



# Rhizosphere Microorganisms for Climate Resilient and Sustainable Crop Production

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## Abstract

Climate change is a major threat to crop production's sustainability in present-day agriculture. Consequently, the need for improved farming techniques and environment-responsive and climate-resilient technologies is realized as one of the top priorities. Recently, research efforts have been on the rise to develop sustainable crop production strategies by exploring the hidden potential of soil-root-microbiome to establish a sustainable food production system and maintain soil and plant health. Published literature indicated that rhizosphere-associated microbes are the prime force for governing the earth's biogeochemical processes because of their insidious and copious existence in the soil environment. The scientific community is betrothed in extensive research to select and commercialize the microorganisms of biotechnological and environmental significance. It is well-established that microbes aid in providing ecological sustainability in the agrarian system by protecting plants from damaging pests and diseases, promoting plant development, reducing environmental and nutritional stressors, and boosting plant resilience to various abiotic and biotic stress situations. Most importantly, crop growth and yield are directly linked to rhizosphere microbiota. Therefore, attempts have been made to review and synthesize the available literature on rhizosphere microorganisms' role in climate-resilient and sustainable crop production. Besides, a new novel and emerging strategies to deploy microbial consortia as potential bio-inoculants for rhizosphere engineering has been highlighted to improve crop yields and environmental protection that are currently in practice to combat the challenges imposed by ever-changing climate change in a sustainable and eco-compatible manner.

**Keywords** Agriculture · Bio-inoculants · Climate change · Mycorrhizae · Soil microbes · Stress

## Introduction

Microbes power all ecosystems. Hundreds of bacteria, actinobacteria, and fungal cell species can be found in one gram of soil. Soil microorganisms are numerous (Microbes 2010). These bacteria regulate 80–90% of soil processes that maintain soil fertility and provide ecosystem services, including plant nourishment, nitrogen, carbon cycling, soil formation, etc. (Saccà et al. 2017). Climate change is a complex environmental issue. A global issue. Increasing air temperatures, changed precipitation patterns, increased UV radiation, and more extreme weather events like droughts and floods pose new threats to agricultural production (Tirado et al. 2010). Climate change may cause localized cooling, extreme weather, and shifting vegetation zones. These changes will indirectly affect soil organisms and microbial activity (Philippot et al. 2013). India's climate has evolved throughout the past century, with annual temperature trends rising by 0.56 °C (Rao et al. 2009). Climate change will exacerbate climate-related stressors

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such as high temperature, low soil moisture, and salinity (Singh and Bainsla 2015).

Mechanized farming, synthetic inputs, and high-yielding crop varieties have driven farm-level productivity for the growing global population. Yet, sustainable methods that use the soil-plant microbiome to provide a sustainable food supply and maintain soil and plant health are becoming more popular. The intricate soil-plant microbiome complex is hard to explain to society's many audiences. Recent years have shown the need to prepare and streamline the global dissemination of plant microbiome interaction data.

There is an urgent need to develop sustainable agricultural practices that improve crop yield (Cerda et al. 2017), combat climate change (Rosenzweig et al. 2014), minimize soil and environmental degradation (Reddy 2014; Nelson et al. 2014), and protect human health for the present and future. Healthy soil microbial communities ensure macro- and micronutrient cycling for optimal agricultural development (Ney et al. 2019). Plant-microbial interactions give the rhizosphere its dynamic quality for crop development (Basu et al. 2021; Bhat et al. 2022; Hamid et al. 2021). Knowing how endophytic and epiphytic bacteria interact with plants can enable us to exploit and modify germs for useful reasons (Chakraborty et al. 2020; Rana et al. 2022; Verma et al. 2022; Rustamova et al. 2022). Rhizosphere microorganisms are less diverse but abundant and active. The rhizosphere's microbiome is highly influenced by plant-derived metabolites, or root exudates, vital to its establishment and growth (Haney et al. 2015). Arabidopsis root exudates may release more sugar early in the plant's growth cycle than later (Chaparro et al. 2012). Another example is the soybean root rhizome-microbiome assembly, which was affected by plant growth and revealed that more complex microbial communities evolved later (Jaborova et al. 2021, 2022; Xu et al. 2021). Plants choose and maintain microbiome assemblages based on a selection trait.

Plant growth-promoting rhizobacteria (PGPR) such *Bacillus* spp., *Pseudomonas* spp., *Enterobacter* spp., *Acinetobacter* spp., *Burkholderia* spp., and *Arthrobacter* spp. affect many ecological processes and form hostile or synergistic partnerships with native soil microbes (Finkel et al. 2017). PGPR helps plants develop and resist biotic and abiotic stress (Basu et al. 2021 such as drought Gowtham et al. 2022; Khan et al. 2020; Hoseini et al. 2022; Ilyas et al. 2020; Najafi et al. 2021; Tanvere et al. 2023), salinity (Sagar et al., 2020; Kusale et al. 2021a; 2021b), heavy metal ion (Akhtar et al. 2021; Budamagunta et al. 2023), and cold (Sheikh et al. 2022).

### Rhizosphere Microbiome Resilience

Researchers have looked at the direct impacts of climatic change on the makeup and functionality of microbes in

great detail. Several factors of the stability of the microbial community, including resistance and resilience, have been examined to anticipate how a microbial community would react to a disruption (Shade et al. 2012). Changes to soil microbial communities may only occur when abiotic factors are beyond the range that the communities typically encounter (Cruz-Martinez et al. 2009). Soil microbial communities may be more resistant to environmental change than their aboveground plant counterparts. Microbial communities adapt to warming and other disturbances through resilience, made possible by the flexibility of microbial traits or resistance. After the stress has gone, the community reverts to its original makeup (Allison and Martiny 2008). A system's or person's resilience is their capacity or ability to respond to an outside force or disturbance while also meeting certain additional requirements as a result of that reaction (outcome). A system's or person's resilience is their capacity or ability to respond to an outside force or disturbance while also meeting certain additional requirements as a result of that reaction (outcome). The Latin word *resilire*, which means "to spring back," is the root of the English term "resilience." The resistance of the soil system is the amount to which stress harms soil organisms, and its resilience is the rate and extent of recovery (Doring et al. 2015). In light of climate change, resilience has increased significance in agricultural and semi-natural ecosystems. It has been described as a flexible and pertinent health criterion for all levels and types of agriculture (Doring et al. 2015). The soil is an excellent medium for the growth and development of plants and microbes. Insight into the biological basis of resistance and resilience of soil functions has been growing. It has been suggested that resistance and resilience might be related to microbial communities and the properties of the resident soil microorganisms (Griffiths and Philippot 2013).

The soil microbial communities are a fantastic approach to investigating resilience since they may respond to disruptions within days or weeks (Griffiths and Philippot, 2013; Cregger et al. 2012). According to (Cruz-Martinez et al. 2009), the makeup of microbial communities can resilient to changes in the climate as well as in plant productivity and species composition that are brought on by such modifications. Even though the microbial composition is susceptible to a disturbance, the community may be robust and soon recover to its pre-disturbance composition, claim Allison and Martiny (2008). This might result from several microbe characteristics, including their quick growth rates, rapid evolution through mutations, or horizontal gene transfer. Due to their quick generation rates and rapid development under optimum conditions, microbial communities may be among an ecosystem's fastest-responding components to changing environmental conditions. On the other hand, bacteria may be able to adapt to environmental change

more slowly due to their enormous functional and genetic diversity, the potential for fast evolutionary rates, and extensive dispersion ability.

The concentration and composition of certain macronutrients, micronutrients, and trace elements in the soil are necessary for the development and health of plants (Hodges 2010). To influence plant development and production, essential nutrients must be present in a physiologically accessible form. For instance, even though phosphate and sulphate are abundant in the soil, only the soluble ionic form of these nutrients is absorbed by plants through various processes, leaving the remainder unused (Solomon et al. 2003; White and Hammond 2008). Microorganisms are crucial for plants to mobilize and absorb nutrients (Sahu et al. 2018). Arbuscular mycorrhizal fungi (AMF) and plant growth-promoting rhizobacteria (PGPR) are two types of soil microorganisms that are known to benefit plant health, growth, and nutrition (Jaborova et al. 2022).

Overusing pesticides to increase agricultural productivity has seriously disrupted the equilibrium of the soil microbial community. As a result, this has impacted nature's geochemical cycle and contributed to environmental contamination. The employment of microorganisms as bioinoculants is preferable to using pesticides to increase crop production and quality and replenish soil nutrients for sustainable agriculture and the environment (Alori and Babalola 2018). Their use was often suggested to reduce the input of chemicals in agriculture.

Undoubtedly, soil quality and plant health, plant health, and productivity depend on the variety and efficiency of the soil's microbiota. Through various processes, mostly mainly carried out by rhizosphere microbiota members, which are known to improve soil and plant quality, soil microbial dynamics significantly regulate ecosystem functioning. The related processes include enhancing plant establishment, increasing nutrient availability, enhancing nutrient absorption, safeguarding against social and environmental pressures, enhancing soil structure, etc. (Kalam et al. 2020).

The provision of nutrients to plants, including those generated from microbial activity, and the supply of plant photosynthates as substrates for the root-associated microbiota are key elements in creating and operating the rhizosphere. Creating root-soil interfaces produces dynamic microenvironments where microorganisms, plant roots, and soil elements collaborate to carry out processes that are known to impact soil quality and plant health significantly (Jaborova et al. 2022). The rhizosphere is the area of soil impacted by roots, which exude carbon-containing substrates mostly as root exudates, carbon-containing substrates that affect microbial activity. The surface of a plant's root, known as the rhizoplane, is covered in firmly adherent soil particles. Certain microbes can colonize the region inside the root to produce processes that promote plant development

and protect plants (Kalam et al. 2020). Instead of colonizing a segment of the rhizosphere, it is possible to think of these microbes—known as endophytes—as populating the root itself. From a methodological standpoint, some overlap between the rhizoplane and the rhizosphere may be discovered because it is acknowledged that the rhizosphere extends from 1 to 4–5 mm below the root surface and that the rhizoplane with adherent soil can be up to 2 mm wide. Root colonization is the term for microbial invasion of the rhizoplane and/or root tissue. In contrast, rhizosphere colonization refers to invading the nearby soil volume influenced by the roots (Kalam et al. 2020). Microorganisms are encouraged to develop around plant roots by the plant, which provides exudates and other kinds of carbon compounds to microbial populations as either signals or growth substrates.

Due to their vital roles in the sustainability of the agroecosystem and natural ecosystems, beneficial microbes can be employed as inoculants to enhance plant growth and health (Sarkar et al. 2021a). The word “rhizobacteria” refers to a subset of the rhizosphere bacterial community known to have a very specialized capacity for root colonization. This notion is an essential since it focuses on rhizosphere bacteria. The so-called plant growth-promoting rhizobacteria (PGPR), which are helpful root colonist bacteria, perform several significant ecosystem functions, such as those involved in the biological control of plant diseases (Sayyed et al. 2005; Sukmawati et al. 2021; Suriani et al. 2020), nutrient cycling (Jaborova et al. 2021, 2022), and/or seedling establishment (Mondal et al. 2021; Sarkar et al. 2021b). Bashan and Holguin (1998) recently recommended dividing PGPR into two categories to differentiate whether or not they function as biocontrol agents. Relevant mutualistic symbionts include nitrogen ( $N_2$ )-fixing bacteria and mycorrhizal fungi. Most plant species create what are known as mycorrhiza, which are symbiotic relationships between their roots and certain soil fungus. Following the biotrophic colonization of the root cortex, the mycorrhizal fungi create an external mycelium that links the root and the nearby soil microhabitats. In soil-plant systems, this type of mycorrhizal (fungal-root) symbiosis is essential for nutrient cycling. The external al mycorrhizal mycelium creates the water-stable aggregates required for excellent soil tilth in collaboration with other soil organisms. Increased resistance to biotic and abiotic challenges is another way that mycorrhizas benefit plant health, making them potentially valuable for biocontrol and bioremediation.

There is growing interest in determining the usefulness of AM symbiosis in certain plant production systems and, accordingly, in modifying them, where practical, so that they may be included in production practices. This is because AM symbiosis can promote plant growth and health. There is growing evidence that native and/or introduced

AM fungus can improve both transplantable horticultural crops and field-sown and plantation crops. AM activity is connected to various plant crops that are economically significant. These include annual crops that allow the naturally occurring endophytes often present in arable soils to function, such as cereals and legumes. However, in these situations, the biotechnological techniques necessary for properly regulating AM potential are rather complicated. However, mycorrhizal biotechnology may be used in various plant production systems. These are, in general, horticulture (including fruit culture) plant crops and include vegetable crops, temperate fruit trees or bushes, tropical plantation crops, ornamentals, spices, etc.

After being inoculated with PGPBs, plants can develop a state of induced systemic resistance (ISR) to pathogens (Lim and Kim 2013). With little to no effect on production and growth, PGPBs in connection with plant roots can activate the plant's innate immune system and give resistance to a wide range of diseases. In greenhouse and field tests, several PGPBs, including *Pseudomonas fluorescens*, *Pseudomonas putida*, *Bacillus pumilus*, *Serratia marcescens*, *Paenibacillus alvei*, *Acinetobacter lwoffii*, *Chryseobacterium balustinum*, and *Azospirillum brasilense* invade roots and shield a wide range of plant species (Mahapatra et al. 2022b).

A deeper level of specialization is revealed by comparing various fungal endophytes: Heat is passed on by *C. protuberata*, but neither illness nor salt tolerance. Contrarily, *Curvularia magna* and *Fusarium culmorum* both solely offer disease tolerance (Rodríguez-Moreno et al. 2008). It seems that some plants have the potential to grow and survive in harsh environments because of these particular characteristics.

The nitrogen-fixing bacteria, mycorrhizal fungi, plant growth-promoting rhizobacteria (PGPR), biocontrol microorganisms, mycoparasitic fungi, and protozoa are rhizosphere organisms that have been extensively investigated for their favorable impact on plant development and health. The rhizosphere's pathogenic fungus, oomycetes, bacteria, and nematodes are harmful to plant development and health. The human pathogens make up a third class of bacteria in the rhizosphere. There have been more studies during the past ten years describing the spread of human pathogenic bacteria in and on plant tissues (Kaestli et al. 2012). It is crucial to comprehend the mechanisms that influence the rhizosphere microbiome's composition and behavior to protect both human health and plant production. Rhizosphere microorganisms the impact the composition and productivity (*i.e.*, biomass) of natural plant communities in both direct and indirect ways (Schnitzer et al. 2011). As a result, it has been suggested that the abundance of microbial species below ground might predict the variety and productivity of plants above ground (Wagg et al. 2011).

Furthermore, he hypothesized that belowground variety would serve as insurance for preserving plant production under various environmental circumstances. Microorganisms in the soil and rhizosphere are considered bioindicators of soil quality because of their sensitivity to tiny changes in abiotic circumstances, such as environmental stress and disturbance.

Rhizobacteria create compounds that prevent rival microbes from proliferating or functioning. Additionally, rhizosphere fungi produce large quantities of antibiotic compounds. *Trichoderma* species, in particular, they have attracted much interest in producing antibacterial chemicals (Druzhinina et al. 2011). Most bacterial and fungal biocontrol strains generate several antibiotic compounds with varying levels of antimicrobial activity. For instance, several polyketide and non-ribosomal peptide antibiotics have broad-spectrum activity, while bacteriocins such as Agrocin 84 generated by *Agrobacterium radiobacter* demonstrate antibiotic properties against closely related taxa. It's interesting to note that many antibiotic substances have various effects on other bacteria at sub-inhibitory doses. This finding inspired an intriguing new line of inquiry into the biological effects of antibiotics. Recent research has demonstrated that antibiotics work differently depending on their concentration, serving as growth inhibitors at high doses and intercellular signaling mediators at low ones (Romero et al. 2011). Antibiotics are also thought to play a part in motility, biofilm development, defense against predatory protozoa, and feeding (Raaijmakers and Mazzola 2012).

Depending on the endophyte, symbiotically given disease tolerance appears to involve several pathways. For instance, a pathogen challenge, a non-pathogenic *Colletotrichum* strain that imparts disease resistance does not activate host defense. Furthermore, disease resistance is not widespread; rather, it is limited to tissues where the fungus has colonized.

The rhizosphere serves as the first line of defense for plant roots against infections carried by soil (Cook et al. 1995). The rhizosphere microbiome contains a variety of organisms that may combat soilborne diseases before and during initial infection, as well as during secondary dissemination on and in root tissue. The primary strategies used by rhizosphere microorganisms to combat plant pathogens include antibiosis (Raaijmakers and Mazzola 2012), competition for trace elements, nutrients, and microsites (Duffy 2001), parasitism (Druzhinina et al. 2011), interference with quorum sensing that affects virulence (Schenk et al. 2012).

## Climate Change and Agriculture

Many environmental elements, such as moisture and temperature, impact plant systems and, consequently, crop



yields. These factors may work in conjunction with or in opposition to other factors to affect crop yields. Controlled field studies can provide data on how a particular crop variety's yield reacts to a specific stimulus, such as water or fertilizer. Such controlled tests, however, only take a small number of environmental elements into account by nature. Utilizing crop biophysical simulation models with embedded parameters from field trials is an alternate method for estimating crop yield (changes). The majority of quantitative estimates of climate change effects on crop yields are generated from these crop simulation models since climate change is anticipated to impact a variety of environmental parameters (e.g., Rosenzweig and Parry 1994). While the evaluation of climatic effects across a variety of crops is made manageable by using crop simulation models, such models also have drawbacks, such as their exclusion from the diversity and unpredictability of elements and situations that affect productivity in the field. Increasing temperatures, altering precipitation patterns, and increasing atmospheric CO<sub>2</sub> concentrations are all plausible possibilities for climate change. Although temperature rises can affect crop yields both favorably and unfavorably, it has been discovered that temperature increases decrease the yields and quality of many crops, most notably cereal and feed grains. Increases in precipitation (amount, timing, and variability) may help semi-arid and other water-scarce places by boosting soil moisture. Still, they may exacerbate issues in locations with a abundant water. Greater net photosynthetic rates would be made by an environment with a higher CO<sub>2</sub> content (Allen et al. 1987). Conversely, a decrease in precipitation may have the opposite effect. Microbes have many benefits of biofilm, as it acts as a sink for the nutrients in the rhizosphere and aids bacteria to survive under unfavorable conditions. Besides that, it helps in exchanging genetic material (Rayanoothala et al. 2021).

Higher concentrations may also cause plants to close their stomatal apertures, tiny holes in their leaves through which CO<sub>2</sub> and water vapor are exchanged with the atmosphere. This could result in decreased transpiration (i.e., water loss), faster rates of soil erosion and degradation, and higher levels of tropospheric ozone due to the warming climate. Changes in runoff and groundwater recharge rates, which impact water supply, as well as adjustments to capital or technology needs, such as surface water storage and irrigation techniques, may have further indirect consequences. Typically, these indirect consequences are not considered in current evaluations (the exceptions are changes in water supplies).

It has been suggested that some plant species' capacity to endure harsh environments may be influenced by the rhizosphere microbiome. For instance, a soil isolate from an arid and salty environment called *Achromobacter piechaudii* ARV8 dramatically boosted the biomass of

tomato and pepper seedlings subjected to brief drought stress (Mayak et al. 2004). It was also shown that rhizobacteria might help plants develop when there is flooding (Grichko et al. 2005). Soil salinity caused by osmotic and drought stress can have a significant impact on plant productivity in a variety of agricultural systems. Halotolerant bacteria flourish in salt-stressed environments and can exhibit characteristics that aid in the development of the host plant when they are present. Upadhyay et al. (2009) demonstrated that 24 of 130 rhizobacterial isolates from the rhizosphere of wheat plants cultivated in a saline zone were resistant to quite high NaCl levels (8%). The 24 salt-tolerant isolates all generated indole-3-acetic acid ten of them solubilized phosphorus, eight of them produced siderophores, six of them produced gibberellin, and two of them had the *nif H* gene, which indicated that they might be able to fix nitrogen. *Bacillus* was the most prevalent bacterial genus found under these circumstances (Upadhyay et al. 2009). Also, halotolerant bacterial strains were discovered among halophytic plant species in Korea's coastal soils. The decrease in ET synthesis via ACC deaminase activity was hypothesized as the underlying mechanism of the discovered isolates' enhancement of plant development under salt stress (Siddique et al. 2010). Roots of the extreme halophyte *Salicornia brachiata* were used to identify new halotolerant diazotrophic bacteria that produce indole acetic acid, solubilize phosphate, and have ACC deaminase activity (Belimov et al. 2012). The isolates were identified as *Cronobactersakazakii*, *Pseudomonas* spp., *Rhizobium radiobacter*, *Mesorhizobium* sp., *Zhihengliuella* sp., *Haererehalobacter* sp., *Halomonass* sp., *Vibrio* sp., and *Brachy bacterium saurashtrense* sp. nov (Belimov et al. 2012).

Low-temperature environments are home to microorganisms that have evolved to survive there. It is noteworthy to note that native legumes in the high arctic may nodulate and fix nitrogen at rates equivalent to those reported for legumes in temperate regions, despite the effect of cold temperatures on nodule formation and nitrogen fixation. Microbial inoculants that promote plant development under cold circumstances are of major interest in agriculture and horticulture. For instance, at 4 °C, *Burkholderia phytofirmans* PsJN boosted physiological activity and grapevine root development (Barka et al. 2006). At 15 °C, where soybean nodule infection and nitrogen fixation are often hindered, *Serratia proteamaculans* promoted soybean growth when co-inoculated with *Bradyrhizobium japonicum* (Katiyar and Goel 2003) chose cold-tolerant mutants of several *P. fluorescens* strains for their capacity to solubilize phosphorus and stimulate plant development. This was done to determine the processes involved in the stimulation of plant growth at low temperatures. They discovered two cold-tolerant mutants more effective at solubilizing phosphorus at 10 °C than the corresponding wild kinds (Katiyar and Goel 2003).

Additionally, two mutants (out of 115) were discovered by (Trivedi and Sa 2008) to be more effective than the wild-type strain of *Pseudomonas corrugata* in solubilizing phosphorus throughout a temperature range of 4 to 28 °C. The names of the genes linked to phosphorus solubilization and cold tolerance were not disclosed in either study.

Crops grown for food, feed, fiber, and fuel suffer significant yield decreases due to soilborne plant diseases. The two primary categories of soilborne plant diseases are the nematodes and fungus, which include both genuine fungi and oomycetes that resemble fungi. Plant pathogenic fungi, oomycetes, and nematodes are agronomically more significant in temperate regions than plant pathogenic bacteria, even though some bacterial species (such as *Pectobacterium* and *Ralstonia*) may significantly harm particular crops economically. *Agrobacterium tumefaciens*, *Ralstonia solanacearum*, *Dickeya dadanthi* and *Dickeyasolani*, *Pectobacterium carotovorum*, and *Pectobacterium atrosepticum*, and *Dickeya solani* are among the top 10 most infamous bacterial pathogens that infect plants through their roots (Mansfield et al. 2012). Viruses may also harm plants by entering their roots, but they need the help of nematodes or zoosporic fungus (Voigt et al. 2013). Information on root exudates that activate and attract soilborne plant diseases is more scant and fragmented than our knowledge of the function of rhizo-deposits in the communication between symbionts and plants. According to (Weston et al. 2012a, 2012b), a lack of awareness of the complicated physical-chemical conditions in soil and rhizosphere settings is primarily to blame for the limited understanding of the communication between plants and root diseases. Thus, it will be crucial to develop our analytical capabilities to clarify the chemistry of rhizodeposits and their spatiotemporal production and dispersion patterns, generally referred to as “ecometabolomics” (Sardans et al. 2011; Weston et al. 2012a, 2012b).

The rhizosphere serves as a cradle for many microorganisms advantageous to plants. Environmental changes dynamically alter the organization of the microbial community in a plant’s rhizosphere. Hence, strategically managing plants’ rhizospheric microbiomes can be essential for reducing stress and managing disease (Sarker et al. 2021).

## Techniques for Decoding Rhizosphere Microbes:

### Resource Partitioning

While resource competition is common across microbial communities, niche differentiation guarantees no competitive exclusion. Resource partitioning, which prevents mul-

tipale community members from competing for the same resource in favor of relying on different metabolites for energy, is the main mechanism underlying niche differentiation. As a result, other pools of secondary metabolites are secreted, which furthers niche differentiation. This frequently happens in natural consortia since no one nutrition supply is usually adequate to support the diversity of organisms in a community. Any consortium operating in soil with non-uniform nutrient content would benefit most from resource partitioning. For instance, heterogeneity in soil’s carbonaceous sources prevents competition between various consortium members, resulting in a very diverse variety (Pinton et al. 2007). *Pseudomonas syringae* and several other strains’ coexistence in a consortium coexistence research in the 1990s was inversely proportionate to how similar their carbon usage patterns were (Zhou et al. 2002). On the other hand, resource partitioning can be created for artificial consortia for overall better production. This has been demonstrated, for instance, in a co-culture of synthetically produced *E. coli* strains that may make lactate by simultaneous metabolism utilizing either glucose or xylose as a substrate (Wilson et al. 1995).

### Horizontal Gene Transfer (HGT)

The horizontal gene transfer between microbial species may be the main driving mechanism behind microbial evolution (Zhou et al. 2015). The creation of varied phenotypes these non-genealogical transfers can allow for the coexistence of numerous, highly specialized microbial species in various ecological niches where they exhibit cooperative behaviors (Gogarten et al. 2002). HGT also permits the diversification of symbiotic populations into distinct groups, such as pioneers, harvesters, and scavengers. Pioneers build and destroy insoluble substances, which harvesters then ingest, while scavengers using their feces. Without HGT, it could not be able to lose genetic features or acquire new ones (Polz et al. 2013). On the other hand, if HGT is inhibited in a consortium, coexistence can be hampered (Dutta and Pan 2002).

### Microbial-based Strategies

According to reports, the core microbiota members play a vital role in directing the development and operation of other microbial assemblage members. Thus, these bacteria may be mined for potential use in agricultural operations to attract additional advantageous plant microbiome members, particularly during the early phases of plant growth (Philippot et al. 2013). Research described a plant breeding strategy inspired by microbial assemblages to create plant core microbial communities *in situ*. A step-by-step inoculation methodology was used to choose the next gen-

eration of beneficial microbiota (Qiu et al. 2019). Following next-generation sequencing, statistical analysis, and fitting them into network analysis models, the core and the central microbiomes are defined. The interconnected core microbiomes that play key functions are then identified using metagenomics, followed by their isolation from the plant and subsequent application as a microbial cocktail. Before a seedling forms and is passed on to offspring, the parental flowers can be sprayed with the microbial cocktail, perhaps resulting in seeds augmented with certain central microbiota (Qiu et al. 2019).

### Biochemical Strategies

Under challenged environmental situations, when the root exudates themselves serve as the regulators against the stressors, microbiome assembly in the plant rhizosphere through root exudates may modify the rhizobium population by possibly recruiting bacteria with advantageous features (Stringlis et al. 2018). Therefore, native microbiomes may be engineered using biochemical techniques to encourage the release of chemical compounds produced naturally by plants and microorganisms. According to a recent study, some VOCs may be used to strengthen plant defense systems by synthesizing the soil microbe in situ. These VOCs might notify soil bacteria from a distance or “call from a distance” to reduce pathogens (Kwak et al. 2018). Alternately, in situ engineering techniques that resemble microbial quorum sensing, in which particular microbial communities act differentially depending on the complex arrays of signal molecules for communications, may be used to increase potentially beneficial microbiomes in the rhizosphere (Rayanothala et al. 2021). This is particularly true in the rhizosphere, where plants respond to microbial signals from heat shock and dehydration by generating heat shock proteins and sudden reactive oxygen species, respectively (Papenfort and Bassler 2016). These signal molecules can also be employed to selectively promote central microbiome assembly in the “core” microbiota to mobilize, solubilize, or mineralize nutrients for use in nutrition uptake or simply to ward off harmful organisms.

### Molecular Strategies

The plant genetics that hosts the abovementioned biom heavy influence and intimately intertwine with the entire microbiome makeup, functions, and richness (Horton et al. 2014). The idea of “Plant with Better Microbiome” may be based on capturing the essence of this mutualism between the microbiome and the plant genome. Quantitative genetic methods, such as QTL (quantitative trait loci) mapping, can be very helpful in this situation because they enable us to recognize advantageous genetic features (phenotypes)

of the host or the microbiome that could clarify a new defensive mechanism against pathogens or energy route. The plant genetics that hosts the aforementioned biome heavily influences and intimately intertwine with the entire microbiome makeup, functions, and richness (Horton et al. 2014). The idea of “Plant with Better Microbiome” may be based on capturing the essence of this mutualism between the microbiome and the plant genome. Quantitative genetic methods, such as QTL (quantitative trait loci) mapping, can be very helpful in this situation because they enable us to recognize advantageous genetic features (phenotypes) of the host or the microbiome that could clarify a new defensive mechanism against a pathogen or energy route. The mutant strain, M1 (deletion of surfactin synthase gene) of *B. subtilis*, was found ineffective as a biocontrol agent against *P. syringae* in both infectivities and in biofilm formation on either root or inert surfaces (Bais et al. 2004; Mahapatra et al. 2020).

### Rhizosphere-associated Microbial Communities Under Stress

The rhizosphere, which comprises a complex web of plant roots, soil, and a wide variety of bacteria, fungi, eukaryotes, and archaea, is unquestionably the most complicated microhabitat. The rhizosphere conditions impact crop growth and yield. Nutrient-rich rhizosphere conditions promote plant development and yield, and vice versa. The majority of soils that need to be nurtured before or during the next harvest are exhausted by extensive agriculture. The primary source of crop nutrients is chemical fertilizers. Still, due to their unchecked and widespread use, the viability of agriculture and the stability of an ecosystem are seriously threatened. These chemicals build up in the soil, drain into the water, and are released into the atmosphere, where they linger for years and pose a major hazard to the ecosystem. Common microbes are *Arthrobacter nicotianae*, *Bacillus amyloliquefaciens*, *B. sphaericus*, *B. subtilis*, *Paenibacillus amylolyticus*, *P. polymyxa*, *Micrococcus luteus*, *Pseudomonas aeruginosa*, and *P. azotoformans*, and most predominant species were reported from various parts of the plant such as phyllosphere, rhizosphere and internal tissues (Verma and Suman 2018; Mahapatra et al. 2020) (Table 1).

The need for more reliable techniques has been highlighted by the inherent drawbacks connected with the use of microorganisms that promote plant development and act as biocontrol agents. Sustainable agriculture can be achieved by utilizing the advantages of microbiome-based rhizospheric engineering, facilitating crop improvement, and ensuring abiotic and biotic stress management (Kaul et al. 2021; Ke et al. 2021; Rai et al. 2023) (Table 2).

**Table 1** Various techniques used to identify the microbes which are resided in rhizosphere

HOST	APPROACH	TYPE OF MICROBIOTA	REFERENCES
Maize	nifH Cluster I clone library	<i>Azospirillum</i> , <i>Bradyrhizobium</i> , and <i>Ideonella</i> were the most abundant genera found in the rhizosphere	Roesch et al. (2007)
<i>Erica andevalensis</i> in a naturally metal-enriched and extremely acidic environment	16S rRNA gene clone library	Actinobacteria (38 clones; 12 OTUs) followed by the Acidobacteria (21 clones; 10 OTUs), and Proteobacteria (18 clones; eight OTUs). Archaea: considering 27 clones, the community was composed by Crenarchaeota (21 clones; four OTUs) and Euryarchaeota (six clones; two OTUs)	Mirete et al. (2007)
Potato	16S rRNA gene microarray	Proteobacteria (46%), followed by Firmicutes (18%), Actinobacteria (11%), Bacteroidetes (7%), and Acidobacteria (3%). The bacterial families Streptomycetaceae, Micromonosporaceae, and Pseudomonadaceae	Weinert et al. (2011)
Sugarbeet	16S rRNA gene microarray	Proteobacteria (39%), Firmicutes (20%), and Actinobacteria (9%). The Gamma- and Betaproteobacteria and Firmicutes were identified as the most dynamic taxa associated with disease suppression	Mendes et al. (2011)
<i>Rhizophora mangle</i> and <i>Laguncularia racemosa</i> in mangroove	Archaeal 16S rRNA gene pyrosequencing	About 300 archaeal OTUs were identified. Four classes were found: Halobacteria, Methanobacteria, Methanomicrobia, and Thermoprotei	Pires et al. (2012)
Oak in a forest soil	16S rRNA gene pyrosequencing	The predominant phyla were Proteobacteria (38%), Acidobacteria (24%), and Actinobacteria (11%). A high proportion of unclassified bacteria (20%) were observed	Uroz et al. (2012)
<i>Deschampsia antarctica</i> and <i>Colobanthus quitensis</i> in the Arctic	16S rRNA gene pyrosequencing	Firmicutes was the most abundant group found, and Acidobacteria was rarely detected. The predominant genera found were Bifidobacterium (phylum Actinobacteria), Arcobacter (phylum Proteobacteria), and Faecalibacterium (phylum Firmicutes)	Teixeira et al. (2010)

OTUs operational taxonomic units

Salinity in agricultural soils refers to the buildup of salt at concentrations that can sufficiently hinder crop growth and productivity. Poor irrigation water quality or an excessive amount of salts that are naturally present in the soil due to mineral weathering are the two main causes of salinity (Kusale et al. 2021a; 2021b, Sagar et al. 2020; Bhardwaj and Kumar 2020). The “playhouse” where soil, plants, and microorganisms are interconnected to create a platform for interactions between soil, plants, and microbes is known as the rhizosphere, which is near the soil and root zone (Backer et al. 2018). The most crucial rhizosphere actors may use their interplaying physics, chemistry, and biology to transform the rhizosphere into a home for small soil drivers like bacteria, fungi, and archaea (Hassan et al. 2019). A brief contact between rhizospheric bacteria and plant roots depends on transferring nutrients and carbon sources between the collaborating organisms. “Root exudates” cause the enhanced interaction between rhizobacteria and plant roots in the rhizosphere zone (Sharaff et al. 2020). The nutritional elements included in root exudates, including carbohydrates, organic acids, and hormones, may function as a signaling chemical to colonize in the rhizospheric root for soil-dwelling microbes, including beneficial rhizobacteria (Chakraborty et al. 2022). According to studies, soil organic amendment is the main cause of the dramatic shift in the rhizobacterial population (Milkereit et al. 2021). Interactions between the nematode and the N-cycler bacterial

population progressively enhance nutrient cycling. To better understand the relationship between plants and bacteria, a multidimensional interaction has been observed in the rhizospheric zone. Rhizosphere interactions between plants and microbes may aid plant growth and lessen biotic and abiotic stress conditions (Goswami and Deka 2020; Kapadia et al. 2021). Therefore, the related microorganisms, including beneficial rhizobacteria, use the rhizosphere as a playground (Kumar et al. 2017) (Table 3).

Due to their sessile nature, plants experience abiotic and biotic stressors continuously during their entire life cycle (Perez and Brown 2013). Their ability to persevere in these circumstances is crucial to their existence. It is well known that certain non-pathogenic bacteria called PGPR can improve plants’ physiological status under these challenging circumstances (Han et al. 2014). Both of the strains employed in this study have proven developing resistance in tomato plants and from developing resistance from biotic and abiotic stressors. L81 is a member of the genus *Bacillus*, often known as PGPR (Han et al. 2014). An *Aeromonas* strain called PGPR is AMG272 (Ashraf 2004).

The ability of PGPR to prime plants through physiological modifications to the metabolic processes alters the distribution of energetic resources, compromising plant growth in favor of a secondary metabolism involved in defense that is more active. When under stress, highly oxidizing ROS are produced, which instantly disrupt photosynthesis.



**Table 2** List of potential rhizobacteria which mitigates various biotic stresses

HOST	Stress	Rhizosphere microbe	REFERENCES
<i>Solanum lycopersicum</i>	<i>Spodoptera litura</i>	<i>Pseudomonas putida</i> and <i>Rothiasp</i>	Bano and Muqarab 2017
<i>Oryza sativa</i>	<i>Rhizoctonia solani</i>	<i>Bacillus amyloliquefaciens</i> (SN13)	Srivastava et al. 2016
<i>Cucurbita pepo</i>	<i>Aphis gossypii</i> Glover	<i>Rhizobium etlistrain G12</i>	Martinuz et al. 2012
<i>Nicotiana tabacum</i> cv White burley	Cucumber mosaic virus	<i>Peanibacillus lentimorbus</i> B-30488	Kumar et al. 2016
<i>Solanum lycopersicum</i> L	<i>Clavibacter michiganensis</i>	<i>Pseudomonas</i> sp. 23S	Takishita et al. 2018
<i>Physalis peruviana</i>	<i>Fusarium oxysporum</i>	<i>Tricoderma koningiopsis</i> Th003 WP	Díaz et al. 2013
<i>Solanum tuberosum</i>	<i>Phytophthora infestans</i>	<i>Pseudomonas chlororaphis</i> R47	Dixit et al. 2016
<i>Glycine max</i> L	<i>Rhizopus</i> sp. and, <i>Fusarium</i> sp	<i>Bradyrhizobium japonicum</i> NCIM 2746	Khandelwal et al. 2002
<i>Gossypium</i> sp	<i>Pythium ultimum</i>	<i>Pseudomonas fluorescens</i>	Hassen et al. 2016
<i>Lycopersicon esculentum</i>	<i>Pythium splendens</i>	<i>Pseudomonas aeruginosa</i> 7NSK2	Buydens et al. 1996
<i>Capsicum</i> spp	<i>Phytophthora capsici</i>	<i>Serratia plymuthica</i> strain C-1, <i>Chromobacterium</i> sp. strain C-61 and <i>Lysobacter</i> <i>enzymogenes</i> strain C-3 consortium	Kim et al. 2008
<i>Triticum aestivum</i> (wheat) cv. Tabuki	<i>Fusarium graminearum</i>	<i>Pseudomonas fluorescens</i>	Moussa et al. 2013
<i>Oryza sativa</i>	<i>Pyricularia oryzae</i>	<i>Corynebacterium agropyri</i> (UPMP7)	Ng et al. 2016

**Table 3** List of potential rhizobacteria which mitigates various abiotic stresses

HOST	Stress	Rhizosphere microbe	REFERENCES
Green gram ( <i>Vigna radiata</i> )	Drought	<i>P. fluorescens</i> (Pf1) <i>B. subtilis</i> (EPB5, EPB22, and EPB 31)	Saravanakumar et al. 2010
<i>Capsicum annuum</i>	Drought	<i>B. licheniformis</i> (K11)	Lim and Kim 2013
<i>Helianthus annuus</i>	Drought	<i>Achromobacter xylosoxidans</i> (SF2) <i>B. pumilis</i> (SF3) and SF4)	Castillo et al. 2013
<i>T. aestivum</i>	Salinity	<i>Dietzianatronolimnaea</i> (STR1)	Timmusk et al. 2014
<i>T. aestivum</i>	Drought and Salinity	<i>B. subtilis</i> <i>A. protophormiae</i> (SA3) <i>D. natronolimnaea</i> (STR1)	Timmusk et al. 2014
<i>Oryza sativa</i>	Salinity	<i>Halobacillus dabanensis</i> (SB-26) <i>Halobacillus</i> sp. (GSP 34)	Rima et al. 2018
<i>Pisum sativum</i>	Salinity	<i>Acinetobacter bereziniae</i> (IG 2) <i>Enterobacter ludwigii</i> (IG 10), <i>Alcaligenes faecalis</i> (IG 27)	Sapre et al. 2021
<i>Triticum aestivum</i> L	Heat stress	<i>Rhizophagus irregularis</i>	Cabral et al. 2016
<i>Oryza sativa</i>	Salt tolerance	<i>Bacillus pumilus</i> strain JPV511	Kumar et al. 2020
<i>Avicennia marina</i>	Heavy metal stress	<i>Halomonas</i> sp	Mukherjee et al. 2019

**Table 4** Techniques used for modifying plant microbiomes

Method	Brief about the method	Reference
Metabolic network monitoring	Building species-level models for foreseeing how microbial communities will evolve in response to environmental variables such substrate availability, metabolic interdependence, competitive pressures, and spatial heterogeneity	Kessell et al. 2020
Single-cell genomics, whole-community metagenomics, and metaproteomics	Integrating genetic, transcriptomic, and metabolomic data to enhance the function and network connections of the microbiome in the individual	Hadadi et al. 2020

Therefore, even before symptoms are seen on the leaves, the photosynthetic apparatus is the first physiological function to be impacted by a stress scenario. For this reason, metrics linked to photosynthetic efficiency as Fv/Fm, PSII, and NPQ, can be used to measure the effects of stress (Lucas et al. 2014).

Sugars, amino acids, flavonoids, proteins, and fatty acids all make up root exudates (Badri and Vivanco 2009). These compounds have multiple functions in the microbiome, including as antimicrobials or growth deterrents for some microorganisms and as growth substrates or signals for others (Bais et al. 2006). Many well-known examples of symbiosis involve complex chemical signaling interactions between plant and microbe partners. Fixation of atmospheric nitrogen in nodules, for instance, results from a series of complex and specific interactions that begin when legumes release flavonoids that alter gene expression patterns in rhizobia (Oldroyd and Downie 2008). Future work needs to determine if chemical signaling plays a role in plant microbiome interactions beyond the rhizosphere. Evidence suggests that chemical signaling plays a significant role in facilitating interactions between different kingdoms. Plants, for instance, have been shown to increase anti-fungal gene expression in root-associated bacteria and to interact with the acyl-homoserine lactone signaling mechanisms involved in bacterial cell-to-cell communication (Jousset et al. 2011).

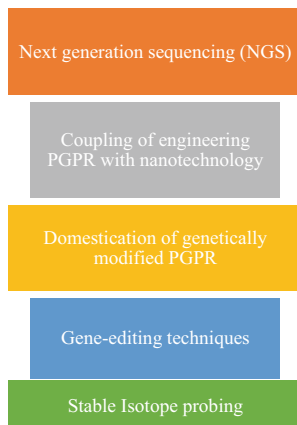
Due to population growth and climatic change, crop production (Hamilton et al. 2016). Sustainable agriculture requires plant-microbial interactions. Mutualism provides biotic and abiotic resistance, plant health, and production. Microbiota diversity influences the host plant's inherent traits, and natural and regulated selection pressure. Lumibao et al. (2020) revealed the fundamentals of how artificial ecosystem rhizospheric microbial variation plant provenance. They discovered plant-soil-microbe feedback mechanisms Interaction in forming plant intraspecific variation depleted ecosystem. However, the reverse theory of understanding how plant genotype affects phylogeny rhizosphere microbiome signatures was first experimentally by Perez-Izquierdo et al. (2019). Their discovery improves communication. Host-genotypic influences and environmental causes more remarkable performance. Hybrid banana endosphere bacteria cell walls (Enterobacteriaceae). ACC deaminase is promising in preventing the Fusarium wilt of banana. Synthetic microbial community implicated in investigating

priority effects and keystone species gnotobiotic Arabidopsis model phyllosphere (Carlstrom et al. 2019). This useful method aids in testing the fundamentals that shape the phyllosphere community. Hence, engineering the host plant's unique microbiome helps explain microbiota structure and genes. It is essential to know the Techniques used for modifying plant microbiomes (Table 4).

According to Kang et al. (2012), who showed that salicylic acid (SA) up-regulates some defense proteins as APX, these data suggest that the mechanisms used by L81 to relieve salt stress in plants may be mediated by an increase in APX activity an increase in APX activity may mediate the mechanisms used by L81 to relieve salt stress in plants. As observed by Lucas et al. (2014) Lucas et al. (2014) observed with other PGPR in rice, L81 boosted APX activity at the three sample times during salt stress. In both cases, bacteria were able to protect plants from salt conditions. However, AMG272 only slightly boosted SOD activity 48 h after pathogen injection, which was linked to less protection.

## Management of Rhizosphere for Sustainable Agriculture

There are many advanced biotechnological tools for improving beneficial rhizobacteria (Fig. 1) (Sarker et al. 2021). Microbial inoculation is generally necessary as part of agricultural practise due to topsoil degradation, soil sterility, poor plant development, low yield index, and insufficient diversity of native bacteria. Utilizing plant-microbe interactions will support the green economy's growth for establishing economic stability and assisting in mitigating climate change. It results in the creation of plant cultivars that may flourish when faced with the challenges of a warming world and high CO<sub>2</sub> levels (Philippot et al. 2013). By lowering the need for synthetic z fertilizers, and pesticides and supporting a variety of ecosystem processes, beneficial soil microorganisms can also provide significant socio-economic benefits to the global economy. To increase nutrient availability for high-yielding, high-quality crop production, (ii) protect crops from pests, pathogens, and weeds, and (iii) manage other factors limiting production, providing ecosystem services, and resilience to stresses like droughts,

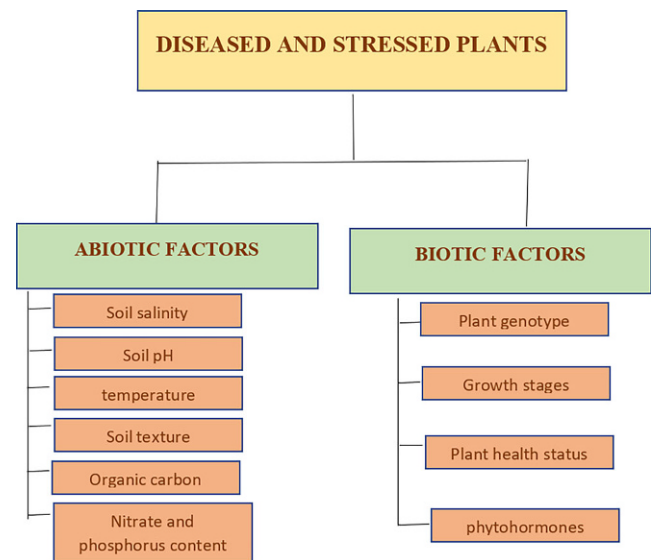


**Fig. 1** Biotechnological tools for improving beneficial rhizobacteria (Sarker et al. 2021)

beneficial microbes can be introduced into the soil environment (Lehman et al. 2015).

In the rhizosphere of actively growing plants, root exudates are particularly important to plant-microbe interactions (Badri et al. 2013). The composition of root exudates varies by plant species and even cultivars within a species (Micallef et al. 2009). As a result, so does the soil microbial community (Kuklinsky-Sobral et al. 2004; Salles et al. 2004). Variation in root exudation among plant species and genotypes suggests the potential for manipulation of root exudation in agricultural cultivars to create specific selective effects on the rhizosphere microbiome (Fig. 2). The Sugars, amino acids, flavonoids, proteins, and fatty acids are present in root exudates (Badri and Vivanco 2009). These compounds can act as signals or growth substrates for appropriate microbial partners and antimicrobials or growth inhibitors for other organisms (Bais et al. 2006; Chakraborty et al. 2022; Mahapatra et al. 2022a). Plant-microbe interactions are mediated by a very complex interplay of chemical communication in a number of classic examples of symbiosis. For instance, when legumes produce flavonoids, they cause rhizobia to change their gene expression patterns. This sets off a series of intricate interactions that eventually cause nodules to fix atmospheric nitrogen (Oldroyd and Downie 2008). Identifying if chemical signaling plays a larger role in plant-microbiome interactions in the rhizosphere is a crucial task that lies ahead.

The inability to examine root exudation in situ has been a significant barrier to advancing notions relating to interactions between root exudates and soil bacteria—however, recent advances in this field. For instance, exudates have been collected using anion exchange membranes, and comparisons between bulk and rhizosphere soil have been made to account for soil-derived chemicals (Chiang et al. 2011). When image analysis is combined with placing anion exchange membranes in contact with roots, it is possible to repeatedly sample root exudates from the same roots over time and calculate exudation rates (Shi et al. 2011). By flushing intact live roots with an aqueous solution to gather

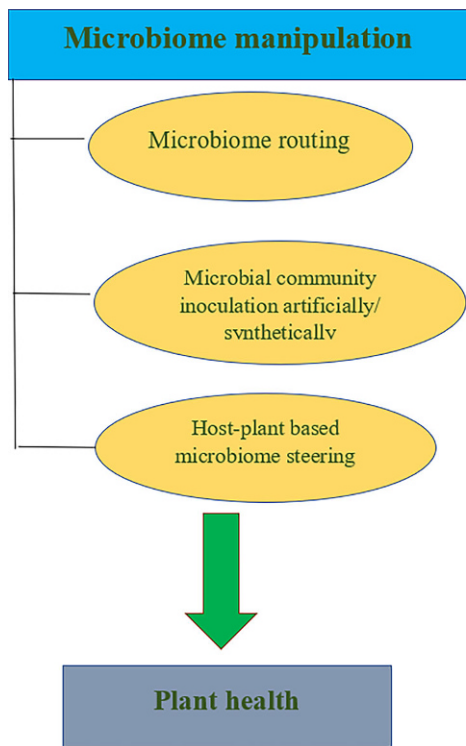


**Fig. 2** The scenario of a diseases/stressed plant when influenced by various abiotic and biotic factors

the soluble exudate components, exudates have also been recovered from intact live roots (Phillips et al. 2008). It may be feasible to employ plants to influence soil microbial communities more widely than just in the rhizosphere, as host plant effects have been found in the bulk soil microbiome (Bremer et al. 2009; Mahapatra et al. 2022b). This possibility is crucial in agricultural systems because, during crop rotation, as hosts change, microbial colonizers for the newly developing rhizosphere are taken from the general soil community (Jones et al. 2004). The effects of the host plant on the soil microbiome increase over time, and microbial partners likely adapt to the host plant. There is evidence of co-evolution between plants and rhizosphere microorganisms, at least in tight mutualistic symbioses (Lambers et al. 2009) (Fig. 3).

Because the plant provides nutrients for which microbial metabolic capability has not developed or becomes common, a lack of shared history between the host plant and soil microbiome may prevent niche saturation in the rhizosphere. Untrained microbes could easily use components of common root exudate. Non-pathogens and pathogens may compete, for instance, for space on root surfaces or access to nutrients secreted from roots. A host-adapted microbiome's quick colonization of roots could stop pathogen establishment. Ecological investigations of plant-soil interactions reveal information that could be useful for agriculture. Contrary to the findings above, the buildup of pathogens with recurrent cultivation has also been noted in agricultural settings, providing support for crop rotation (Hwang et al. 2009).

Rhizosphere microorganisms have a variety of potential positive effects on plant performance. Agricultural produc-



**Fig. 3** The positive approach to manipulate microbiota which directs to plant health

tivity may be increased by utilizing advantageous microbial functions more completely wherever host plants utilize microbiome services. The provision of nutrients (Janos 2007), increased resistance to abiotic stresses, activation of the plant's innate immune response system (Jain et al. 2011), modification of functional plant traits (Friesen et al. 2011), or alteration of tissue chemistry (Larsen et al. 2006) are a few examples of the microbial services that may be provided. A more practical method of utilizing beneficial microbial functions in agricultural systems is urgently needed.

## Research Gaps and Challenges

The objective of utilizing plants as selective agents to enhance beneficial microbial functions in the soil is significantly hampered by the variability across habitats, soil types, and microbial communities. These factors interact with one another: differing soil types influence plant physiology (Taiz and Zeiger 2006), which in turn will change interactions with soil microorganisms (Wakelin et al. 2008) to shaping the microbial communities that exist there. Broad surveys that test specific plant genotypes across treatments in which environment, soil qualities, and microbial communities are systematically and independently modified will be necessary to get a clear image of how challenging it may be to overcome this variability.

One facet of this environmental variability is the soil microbiome, and interaction with the local microbiome adds to the site-to-site variability in plant performance. From this angle, selecting plants with consistent performance across environments can lessen the sensitivity of the host plant to microbial activity. For instance, it has been demonstrated that current wheat cultivars have lower mycorrhizal dependency than earlier landraces. If this is the case, it may be necessary to reintroduce genes into elite germplasm that mediate advantageous interactions with related microorganisms (Schweitzer et al. 2008).

A crucial aspect of many plant advantages mediated by microbes is context dependence. For instance, microbial interference with plant hormone signaling may be advantageous in drought-like conditions but not always in other ones (Shaharoon et al. 2011). To perform at their best, plants must be able to quickly recruit or improve specific microbial services in environments where their net benefits would be greatest. The host plant's known geographical and temporal variability in root exudation may tolerate this adaptive flexibility (Wu et al. 2018).

Future research could create cultivars or transgenic plants with exudation traits that promote advantageous microbiome traits and microbial functions while deterring pathogens. But before that can happen, we must have a far more thorough understanding of how different exudate components interact with one another to influence the soil microbiome. Comparative studies of plant hosts with various traits of root exudation have started to fill this gap. For instance, compared to the wild-type plant, root exudates from an *Arabidopsis* mutant were found to contain relatively more phenolic compounds and fewer sugars. This change resulted in a relatively higher abundance of beneficial soil bacteria, including rhizobacteria that promote plant growth, nitrogen-fixing bacteria, and bacteria involved in heavy metal remediation (Badri et al. 2013). Before plant breeders can develop plants that support their advantageous microbiome, however, more research of this kind will need to be done. The possibility that additional, previously unrecognized pathways exist for plants to profit from linked rhizosphere bacteria should also be addressed. For instance, recent research has suggested that plant roots may consume microbial cells for digestion and use as a source of nutrients (Paungfoo-Lonhienne et al. 2010; Mahapatra et al. 2022a). Future research is, therefore likely to identify fresh targets for breeding plants to improve access to nutrient pools and boost plant development in low-input farming settings.

There is more proof that the way we now classify bacteria as pathogenic or beneficial is flawed. *F. culmorum*, for instance, was classified as pathogenic because it can wreak damage on numerous crop plants. On the other hand, the *F. culmorum* isolate FcRed1 performs as a helpful microbe and bestows salt tolerance on its host dunegrass *Leymus-*



*mollis*, whereas isolates from non-coastal dunegrass do not have this ability. However, *C. protuberata* is a plant disease that affects various monocots isolate Cp4666D makes its host plant, *D. lanuginosum*, more tolerant to heat and drought, although *Curvularia* species are not known to have widespread disease-host ranges, tomato is also given heat tolerance by the monocot *D. lanuginosum* attributed to *C. protuberata* (Rodríguez-Moreno et al. 2008).

## Conclusions

A comprehensive approach will be needed to establish plans in the following years that aim to sustainably enhance agricultural production due to the climate change scenario's significant challenges to agricultural sustainability. Numerous microbial species that are important to ecosystem functions can be found in soil. In this shifting climatic scenario, the agrarian management techniques currently in use may impact their role in soil fertility and productivity. The microbes may lose their innate ability to carry out various biological activities, such as suppressing soil-borne plant pathogens and converting nutrient pools into forms that plants can use, which are crucial for the growth, development, protection, and productivity of crop plants in the absence of potential management strategies to address climate change. Utilizing plant-microbe interactions for agricultural practices such as integrated nutrient and soil management, integrated pest and weed management, and organic agriculture that uses microorganisms in the form of bio-inoculants, biofertilizers, biopesticides, and biological weed control, among other practices, will help to contribute to climate change. The demand for sustainable farming practices has increased as a result of chemical pollution, population growth, and the depletion of energy and resource reserves. Increased dependence on the advantages the soil microbiome is one step toward sustainability. We have emphasized study topics that are essential to our capacity to utilize better utilize the plant-associated microbiome in crop production, whether through direct manipulation or by employing crop plants as selective agents to enrich for beneficial bacteria.

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**Conflict of interest** P. Rayanoothala, Sk. Hasibul Alam, S. Mahapatra, A. Gafur and S. Antonius declare that they have no competing interests.

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