest China. *Journal of Integrative Plant Biology* 63(12):2093-2109.
- Luo J, Gu S, Guo X, Liu Y, Tao Q, Zhao HP, Liang Y, Banerjee S, Li T (2022). Core microbiota in the rhizosphere of heavy metal accumulators and its contribution to plant performance. *Environmental Science and Technology* 56(18):12975-12987. <https://doi.org/10.1021/acs.est.1c08832>
- Maya MA, Matsubara Y (2013). Influence of arbuscular mycorrhiza on the growth and antioxidative activity in cyclamen under heat stress. *Mycorrhiza* 23(5):381-390. <https://doi.org/10.1007/s00572-013-0477-z>
- Mendes, Rodrigo, Pizzirani-Kleiner, Aline A, Araujo Wellington L, Raaijmakers, Jos M (2007). Diversity of cultivated endophytic bacteria from sugarcane: Genetic and biochemical characterization of *Burkholderia cepacia* complex isolates. *Applied and Environmental Microbiology* 73(22):7259-7267. <https://doi.org/10.1128/AEM.01222-07>
- Munir N, Hanif M, Abideen Z, Sohail M, El-Keblawy A, Radicetti E, Mancinelli R, Haider G (2022). Mechanisms and strategies of plant microbiome interactions to mitigate abiotic stresses. *Agronomy* 12(9). <https://doi.org/10.3390/agronomy12092069>
- Naylor D, Coleman-Derr D (2018). Drought stress and root-associated bacterial communities. *Frontiers of Plant Science* 8:2223.
- Onwuka B, Mang B (2018). Effects of soil temperature on some soil properties and plant growth. *Advances in plants & agriculture research* 8(1):34-37. <https://doi.org/10.15406/APAR.2018.08.00288>
- Pais AKL, Silva JR, da Santos LVS, dos Albuquerque GMR, Farias ARG, de Silva Junior WJ, Balbino V, de Q, Silva AMF, Gama MAS, da Souza EB de, (2021). Genomic sequencing of different sequvars of *Ralstonia solanacearum* belonging to the Moko ecotype. *Genetics and Molecular Biology* 44. <https://doi.org/10.1590/1678-4685-GMB-2020-0172>
- Pal G, Saxena S, Kumar K, Verma A, Sahu PK, Pandey S, White JF, Verma SK (2022). Endophytic Burkholderia: Multifunctional roles in plant growth promotion and stress tolerance. *Microbiological Research* 265:127201. <https://doi.org/10.1016/j.micres.2022.127201>
- Pan C, Zhang H, Ma Q, Fan F, Fu R, Ahammed GJ, Yu J, Shi K (2019). Role of ethylenebiosynthesis and signaling in elevated CO<sub>2</sub>-induced heat stress response in tomato. *Planta* 250(2):563-572. <https://doi.org/10.1007/s00425-019-03192-5>
- Pandey SS, Singh S, Babu CSV, Shanker K, Srivastava NK, Shukla AK, Kalra A (2016). Fungal endophytes of *Catharanthus roseus* enhance vindoline content by modulating structural and regulatory genes related to terpenoid indole alkaloid biosynthesis. *Scientific Reports* 6(1):26583. <https://doi.org/10.1038/srep26583>

- Pang Z, Zhao Y, Xu P, Yu D (2020). Microbial diversity of upland rice roots and their influence on rice growth and drought tolerance. *Microorganisms* 31(9):1329. <https://doi.org/10.3390/microorgan-isms8091329>
- Patriquin DG, Doˆbereiner J (1978). Light microscopy observations of tetrazoliumreducing bacteria in the endorhizosphere of maize and other grasses in Brazil. *Canadian Journal of Microbiology* 24(6):734-742. <https://doi.org/10.1139/m78-122>
- Rajesh M, Samsudeen K, Rejusha P, Manjula C, Rahman S, Karun A (2014). Characterization of annur and bedakam ecotypes of coconut from Kerala state, India, using micro-satellite markers. *International Journal of Biodiversity* 2014(4). <https://doi.org/10.1155/2014/260895>
- Ramirez-Estrada K, Osuna L, Moyano E, Bonfill M, Tapia N, Cusido RM, Palazon J (2015). Changes in gene transcription and taxane production in elicited cell cultures of *Taxus media* and *Taxus globosa*. *Phytochemistry* 117:174-184. <https://doi.org/10.1016/j.phytochem.2015.06.013>
- Sacristan S, Garca-arenal F (2008). The evolution of virulence and pathogenicity in plant pathogen populations. *Molecular Plant Pathology* 9(3):369-384. <https://doi.org/10.1111/j.1364-3703.2007.00460.x>
- Santos-Medellın C, Edwards J, Liechty Z, Nguyen B, Sundaresan V (2017). Drought stress results in a compartment-specific restructuring of the rice root-associated microbiomes. *MBio* 8(4):e007644817. <https://doi.org/10.1128/mBio.00764-17>
- Santoyo G, Gamalero E, Glick BR (2021). Mycorrhizal-bacterial amelioration of plant abiotic and biotic stress. *Frontiers in Sustainable Food Systems* 5:672881.
- Sarkar S, Kamke A, Ward K, Rudick AK, Baer SG, Ran Q, ... Lee STM (2022). Bacterial but not fungal rhizosphere community composition differ among perennial grass ecotypes under abiotic environmental stress. *Microbiology Spectrum* 10(3):e02391-2421. <https://doi.org/10.1128/spectrum.02391-21>
- Schimel J, Balsler TC, Wallenstein M (2007). Microbial stress-response physiology and its implications for ecosystem function. *Ecology* 88(6):1386-1394. <https://doi.org/10.1146/annurev-ecolsys-110617-062614>
- Schimel JP (2018). Life in dry soils: Effects of drought on soil microbial communities and processes. *Annual Review of Ecology Evolution and Systematics* 49(1):409-432. <https://doi.org/10.1890/06-0219>
- Schlaeppli K, Bulgarelli D (2015). The plant microbiome at work. *Molecular Plant-Microbe Interactions* 28(3):212-217. <https://doi.org/10.1094/MPMI-10-14-0334-FI>
- Shah DA, Sen S, S A, Ghosh D, Grover M, Mohapatra S (2017). An auxin secreting *Pseudomonas putida* rhizobacterial strain that negatively impacts water-stress tolerance in *Arabidopsis thaliana*. *Rhizosphere* 3:16-19. <https://doi.org/10.1016/j.rhisph.2016.11.002>
- Sheibani-Tezerji, Raheleh, Rattei, Thomas, Sessitsch, Angela, Trognitz, Friederike, Mitter, Birgit (2015). Transcriptome profiling of the endophyte *Burkholderia phytofirmans* PsJN indicates sensing of the plant environment and drought stress. *MBio* 6(5):006211715. <https://doi.org/10.1128/mBio.00621-15>
- Shekhawat K, Saad MM, Sheikh A, Mariappan K, Al-Mahmoudi H, Abdulkakim F, Eida AA, Jalal R, Masmoudi K, Hirt H (2021). Root endophyte induced plant thermotolerance by constitutive chromatin modification at heat stress memory gene loci. *EMBO Reports* 22(3):51049. <https://doi.org/10.15252/embr.202051049>
- Sher A, Molles M (2015). *Ecology: Concepts and Applications*. McGraw-Hill Education. ISBN10:1260722201 / ISBN13: 9781260722208.
- Singer E, Bonnette J, Kenaley SC, Woyke T, Juenger, TE (2019). Plant compartment and genetic variation drive microbiome composition in switchgrass roots. *Environmental Microbiology Reports* 11(2):185-195. <https://doi.org/10.1111/1758-2229.12727>
- Singh R, Hou W, Marslin G, Dias A, Franklin G (2014). Lignin and flavonoid content increases in *Hypericum perforatum* cell wall after *Agrobacterium tumefaciens* co-cultivation. *Planta Medica* 80(16):P1M22. <https://doi.org/10.1055/s-0034-1394589>
- Subrahmanyam G, Kumar A, Sandilya SP, Chutia M, Yadav AN (2020). Diversity, plant growth promoting attributes, and agricultural applications of rhizospheric microbes. In: Yadav AN, Singh J, Rastegari AA, Yadav N (Eds). *Plant Microbiomes for Sustainable Agriculture*. Springer International Publishing, pp 1-52. [https://doi.org/10.1007/978-3-030-38453-1\\_1](https://doi.org/10.1007/978-3-030-38453-1_1)
- Suman A, Verma P, Yadav AN, Srinivasamurthy R, Singh A, Prasanna R (2016). Development of hydrogel-based bio-inoculant formulations and their impact on plant biometric parameters of wheat (*Triticum aestivum* L.).

- International Journal of Current Microbiology and Applied Sciences 5(3):890-901. <https://doi.org/10.3389/jsoil.2022.821589>
- Suman J, Rakshit A, Ogireddy SD, Singh S, Gupta C, Chandrakala J (2022). Microbiome as a key player in sustainable agriculture and human health. *Frontiers in Soil Science* 12. <https://doi.org/10.20546/ijemas.2016.503.103>
- Tiwari R, Awasthi A, Mall M, Shukla AK, Srinivas KVNS, Syamasundar KV, Kalra A (2013). Bacterial endophyte-mediated enhancement of in planta content of key terpenoid indole alkaloids and growth parameters of *Catharanthus roseus*. *Industrial Crops and Products* 43:306-310. <https://doi.org/10.1016/j.indcrop.2012.07.045>
- Trenberth KE (2011). Changes in precipitation with climate change. *Climate Research* 47(1e2):123-138.
- Van Wallendael A, Lowry DB, Hamilton JA (2022). One hundred years into the study of ecotypes, new advances are being made through large scale field experiments in perennial plant systems. *Current Opinion in Plant Biology* 66:102-152. <https://doi.org/10.1016/j.pbi.2021.102152>
- Voesenek LACJ, Colmer TD, Pierik R, Millenaar FF, Peeters AJM (2006). How plants cope with complete submergence. *New Phytologist* 170(2):213-226. <https://doi.org/10.1111/j.1469-8137.2006.01692.x>
- Wagg C, Bender SF, Widmer F, Van Der Heijden MG (2014). Soil biodiversity and soil community composition determine ecosystem multifunctionality. *Proceedings of the National Academy of Sciences* 111(14):5266-5270. <https://doi.org/10.1073/pnas.1320054111>
- Walker V, Bertrand C, Bellvert F, Moe`nne-Loccoz Y, Bally R, Comte G (2011). Host plant secondary metabolite profiling shows a complex, strain-dependent response of maize to plant growth-promoting rhizobacteria of the genus *Azospirillum*. *New Phytologist* 189(2):494-506. <https://doi.org/10.1111/j.1469-8137.2010.03484.x>
- Whipps JM, Hand P, Pink D, Bending GD (2008). Phyllosphere microbiology with special reference to diversity and plant genotype. *Journal of Applied Microbiology* 105(6):1744-1755. <https://doi.org/10.1111/j.1365-2672.2008.03906.x>
- Whitman WB, Rainey F, Kampfer P, Trujillo M, Chun J, DeVos P (2015). *Bergey's manual of systematics of Archaea and Bacteria*. Vol. 410. Wiley Online Library. <https://doi.org/10.1007/978-0-387-68572-4>
- Winston ME, Hampton-Marcell J, Zarraindia I, Owens SM, Moreau CS, Gilbert JA, Hartsel J, Kennedy SJ, Gibbons SM (2014). Understanding cultivar-specificity and soil determinants of the cannabis microbiome. *PLoS One* 9(6):99641. <https://doi.org/10.1371/journal.pone.0099641>
- Wipf HML, Bu`i TN, Coleman-Derr D (2021). Distinguishing between the impacts of heat and drought stress on the root microbiome of *Sorghum bicolor*. *Phytobiomes Journal* 5(2):166-176. <https://doi.org/10.1094/PBIOMES-07-20-0052-R>
- Wippel K, Tao K, Niu Y, Zgadzaj R, Kiel N, Guan R, Dahms E, Zhang P, Jensen DB, Logemann E, Radutoiu S, Schulze-Lefert P, Garrido-Oter R (2021). Host preference and invasiveness of commensal bacteria in the lotus and *Arabidopsis* root microbiota. *Nature Microbiology* 6(9):1150-1162. <https://doi.org/10.1038/s41564-021-00941-9>
- Wu N, Li Z, Meng S, Wu F (2021) Effects of arbuscular mycorrhizal inoculation on the growth, photosynthesis and antioxidant enzymatic activity of *Euonymus maackii* Rupr. under gradient water deficit levels. *PLoS One* 16(11):0259959. <https://doi.org/10.1371/journal.pone.0259959>
- Xiong Q, Hu J, Wei H, Zhang H, Zhu J (2021a). Relationship between plant roots, rhizosphere microorganisms, and nitrogen and its special focus on rice. *Agriculture* 11(3). <https://doi.org/10.3390/agriculture11030234>
- Yadav AN, Kumar V, Dhaliwal HS, Prasad R, Saxena AK (2018). Microbiome in crops: Diversity, distribution, and potential role in crop improvement. In: Prasad R, Gill SS, Tuteja N (Eds). *Crop Improvement Through Microbial Biotechnology*. Elsevier, pp 305-332. <https://doi.org/10.1016/B978-0-444-63987-5.00015-3>
- Yasuda M, Isawa T, Shinozaki S, Minamisawa K, Nakashita H (2009). Effects of colonization of a bacterial endophyte, *Azospirillum* sp. B510, on disease resistance in rice. *Bioscience, Biotechnology, and Biochemistry* 73(12):2595-2599. <https://doi.org/10.1080/09168451.2017.1329621>
- Young E, Carey M, Meharg AA, Meharg C (2018). Microbiome and ecotypic adaptation of *Holcus lanatus* (L.) to extremes of its soil pH range, investigated through transcriptome sequencing. *Microbiome* 6(1):48. <https://doi.org/10.1186/s40168-018-0434-3>



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