An Overview of the Investigation of Plant-Microbe Interactions in Climate Change Adaptation to Abiotic Stress

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Abstract:

The challenges of extreme weather events and climate change are posing a serious problem for agricultural production globally. Plants exist with microorganisms, and their presence and behavior have a significant influence on microorganisms. Chemically, the rhizosphere is a complicated ecosystem that favors the growth and incursion of numerous microorganisms interacting with the plants. It also acts as an ecological niche comprising plant roots. Although there has been in-depth knowledge on interactions between plants and microbes, little is known on the effect of abiotic stressors on the composition and structure of microbial communities in the rhizosphere. The article in this paper stresses the effects of climate on microbe populations and functional characteristics and plant growth. It is exploring the mechanisms with which plants counteract abiotic stress by eliminating reactive oxygen species (ROS), regulating antioxidants and production of indole-3-acetic acid (IAA), and restricting growth-inhibitory ethylene by colonizing bacteria that produce ACC deaminase. In addition, we explained the systematic communication system that is aided by root exudation and a hormone crosstalk, which can moderate and initiate dialogs between plants and other microorganisms that are in close proximity. Finally, this group supports bacteria to migrate chemotactically towards the rhizosphere in order to accelerate colony formation. Finally, we reviewed the most recent advances on how correspondence between microbial communities and plants enhances resilience to climatic stress.

Keywords: Nutrient Acquisition, Phytohormones, Sustainable Ecosystem, Climate Factors, Rhizosphere

1 Introduction

Climatic patterns have shown that after the 1970s, the average global temperature rose considerably, and precipitation patterns and the instances of extreme weather conditions altered too (Capua and Rahmstorf, 2023). The agriculture industry is directly affected by the prevailing climatic conditions, as witnessed by the reduction in the agricultural output. Additionally, climate change has increased diseases and pests that could cause more severe and regular outbreaks of diseases (De Wolf and Isard, 2007; Garrett et al., 2021). Recent research shows that abiotic stressors are exceedingly vulnerable to global agricultural productivity (Bowerman et al., 2023). In addition, by 2029, agricultural production has to increase by nearly 50 percent meet the needs of the growing human population (Nawaz et al., 2024b). Thus, the activity of deforestation and displacement of natural ecosystems increases significantly acquire more land to cultivate (Foucher et al., 2024). The current approach by development farmers to increase plant resistance to climate change is to provide sustainable food security with limited increase of agricultural land. Plant growth-promoting microorganisms, therefore, are one of the promising resources that can be explored increase the level of agricultural production (Bender et al., 2016).

As indicated by Ojuederie et al. (2019), plants associate with a wide range of microbes undertaking numerous essential activities, such as root formation, development of the plant, effective utilization of nutrients, and adaptation to biotic and abiotic stresses. The rhizosphere is the point of interactions of the plant roots, soil, microbes, and the environment (Trivedi et al., 2020). The bacteria are rhizosphere bacteria, and they exist in the ground and create a specific layer around the root system (Rout and Southworth, 2013). Plants get the macronutrients such as potassium, phosphorus, and nitrogen through the rhizosphere and, thus, become a part of the nutrition cycle (Thepbandit and Athinuwat, 2024). By means of rhizosphere deposition, plants establish symbiotic relationships with an assortment of rhizosphere microorganisms to shape the composition of their communities (Toju et al., 2018). Among a number of symbiotic bacteria that have been shown to promote plant growth by reducing the number of various plant diseases, regulating phytohormones, and enhancing the absorption of nutrients are several types (Kuypers et al., 2018; Hu et al., 2020; Lopes et al., 2021). Plant growth-promoting rhizobacteria (PGPR) can be biofertilizers since they enhance the amount of macro- and microelements available, which improves soil fertility and agricultural yield (Lopes et al., 2021). To make the farm able to produce more agricultural products, a critical understanding of the interaction of microbes and plants in the rhizosphere that is directed through root exudation and hormonal crosstalk is needed.

Abiotic stressors also include impact on soil microbial activities as well as on plant physiology and metabolism. Nonetheless, this is because, based on such factors as period, host plants, intensity, and other environmental conditions, stress produces diverse responses (Georgieva and Vassileva, 2023). As an instance, advanced gagging and grain yield in wheat cultivated in a rainfed environment were severely reduced, primarily due to the adverse impact on photochemical production, leaf area expansion, seed production, and weight (Rahimi-Moghaddam et al., 2023). Conversely, Thymus serphyllum has an increased production of osmolytes that contain sorbitol, mannitol, proline, and other amino acids, thereby saving it during dry spells (Moradi et al., 2017). Moreover, the rhizosphere of groundnuts exhibited a high proportion of Acidobacteria and Cyanobacteria during salt stress that enhanced groundnuts salt tolerance (Xu et al., 2020). Nevertheless, the rice plants experienced significant yield tradeoffs, including reduced germination, growth, and tillering, which had an effect on the plant biomass and plant height (Fang et al., 2023). Consequently, the nature of the interaction of microorganisms and plants under abiotic stress is complex and dynamic. There is an unraveling needed to know how abiotic stresses impact the plants, microbes, and plant-microbe interactions, and this understanding is essential to harness the potential of the plant microbiota in agriculture (Fadiji et al., 2023). This study has already gathered the effects of the changing climatic conditions on plant-microbe interactions as well as those positive impacts that are brought to high agricultural yields using bacteria that are associated with the plant. We also review new trends in the mitigation of stressors and their significance in the achievement of key ends in future study.

2 Understanding the coexistence of soil microbiota and plants

A plant is hypomolecularized at the taxonomic level of a multiplicity of microbiome communities that consist of viruses, fungi, bacteria, and archaea. These microbiomes live together in the roots of plants within the rhizosphere (adjacent soil), endosphere (internal), and phyllosphere (aerial organs), whose influence is harmful to their host's health and fitness regulation. The rhizosphere is one of the most heterogeneous and complex micro-habitats in terms of microbial population existence. The origins of the plant-related microbes may be numerous, such as the soil, seeds, water, and other related species, insects, and animals, to mention but a few. The whole part of these species may be complicated symbionts and join themselves with plants (Fitzpatrick et al., 2018). Specifically, the surrounding environment regulates the plant microbiomes that existed as a symbiotic entity known as the holobiont (Trivedi et al., 2020). A holobiont is a complex and mutual host of organisms inhabiting very closely in any type of environment (Matthews, 2024). They are microorganisms of holobionts that can considerably benefit the health of plants by increasing the solubility of minerals (Lemanceau et al., 2017) and signaling phytohormones that involve auxin (IAA), gibberellins (GA), and cytokinin (CK) (Spaepen and Vanderleyden, 2011), and direct provision of nutrients (Saleem et al., 2024), in addition to increasing phytopathogen resistance (Jin et al.,) Plant-microbe crosstalk starts with the synthesis of the chemical molecules, flavonoids and amino acids, establishing an environment in which bacteria can survive and live and allow the plants to resist stress and maintain development (Stefan et al., 2018). (Figure 1). Early symbiosis is still detected using signals produced by beneficial bacteria by the plants (Ravelo-Ortega et al., 2023). By creating adequate water and nutrient supplies for the plants, Fadiji et al. (2023) argue that rhizosphere bacteria always play a role in establishing plant adaptations to abiotic stressors, which may lead to an increment in agricultural production. In a bid to curb chemical fertilizer-related harmful effects on people, animals, aquatic life, and the environment, several studies are currently being conducted to isolate, identify, and utilize useful symbiotic bacteria to substitute down-the-line chemical fertilizers (Kumar et al., 2022; Shahwar et al., 2023). Abdelaziz et al. (2019) have discovered that incorporation of the root endophytic fungus (Piriformospora indica) into the soil produced significant increases in tomato production and growth. Interactions between plants and rhizobia are highly specific and occur at the species level more than at the genotype level, making symbiosis occur successfully (Wang et al., 2018). In general, rhizobia are valuable components of soil, as they produce and fix nitrogen compounds that help plants to grow and develop under unfavorable conditions, which leads to the growth of ecosystem production.

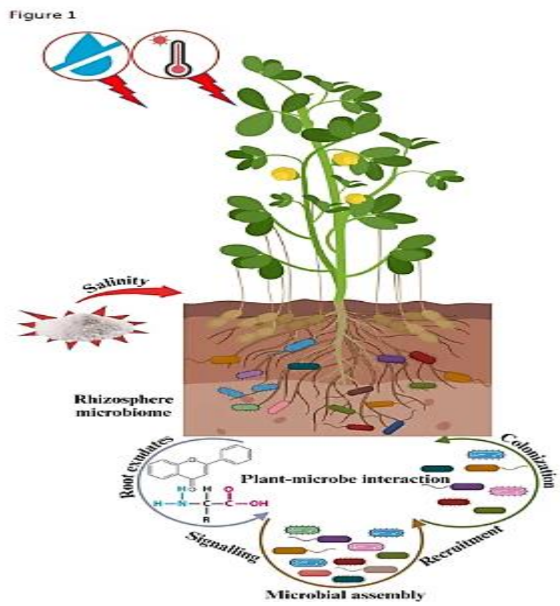

Figure 1 Systematic overview of how microbes and plants cooperate to reduce abiotic pressures in climate change.

3 Abiotic stressors linked to climate change the rhizosphere's bacteria and plants.

The external environment that plants are continuously exposed to is ever-changing in a variety of ways (Nawaz et al., 2024a). severe climate alterations, including drought, salinity, and severe temperatures, are already occurring in certain parts of the planet. Plant-associated microbial communities are negatively impacted by these climatic conditions, and this negatively impacts plant growth and development (Afridi et al., 2022). In order to adjust to these sudden shifts, plants undergo a variety of physiological and morphological changes in reaction to adverse circumstances; as a result, they suffer severe growth and yield penalties (Xu et al., 2023). The composition and function of the microbial population in the rhizosphere may change because of abiotic stressors, among other effects on rhizosphere microbial communities. For example, Actinobacteria and Firmicutes may become more abundant after extended exposure to drought stress (Vescio et al., 2021). Furthermore, when the peanut rhizosphere was subjected to salt stress, a corresponding increase in the abundance of Acidobacteria and Cyanobacteria was noted (Xu et al., 2020). Dollete et al. (2024) recently found that forage legumes' symbiotic nitrogen fixation has decreased, which has an impact on plant growth and development. Additionally, under abiotic stress conditions as pH, temperature, and heavy metals, the biocontrol fungus Trichoderma sp. showed changed phosphate solubilizing efficacy (Rawat and Tewari, 2011).

The potential of plant growth promoting microorganisms (PGPMs) to reduce certain abiotic stressors and improve plant adaptability to adverse environments has been widely studied (Chieb and Gachomo, 2023; Kibret et al., 2024). Plants use a variety of tactics to maintain their growth under stressful conditions, including stomatal closure (physiological adaptation), changes in growth pattern (morphological adaptation), induction of chemical signaling and regulation of phytohormones (biochemical adaptation) (Naamala and Smith, 2020) (Table 1). Plant performance may be limited by climate-associated abiotic stressors that affect plants differently and at various phases of development (Lata et al., 2018). The harmful consequences of these abiotic pressures on plant adaptation—which might impede the creation of a sustainable environment and lower agricultural output—are further explained in depth.

3.1 Using the interaction between microorganisms and plants to reduce temperature stress

According to Kashyap et al. (2017), temperature is a key component that shapes the microbial community that relates to plants as well as their growth and phenological characteristics. According to Compant et al. (2010), the global mean temperature is expected to rise by 1.8 to 3.6°C by the year 2100, causing water scarcity in many parts of the world. This could have a substantial impact on the distribution, activities, and composition of the rhizosphere microbiome (Farooq et al., 2022). Higher temperatures may cause a significant change in the respiration rate of microorganisms, which might hasten their development and proliferation (Classen et al., 2015). In a similar vein, Vargas (2024) found that rising temperatures might cause soil respiration to rise exponentially. Moreover, microbes' use of organic materials may be impacted by warmer temperatures (Frey et al., 2013). Additionally, Velásquez et al. (2018) documented the relationship between temperature fluctuations and the pathogenicity of bacteria. According to Hasegawa et al. (2005), higher temperatures may also facilitate bacterial virulence, such as Pectobacterium atrosepticum, which causes soft rot disease and further impacts cell wall disintegration, increasing the prevalence of illness in plants.

Microbial activities are significantly impacted by temperature stress because, unless they rapidly adapt to temperature changes, they need an ideal range of temperatures to support their growth, reproduction, and capacity to cause illness (Wang et al., 2021a). By effectively allocating carbon, for instance, a number of microorganisms have evolved unique adaptations to withstand harsh climatic conditions and maintain their host plants (Vera-Gargallo et al., 2023). To counteract the negative impacts of thermal stress, they also have sophisticated regulation networks of secondary metabolites and certain enzymes (Raddadi et al., 2015). Many thermotolerant microorganisms, such as arbuscular mycorrhizal fungi (AMF) and endophytic bacteria, alter their structures to withstand high temperatures and shield their host plants from harsh climatic circumstances. Rasmussen et al. (2020) investigated how temperature affected plant-associated AMF colonization and plant performance and found that fungal colonization and plant growth both increased with continuous temperature increases. Similar results about enhanced AMF colonization in response to increasing temperatures were reported by a number of experimental experiments (Compant et al., 2010; Xie et al., 2024). The use of plant growth-promoting endophytic bacteria as biofertilizers to reduce heat stress damage in soybean plants was proposed by Khan et al. (2020a), who also demonstrated the beneficial effects of these bacteria on crop output at higher temperatures. The use of thermotolerant bacteria to increase the amount of chlorophyll in rice and canola was also shown in previous research (Glick et al., 1997; Chaganti et al., 2023).

Additionally, some microbes may help plants deal with a variety of stressors. For example, the Burkholderia phytofirmans PsJN strain has been shown to improve drought tolerance in wheat, heat tolerance in tomatoes, salinity and freezing resistance in Arabidopsis, and cold resilience in grapevines (Miotto-Vilanova et al., 2016; Issa et al., 2018). Heat-resistant bacteria may improve crop growth and development in heat-stressed wheat, rice, tomato, potato, chickpea, sorghum, and canola plants, according to similar results reported for other crops (Table 1). All things considered, for a sustainable ecosystem with increased agricultural productivity, it is essential to comprehend how high temperatures affect plant-microbe interactions and to identify target microorganisms and their associations with crops in a particular setting.

3.2 The function of plant-microbe symbiosis in drought

Food security is at risk due to drought, which is one of the main causes of agricultural losses globally. Severe drought events will worsen due to climate change and global warming, which will increase the danger to agricultural sustainability (Fadiji et al., 2023). Increased fluctuation in precipitation patterns is one of the obvious effects of climate change. This directly affects the amount of moisture in the soil and atmosphere, leading to drought or flood conditions (Tabari, 2020). Drought causes a variety of physiological and morphological reactions in plants due to water constraint (Kumar and Verma, 2018). Drought hinders plants' ability to grow and develop normally, alters their water needs, and lowers their water-use efficiency. A greater root/shoot ratio results from drought stress in seedling plants, which preserves root development while restricting shoot growth (Kou et al., 2022). Extreme water-limiting circumstances can result in delayed leaf growth because they cause plant cells to shrink, which lowers turgor pressure and lowers plant fresh weight (Fahad et al., 2017). In order to maximize the distribution of water and nutrients to various plant parts under drought circumstances, the root shape also adjusts by shrinking, reducing water loss that might impair the leaves' ability to use photosynthesis II (Ma et al., 2020). Long-term water shortage compromises the integrity of the cell wall, which leads to the production of reactive oxygen species (ROS), early leaf senescence, ethylene buildup, changes in chlorophyll content, and inhibition of photosynthetic processes (Kumar and Verma, 2018). Furthermore, dryness hinders salts' ability to dissolve and move, which causes them to build up in the rhizosphere soil and eventually result in salinity stress (Gupta et al., 2022).

Many plant species that have experienced drought for an extended period of time have developed features to withstand drought, such as improved phytohormone use, enhanced osmolyte and heat-shock protein production to maintain growth and yield (Figure 2). Additionally, these plants produce appropriate solutes that support drought tolerance, increase a number of compatible antioxidant enzymes for scavenging excess ROS, and activate cellular mechanisms to maintain water and salt balance by moving excessive salt from cells to other parts of the plant (Gupta et al., 2022). According to a metabolomic investigation, Thymus serphyllum produces more osmolytes, including proline, sorbitol, mannitol, and other amino acids that provide resistance to drought stress (Moradi et al., 2017). The rhizosphere's microbial ecology and soil properties are greatly impacted by drought (Manzanera, 2021). Microorganisms in the rhizosphere and root system interact with one another to affect one another (Figure 1).

Figure 2: Plants adjust to shifting climates and use specific defense systems against abiotic challenges.

By enhancing root architecture and promoting water and nutrient absorption, rhizosphere bacteria work symbiotically to significantly lessen the consequences of drought. Additionally, the release of some advantageous metabolites is encouraged by this association, which may aid plants in improving the root/shoot ratio, increasing biomass production, improving water absorption capacity, and improving nutrient availability (Figure 1) (He et al., 2021; Rawal et al., 2022). Other elements that impact these microorganisms' performance are produced by the host plant's induction of root exudation (Gupta et al., 2022). Thus, rhizosphere microbiome manipulation may increase crops' ability to reduce stress (Xu and Coleman-Derr, 2019; de Vries et al., 2020). For example, by assigning more endosphere Streptomyces, certain plant species may withstand more drought (Fitzpatrick et al., 2018). Similarly, during drought, Streptomyces colonized sorghum seedlings showed higher root development, but under well-watered circumstances, no discernible impacts were seen (Xu et al., 2018). Additionally, by using external hyphae and glomalin, AMF greatly increases crop drought tolerance by boosting water availability (Wang et al., 2023). Similarly, under dry soil conditions, AMF has a significant impact in root growth and development in maize and citrus (Wu et al., 2013; Zhao et al., 2015). The function of PGPMs in plant defense against various abiotic stressors was shown in several related investigations (Table 1). Utilizing rhizosphere microorganisms under drought stress may have a major impact on agricultural productivity by optimizing the allocation of water and nutrients, since these studies demonstrated that plant health is highly reliant on the makeup and activity of the plant-associated microbiome.

3.3 The role of the plant-microbiota interaction in modulating salt tolerance

One of the main abiotic stresses that negatively impacts crop development and production is soil salinity (Julkowska and Testerink, 2015). According to estimates, salinization affects around 7% of the world's fields, or one billion hectares of soil (Bayabil et al., 2021). More significantly, due to improper agricultural practices (increased use of fertilizers and saline water irrigation), industrial pollution, and decreased precipitation and increased surface evaporation, the area occupied by salinity-affected soils is growing by about 10% annually as a result of climate change (Ouhibi et al., 2014; McFarlane et al., 2016). As a consequence of mineral weathering, plants are naturally able to absorb a fair amount of soluble salts. Soluble salts are deposited in the root zone as a result of insufficient precipitation, which prevents salt leaching (Shrivastava and Kumar, 2015). Furthermore, the issue of salinity could have become worse due to the inflow of saltwater via surface or groundwater connections (Bayabil et al., 2021). Additionally, osmotic stress results from the increased salt content in the rhizosphere, which affects the absorption of nutrients and water. By producing more ROS, this situation results in oxidative damage (Isayenkov and Maathuis, 2019; Rahman et al., 2024). Furthermore, the nodulation process is negatively impacted by soil salinity, which lowers crop yields and prevents nitrogen fixation by lowering nitrogenase activity (Kumar and Verma, 2018).

Plants may develop several defensive mechanisms to protect themselves when exposed to saline conditions. These include the development of trichomes or salt-releasing glands (Yuan et al., 2016), the restoration of ionic homeostasis, osmotic, and ROS levels (Yang and Guo, 2018), the modification of stomatal conductance (Li et al., 2020), and the regulation of specific growth patterns such as flowering time (Kazan and Lyons, 2016) (Figure 2). Through specific plant-mediated processes, soil microorganisms significantly increase plant tolerance to salt and drought conditions (Sangiorgio et al., 2020) (Table 1). Additionally, microbes speed up antioxidant reactions to shield plants from oxidative damage. Bacteria often exhibit these adaptive responses because they allow them to endure a variety of challenging environments (Liu et al., 2019). Among these characteristics, the creation of extracellular polymeric substances (EPS) controls a number of functions, such as limiting mass transfer, halting water loss, and controlling vital biomolecules like enzymes, nucleic acids, and exopolysaccharides (López-Ortega et al., 2021). By absorbing sodium ions from the soil and reducing their availability to plants, EPS-producing microorganisms may improve plants' tolerance to salt (Bhagat et al., 2021). Furthermore, via the production of micro and macro-aggregates, bacterial exopolysaccharides significantly contribute to the improvement of soil structure under salt stress (Grover et al., 2011).

A varied set of microorganisms known as halophiles or halo-tolerant are remarkably able to thrive across a wide range of NaCl concentrations (Abbas et al., 2019). Through a variety of adaptation processes, these microorganisms may be classified as halophilic (2.5-5.2 M) or halotolerant (0.3-0.5

M) (López-Ortega et al., 2021). ACC deaminase activity, EPS production, nitrogen fixation, IAA production, biofilm formation, osmolyte accumulation in plant cell cytoplasm, turgor pressure maintenance in salt-stressed cells, and limiting osmotic and oxidative stress by generating plant hormones and antioxidants are some of the major contributions of these microbes (Table 1) (Rajput et al., 2018; Rima et al., 2018; Nawaz et al., 2020; Kumar et al., 2021). Li et al. (2021) claim that plant roots in the rhizosphere of the salt-treated plants attracted a varied microbial population, improving the plants' ability to withstand salt. Similarly, when groundnuts were subjected to salt stress, the rhizosphere showed a significant prevalence of Acidobacteria and Cyanobacteria (Xu et al., 2020). To completely comprehend the effects of salt stress on the plant-associated microorganisms, more thorough mechanistic research employing various plant species under saline conditions is necessary, even though these findings highlight the significance of microbial communities in the defense mechanisms of plants under salt stress.

4 Signaling and communication between microbes and plants

In their natural setting, plants interact dynamically with a variety of environmental cues, which helps microbial populations integrate. Plants can effectively perceive and react to interacting stimuli in these communicative networks. However, they have the ability to form symbioses or trigger immunological responses if they recognize microbial compounds. For stationary organisms like plants, chemical signaling plays a crucial role in sensing and regulation, despite this intricate web of communication networks (Afridi et al., 2022). Chemical cues are used by plants as stimuli to form advantageous connections with nearby microorganisms, either belowground (roots) or aboveground (trunk, shoots, and leaves). Hormonal crosstalk and root exudation guide this complex communication network, which controls the complex interactions between plants and their many biotic and abiotic surroundings.

4.1 How root exudates influence the bacteria in the rhizosphere

Through their roots, plants release a diverse range of metabolites, including primary and secondary metabolites, during different phases of growth. Growth, development, and the uptake of nutrients are among the activities that primary metabolites control. Conversely, secondary metabolites have crucial roles in plant defense and protection against insects and pests, but they are often not engaged in plant survival. Furthermore, plants' ability to adapt to shifting conditions and withstand various biotic and abiotic challenges depends on secondary metabolites. Under biotic and abiotic stressors, these secondary metabolites carry out a wide variety of defensive tasks, including as signaling, photoprotection, antibacterial activity, and structural stability (Ingle et al., 2016). Additionally, plant secondary metabolites regulate microbial communities linked to their hosts, serve as signaling molecules for plant-microbe interactions, and help plants tolerate pests and diseases (Fakhri et al., 2022).

The physico-chemical characteristics of the soil (Sasse et al., 2020) and the genetics and age of the plant species have a significant impact on the chemical makeup of root exudates (Zhang et al., 2021). The complex control of root system architecture (RSA) is primarily responsible for the variation in root exudates across various plant species (Galindo-Castañeda et al., 2024). Although multiple root zones have been shown to be active in different plant species, the region under the root cap is acknowledged as the primary exudation location (Haldar and Sengupta, 2015). Moreover, the exudations of various root sections vary. For example, asparagine and threonine are produced by the root meristem and elongation site, whereas aspartic acid is secreted by the whole root and glutamic acid, valine, leucine, and phenylalanine are exuded by the root hair zone (Haldar and Sengupta, 2015). The primary source of nutrients in the rhizosphere is plant root exudation, which draws in native microorganisms that flourish there (Pascale et al., 2020). In addition to serving as signaling molecules like stimulants and chemoattractants, root exudates may also have repulsion and inhibitory effects under certain conditions. These substances alter the first conversation between plant roots and soil microbes since they constantly vary in response to changes in their immediate surroundings (Wiesenbauer et al., 2024). The development of a microbiome in the rhizosphere requires colonization and chemotaxis. Exudates from roots are thought to be the primary source of signaling molecules for microorganisms, which facilitates early colonization by encouraging their chemotactic migration into the rhizosphere. Therefore, via altering microbial populations, root exudates play a crucial part in plant-soil feedback.

4.2 Hormonal communication for improved stress tolerance in plant-microbe symbiosis

Naturally occurring plants are always interacting with their biotic and abiotic surroundings. Plants evolved a complex and flexible environmental signaling network guided by phytohormones to guarantee their survival and to maintain the impacts of these various and often hostile environments (Jain et al., 2021). Plant responses to very dynamic and diverse situations are fine-tuned by this intricate hormonal interplay. According to Hirayama and Mochida (2022), plant hormones are organic compounds that are created in trace quantities and play a crucial role in regulating the developmental processes of plants. They do this by activating various physiological systems in response to external stimuli. To regulate their development and metabolism, plants naturally produce a wide range of hormones, such as auxins, GA, CK, and ABA (Iqbal et al., 2022). Research shows that applying phytohormones under stress significantly improves plant metabolism and functioning. According to Hu et al. (2013), auxin and ABA are two phytohormones that are essential for reducing abiotic stress. But in several studies, scientists have also figured out the possible functions of additional phytohormones (Singh and Singh, 2017; Sharma et al., 2019). Plant defense against a variety of abiotic stimuli is significantly aided by the interaction of ABA, SA, jasmonates, and ethylene with the main growth-2promoting hormones, including auxins, GA, and CK (Figure 3).

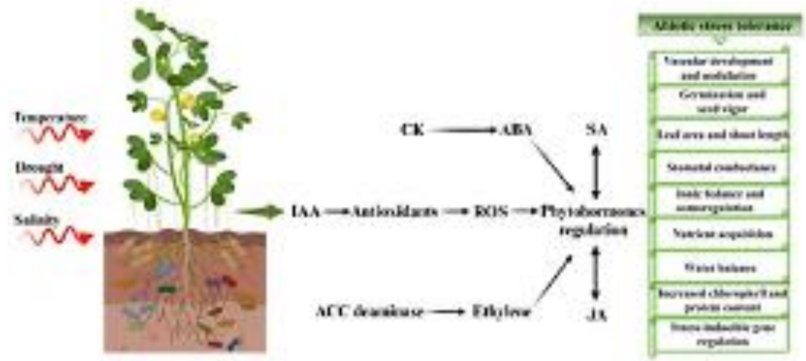

Figure 3. Hormonal crosstalk and signaling mediating abiotic stress tolerance in plants.

By initiating phytohormone signaling and triggering defensive mechanisms, microorganisms form symbiotic relationships with plants to shield them from biotic and abiotic challenges (Khan et al., 2020b). It is important to highlight, too, that the role that bacteria play in controlling phytohormones is important not just for directly boosting plant development but also for a number of other microbial impacts on plants, including improving nutrient uptake and modulating stress tolerance. By controlling essential plant processes such as nutrient uptake, water balance homeostasis, pathogen tolerance, antioxidant activities, elevated chlorophyll and protein content, and stress-inducible gene regulation, phytohormones significantly contribute to the mitigation of abiotic stress (Figure 3).

Since the status of phytohormones is partially dependent on the effectiveness of nutrient acquisition, it is important to note that microbes can indirectly affect the concentration of phytohormones in plants by modulating mineral acquisition through nitrogen fixation or phosphate solubilization (Kudoyarova et al., 2015). Furthermore, most known processes by which microbes stimulate plant development probably include the involvement of rhizosphere bacteria in regulating plant hormonal state. According to Shigenaga et al. (2017), this might include tasks like integrating microbial biocontrol solutions based on plant hormones or designing the interaction of phytohormones. To better comprehend the complex functions of phytohormones in controlling plant defenses and fitness, a thorough review is necessary (Vos et al., 2013; Guo et al., 2018). This will make it easier to maximize the phytohormone network's utilization for useful purposes in plant protection and cultivation.

5 Plant abiotic stress suppression mediated by ACC deaminase

Many PGPR include the enzyme 1-aminocyclopropane-1-carboxylate (ACC) deaminase, which controls plant development by lowering the amount of ethylene generated in response to stress signals (Ali and Kim, 2018). According to Vanderstraeten et al. (2019), ethylene is a gaseous phytohormone that controls plant growth at ideal quantities. However, at larger concentrations, it impacts several plant developmental processes, including as root growth, nodulation, fruit ripening, blooming, and leaf senescence. Increased ethylene buildup from prolonged exposure to different stimuli may have a major effect on plant developmental processes (Dubois et al., 2018). IAA may trigger the synthesis of ACC, which functions as a crucial turning point in the control of ethylene production in plants and an intermediate precursor to ethylene biosynthesis.

ACC deaminase-producing bacteria catalyze the breakdown of α-ketobutyrate and ammonia instead of ethylene when ACC is secreted by plant roots in the presence of high ethylene concentrations. This lowers plant growth-inhibitory ethylene levels in stressed or developing plants (Ratnaningsih et al., 2023). Additionally, these bacteria's production of IAA improves nutrient absorption and root growth, strengthening plants' resistance to a variety of abiotic stressors (Figure 4) (Etesami and Glick, 2024). IAA greatly improves plant resistance to heavy metal stress by encouraging root and shoot development (Shah et al., 2024). For example, it has been shown that IAA availability enhances Pb, Zn, and Cd phytoextraction, hence improving plant development under heavy metal stress (Sytar et al., 2019). Similarly, by reducing the harmful effects of heavy metals on plants, IAA treatment may improve plant development in soil polluted with metals (Sharif et al., 2022). According to different research, applying the fungal endophyte Penicillium roqueforti, which produces IAA, significantly decreased the number of heavy metals that wheat plants absorbed (Ikram et al., 2018). All things considered, microorganisms' production of IAA contributes significantly to improved plant resilience and growth, especially in soils polluted with metals.

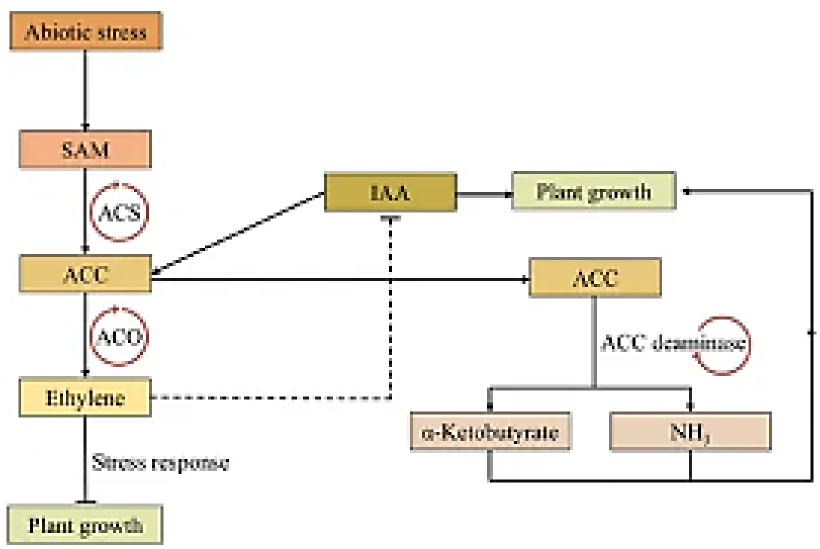

Figure 4. A schematic model proposing how ACC deaminase-producing bacteria promote plant growth by reducing ethylene concentration

Plants may be protected against a variety of challenges by being inoculated with bacteria that produce ACC deaminase (Herpell et al., 2023; Roy Choudhury et al., 2023). In mangrove seedlings, it has been shown that Trichoderma strains with ACC deaminase exhibit phytopathogenic biocontrol and plant growth regulation action (Saravanakumar et al., 2018). Furthermore, during heavy metal stress, the presence of the Serratia K120 bacteria was linked to increased ACC deaminase activity and IAA synthesis (Carlos et al., 2016). According to reports, ACC deaminase activity in Paraburkholderia dioscoreae Msb3, a unique bacterium identified strain, enhances tomato plant development by interacting with other symbionts (Herpell et al., 2023). Comprehensive research on the microbial ACC deaminase activity and plant root ACC exudation under different abiotic stressors is lacking, despite the fact that the significance of ACC deaminase in promoting plant development and abiotic stress resistance has been established. It would be beneficial to conduct a thorough analysis of the plant reactions after using bacteria that produce ACC and IAA deaminase. This would help identify the most effective PGPR application strategy for crop production, which would result in more environmentally friendly practices that lessen the need for chemical fertilizers.

6 Current challenges for optimizing plant-microbe interaction

The sudden changes in climate have had a major influence on plants, leading to serious problems with cellular homeostasis. These effects ultimately result in restricted plant growth and development, underscoring the growing need of switching from traditional breeding methods to more sophisticated and sustainable ones. Genetic engineering has shown promise in addressing these issues by creating microbial strains that are efficient and have long lifespans to increase agricultural yields under drought. Novel genes associated with drought resistance have been discovered as a result of recent advancements in microbiology, molecular biology, and biotechnology (Salvi et al., 2022). The process of bio-inoculation of crops grown in drylands may benefit from additional assessment of these strains according to their stress tolerance. The integration of microbiotechnology concepts in agriculture should be utilized to isolate microbial strains from the stress-affected soils (Kaushal and Wani, 2016).

In plant-microbe interaction research, investigating diverse microbial communities presents a significant challenge because it can be challenging to answer crucial questions such as the fundamental traits of a particular microbial community, the intricate interactions among various community members, and how these members contribute to the survival of plants in such conditions. The ability of plants to control the recruitment of different root-associated microbes for necessary reasons is now well acknowledged (Bag et al., 2022). Furthermore, research is needed to understand the processes behind the many rhizosphere signaling pathways that contribute to the formation and maintenance of the intrinsic microbiome. New discoveries in the field of plant-microbe interactions might have a big effect on agricultural output. Further investigation into these advantageous rhizosphere-based plant-microbe interactions will clarify the ways in which these microorganisms affect the nutritional makeup of plant components. The systematic exploitation and use of these beneficial microbial species that reside in the plant rhizosphere is still a difficult and demanding field of study. Therefore, in order to understand the intricate interactions between plants and the microbiome under shifting environmental circumstances, new and cutting-edge scientific methodologies are desperately needed.

7 Recent innovations in plant-microbe interaction

The rhizosphere is a dynamic habitat that provides researchers with a variety of fascinating features. A new age for extensively examining the intricate plant-microbe interaction for environmentally effective production has arrived with the development of very advanced molecular biology methods. New avenues for investigating the intricate networks of plant-microbe interactions and plant tolerance to various biotic and abiotic challenges have been made possible by the development and ongoing improvement of omics, gene-editing methods, and high-throughput sequencing technology (Kimotho and Maina, 2024). In addition to improving plant resistance to various stressors, genomics has shown itself to be an effective technique for analyzing and forecasting plant-microbe interactions (Frantzeskakis et al., 2020). The vast genetic variability found in the soil microbiome has been analyzed using a variety of sequencing technologies, such as metagenomics (Masuda et al., 2024), fungal internal transcribed spacer (ITS) regions sequencing (Labouyrie et al., 2023), and prokaryotic 16S amplicon sequencing (Qin et al., 2024).

The most thorough and effective method for determining the molecular underpinnings of plant-microbe interactions is transcriptomics based on next generation sequencing (NGS) (Katara et al., 2024). It is mostly used to assess how well plants respond under different stressors, exposing the physiological reactions of plants to infections and clarifying the signaling processes taking place in the rhizosphere (Roy et al., 2024). Investigating advantageous plant-microbe interactions and plant performance under abiotic stressors has been made possible by NGS (Rehman et al., 2024). NGS has been used to uncover, for example, the impact of short-term flooding on the expression profile of orchard grass genes (Qiao et al., 2020), the cold tolerance response in upland cotton (Wang et al., 2024), the enhanced drought tolerance in wild soybean (Kim et al., 2024), and the altered gene expression level in Arabidopsis under cold stress (Zhang et al., 2024). The best method for detecting pathogens at the moment is metagenome sequencing using Oxford Nanopore Technologies (ONT) (Yu et al., 2023). Without requiring an amplification step, it is a reliable and straightforward long-read sequencing technique (Wang et al., 2021b). It may be utilized without previous knowledge of infections since it can directly identify all diseases except RNA viruses (Javaran et al., 2023). Metagenome sequencing of bacteria, fungi, and viruses that impact different crops has already been accomplished using the MinONTM method (Jongman et al., 2020; Mechan Llontop et al., 2020). All things considered, these contemporary molecular approaches have significantly increased agricultural sustainability and production while boosting resistance to several persistent climate difficulties.

8 Future perspectives

Microbes are thriving in plants, particularly in the rhizosphere. Known as the "cry for help" method, plants may release a variety of chemical signals to attract helpful microorganisms to help them cope with adverse circumstances (Bai et al., 2022). Investigating these molecular facets of plant-microbe interactions in the rhizosphere is crucial to comprehending the mechanistic underpinnings of plants' "cry for help" approach (Zancarini et al., 2021). Understanding the signaling cascades that control plant development and stress responses requires the identification of genes with particular roles (Depuydt and Vandepoele, 2021). Regulating plant growth and development processes, such as root architecture, microbial abundance, phytohormones, secondary metabolites, nutrient acquisition, and plant immune responses, will require an understanding of the interaction between plant functional genes and rhizosphere microbes (Liu et al., 2023). One intriguing subject for more research is the MYB72 transcription factor in Arabidopsis, which is known for playing a significant part in the induced systematic response (ISR) mediated by advantageous microorganisms (Vlot et al., 2021). Furthermore, further research is needed to determine how members of the plant multidrug and toxic compound extrusion (MATE) family transport phytohormones and secondary metabolites (Wang et al., 2022). Furthermore, by carefully adjusting their genetic and epigenetic regulation, the co-expression of the Arabidopsis gene AVP1, the rice gene OsSIZ1, and the cyanobacterium flavodoxin gene FId demonstrated their significant contributions to plant growth and resilience to numerous environmental adversities (Zhao et al., 2024).

Novel molecular-level developments in plant-microbe interactions provide a fresh approach to genetic breeding (Nerva et al., 2022). By investigating this link, we may create crop varieties that are more resilient to certain types of stress. It is anticipated that future studies using state-of-the-art technologies, such as multi-omics, NGS, and imaging methods covered in section 7, will improve our comprehension of the microorganisms that interact with host genes in a reciprocal manner and provide new germplasm resources. Furthermore, there is still much to learn about the molecular and mechanistic underpinnings of microbial ACC deaminase activity in response to ACC secreted by roots under different abiotic stressors. A thorough examination of how plants react to bacteria that produce ACC and IAA deaminase would be beneficial, particularly in identifying the most effective methods for applying PGPR in crop production. This would result in more environmentally friendly methods that lessen the need for chemical fertilizers.

9 Conclusions

Increased hardship brought on by climate change has an adverse effect on plant and microbial development and has ramifications for global food security. It is difficult to find creative ways to satisfy the rising need for food in a changing environment, especially when plant diseases and stressors have a significant impact on crop sustainability and productivity. One of the possible needs is to increase agricultural productivity while simultaneously improving plant responses to these stresses. Considering this, the present study delves deeply into the ways that plants and their microbiomes improve resistance to environmental stressors such as salt, drought, and temperature fluctuations. We emphasize important microbial tactics, such as ROS scavenging, antioxidant control, and IAA production, that mediate plant tolerance. Furthermore, we highlight the function of bacteria that produce ACC deaminase in controlling ethylene levels, and we recommend that future studies concentrate on the relationship between microbial ACC deaminase activity and plant root ACC exudation for efficient ethylene mitigation under stress. The chemotactic movement of bacteria fueled by hormonal crosstalk and root exudation is explored, as well as recent developments in molecular tools, such as next-generation sequencing and multi-omics approaches, to optimize these interactions.

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