

The Potential of Rhizobacteria for Plant Growth and Stress Adaptation

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Abstract

Plants host a very rich microbiome comprising fungi, bacteria, and protozoa. Bacteria proliferate inside tissues or around roots, where carbon-rich compounds exert positive chemotaxis. Many physiological functions in crops are related to symbiotic events with Gram-positive or Gram-negative bacteria, which influence growth, development, nutrition, and immunity and fine-tune root tropisms. This potentiates the exploration of the substrate and may confer stress tolerance. The production of secondary metabolites and volatile compounds has been thoroughly investigated in Gram-positive bacteria in recent years, and a few of these info-chemicals increase the endogenous auxin levels and/or response, whereas Gram-negative species releases quorum-sensing signals of the *N*-acylhomoserine type that are recognized by roots to strengthen root branching and immunity. This chapter reviews the contributions of rhizobacteria to enhance crop fitness in the field to make agriculture safer and more sustainable and highlights a few examples of how cross-kingdom signaling influences root behavior.

11.1 Introduction

Agriculture is the primary economic activity enabling food supply worldwide. Starting from the so-called "green revolution" driven by Dr. Norman Borlaug and his coworkers, through the development of crops more efficient to take up nutrients and water and more resistant to environmental challenges along with industrial

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production of fertilizers, now we may have access to fruits and fiber to satisfy world's demand in the few following years. Nevertheless, continuous population growth has led to the undesirable situation of the opening of natural ecosystems to agriculture, despite these lands may not be adequate to support plantations in the long term (Gomiero 2016). Another challenging trend is that the excessive use of agrochemicals has led to soil salinity, water contamination, and environmental risks (Atafar et al. 2008). Recent approaches to make agriculture more sustainable take advantage of the mutualistic relationships that plants establish with microorganisms, mainly bacteria and fungi. The root microbiome contains a great diversity of rhizobacteria that positively impact plant growth, help in phytoremediation, nutrient solubilization, or prevent diseases (Alori et al. 2017; Köhl et al. 2019; Jiang and Fan 2008). Besides, through chemical communication with root cells, rhizobacteria amplify host responses associated with the tolerance to biotic and abiotic challenges (Bano and Muqarab 2017; Chiappero et al. 2019).

The establishment of rhizobacterial populations is promoted by root exudates, which are mainly constituted of carbohydrates, amino acids, organic acids, and secondary metabolites. Changes in the chemical composition of the rhizosphere influence the microbiome and, consequently, modify the overall plant adaptive responses (Sasse et al. 2018). The competition of soil microorganisms for space along roots drives the association between different bacterial taxa (Philippot et al. 2013). Consortia establishment allows the integration of diverse traits related to the growth of the host and health maintenance (Kumar et al. 2016). Recent studies have identified compatible rhizobacteria for consortia formulation and farming practices. Here, we present an overview of the rhizobacterial mechanisms that benefit crops and how these can be modulated when bacteria coexist within plant roots.

11.2 Rhizobacterial Functions in Plant Growth and Development

Plant developmental processes such as embryogenesis, germination, growth, flowering, and reproduction are regulated by a wide range of compounds named phytohormones, many of which can be produced by rhizobacteria. Indole-3-acetic acid (IAA) is the most widely distributed auxin in plants and microorganisms that stimulates root growth and organogenesis (Perrot-Rechenmann 2010). Through changes in the configuration of the root system, bacteria improve soil exploration and, therefore, nutrient uptake (Fig. 11.1). *Pseudomonas, Bradyrhizobium, Streptomyces, Azospirillum, Sphingomonas*, and *Acinetobacter* species that actively produce IAA constitute important options to enhance crop performance (Chouyia et al. 2020; Hashmi et al. 2019; Ijaz et al. 2019; Kumawat et al. 2019; Molina-Romero et al. 2017).

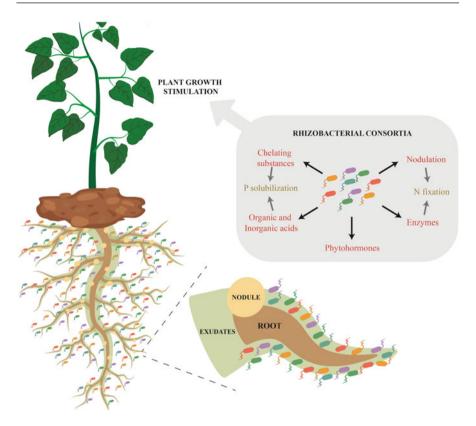


Fig. 11.1 Plant growth enhancement by rhizobacterial species. Soil bacteria can improve plant growth and development contributing to P solubilization by the production of chelating substances and organic acids. The enzymatic machinery of some rhizobacteria allows to convert the atmospheric nitrogen into assimilable N forms for plants. Phytohormones produced by rhizobacteria reconfigure the root system architecture in a way that improves its ability to explore the soil and therefore boosts the uptake of nutrients

11.3 Enhanced Nutrient Uptake

Plants rely on an adequate supply of minerals for growth and development. When a given soil lacks any macro- or micronutrients, various physiological processes are altered, decreasing their productivity. Phosphorus (P) and nitrogen (N) are the most limiting elements for the success of crops due to their structural, metabolic, and signaling functions. Most nutrients should be supplied in their ionic forms as part of chemical fertilizers or as part of organic amendments that farmers use to warrant high productivity (Maathuis 2009). Phosphorus commonly remains in the soil as insoluble phosphate complexes, not easily available for uptake by the root system. The production of organic acids, chelating substances, and enzymes from rhizobacterial species promotes solubilization of organic and inorganic P forms,

which can be taken up by root hairs and lateral roots (Alori et al. 2017). Such ability to solubilize P is an interesting trait of bacteria that increases the growth and yield parameters in tomatoes and maize (Bradáčová et al. 2019, 2020) and supports growth in P-deficient soils (Bradáčová et al. 2019). Noteworthy, a mixture of *Pseudomonas* sp., *Burkholderia* sp., *Enterobacter* sp., and *Serratia* sp. improved both the available P content in soil and its uptake in aloe plants (Gupta et al. 2012).

Rhizobacteria may support N reduction to form nitrate (NO_3^-) and ammonium (NH_4^+) for plant nutrition. Particularly, the *Rhizobium* genus stimulates the growth of legumes through N fixation in root nodules (Vargas et al. 2017). The mineralization of organic matter contributes to enriching the pool of available N in the soil by the activity of lytic enzymes from saprophytic bacteria and fungi (Geisseler et al. 2010). Soybean and common bean seeds inoculated with *Bradyrhizobium* sp. and co-inoculated with *Azospirillum* sp. generated the same yield under N deficiency conditions as in fertilized soils. This consortium is an example of alternatives less expensive for farmers to support productivity (Hungria et al. 2013). Integration of rhizobia species including *Bradyrhizobium* sp., *R. leguminosarum*, and *Sinorhizobium meliloti* synergistically increased the nodule number, biomass, and the N uptake in soybean and pigeon pea (Kumar et al. 2016; Kumawat et al. 2019; Pandey and Maheshwari 2007).

Plant nutrition also demands several trace elements that play critical roles in redox reactions and function as cofactors of several enzymes such as RNA polymerase, cytochromes, and superoxide dismutase (Nagajyoti et al. 2010). Bacteria can help plants, either by solubilizing these micronutrients through acidifying the soil or by releasing siderophores that act as metal chelators (Abbaszadeh-Dahaji et al. 2016; Scavino and Pedraza 2013). Wheat plants whose seeds were treated with *Bacillus* sp., *Providencia* sp., and *Brevundimonas* sp. mixtures showed better content of Fe, Zn, Cu, and Mn (Rana et al. 2012). Another triple consortium (*B. megaterium, Arthrobacter chlorophenolicus*, and *Enterobacter* sp.) applied to wheat seeds increased the content of microelements in the harvested grains (Kumar et al. 2014).

11.4 Tolerance to Abiotic Stress

Soil pollution caused by natural or anthropogenic factors and extreme weather conditions are detrimental to agriculture. Heavy metals, salinity, drought, and drastic temperature fluctuations are the principal abiotic stresses that negatively impact crop growth and productivity (Farooq et al. 2012; Nagajyoti et al. 2010; Parihar et al. 2015; Mathur and Jajoo 2014). Physiological consequences of abiotic stress reside in overproduction of reactive oxygen species (ROS) and the emission of the gaseous phytohormone ethylene (Kumar and Verma 2018). ROS include free radicals that act as messengers in cell signaling through the so-called oxidative stress response. Disturbed ROS homeostasis compromises cell integrity and may cause cell death (Sharma et al. 2012). ROS affect membrane stability via lipoperoxidation and damage proteins and nucleic acids, and thus plants employ scavenging enzymes such as peroxidase, superoxide dismutase, catalase, polyphenol oxidase, and

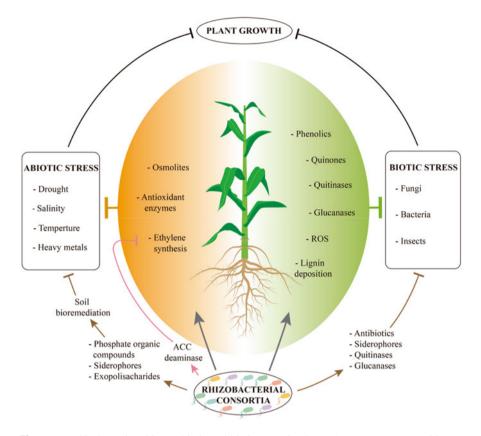


Fig. 11.2 Rhizobacteria mitigate abiotic and biotic stress in plants. Arrows represent positive or negative regulation. Soil bacteria produce numerous enzymes and compounds that directly reduce the soil pollution caused by heavy metals and eliminate the soilborne phytopathogens (brown arrows). The induced systemic tolerance and the induced systemic resistance in plants, which involve components that attenuate the impact of abiotic and biotic stresses, can be activated by rhizobacteria (grey arrows). ACC deaminase from bacteria can decrease ethylene overproduction triggered in plants in response to several stresses (pink arrows). Overall, growth/defense trade-offs are finely modulated in symbiotic interactions

antioxidant compounds including proline, glutathione, ascorbic acid, carotenoids, vitamins, and flavonoids to diminish the oxidative stress (Mehla et al. 2017). Also, as part of adaptive strategies, plants maintain a precise balance in the amount of ethylene synthesized from aminocyclopropane-1-carboxylic acid (AAC) through ACC deaminase enzyme activity that degrades ACC to α -ketobutyrate and ammonia (Shi et al. 2012; Singh et al. 2015).

A practical and eco-friendly strategy to mitigate these nonbiological stresses is the use of probiotic microbes (Fig. 11.2). Rhizobacteria can restore soil fertility by eliminating contaminants and inducing morphological, physiological, and gene expression changes in plants to improve their resistance through a mechanism termed induced systemic tolerance (IST) (Etesami and Maheshwari 2018). Indeed, rhizobacteria provide a combination of different and potential properties that reinforce the plant tolerance to abiotic stresses (Rajput et al. 2018; Saikia et al. 2018; Silambarasan et al. 2019).

11.4.1 Heavy Metals

Fe, Zn, Mn, Mo, Cu, and Ni are heavy metals considered micronutrients for plants in low micromolar or nanomolar concentrations. However, higher concentrations of these minerals (i.e., millimolar range) or other nonessential metals led to adverse effects on germination and shoot and root development not only by oxidative damage, but also by causing enzymatic dysfunction, chlorosis, and senescence (Nagajyoti et al. 2010).

Heavy metal pollution in soils represents a problem for agriculture and human health, and its origin can be natural (i.e., volcanic eruptions and rocks) or industrial (mining and smelting) (Alloway 2013; Ma et al. 2019; Wei et al. 2018). Long-term application of fertilizers and pesticides may also pollute the soils with heavy metals (Atafar et al. 2008). The use of microorganisms is one of the cheapest and most ecological alternatives for the restoration of contaminated soils. Certain bacteria can precipitate, methylate, reduce, oxidize, and chelate heavy metals to attenuate their toxicity (Jiang and Fan 2008; Ojuederie and Babalola 2017). Phosphate organic compounds, as well as siderophores, can interact and bind heavy metals. Shilev et al. (2020) isolated a bacterial consortium (Pseudomonas spp. and Bacillus sp.) tolerant to heavy metals and inoculated it to spinach seeds in soils contaminated with Pb, Zn, and Cd. The consortium showed the capacity to precipitate or immobilize heavy metals forming insoluble complexes and at the same time increased phosphate solubilization and siderophore production. Plants treated with the bacterial mixture had less accumulation of heavy metals in leaves, stems, and roots and sustained remarkable growth. Another bacterial consortium supported the Pb and Cd immobilization, increasing the phosphate solubilization (Yuan et al. 2017). Through interaction with their functional groups, exopolysaccharides from bacteria also retain various heavy metals (Morillo Pérez et al. 2008). Phosphate solubilizing activity, siderophore, and exopolysaccharide production are traits of B. megaterium and Pantoea agglomerans that enhance the growth of mung bean plants in soils polluted with Al reducing its concentration in tissues (Silambarasan et al. 2019).

Plants possess mechanisms to counteract the toxicity of heavy metals. For instance, compounds from root exudates such as organic acids, carbohydrates, and siderophores retain toxic elements by chelation, avoiding their absorption by crops (Nagajyoti et al. 2010). These mechanisms can be over-induced by rhizobacteria, allowing the plants to continue growing, even at high concentrations of heavy metals (Silambarasan et al. 2019).

11.4.2 Salinity

Salinization is a severe problem for plant development that has spread to 20% of irrigated lands. Unlike halophytes, most crops exhibit physiological problems when grown in soils with moderate or high salt concentrations (Abogadallah 2010; Farooq et al. 2015). Saline stress increases the Na⁺ and Cl⁻ levels in the cytoplasm and chloroplasts, provoking an osmotic imbalance that stimulates ROS and ethylene overproduction and affects photosynthesis and plant growth (Amjad et al. 2014; Dar et al. 2017; Farooq et al. 2015). Cellular responses to salinity imply the production of osmoregulatory solutes, increased antioxidant activity, and improved selectivity of ions (Ahanger et al. 2017; Amjad et al. 2014). Highly efficient mechanisms are employed by rhizobacteria isolated from halophytes to improve the host adaptation to saline soils (Abbas et al. 2019; Jiménez-Vázquez et al. 2020). These microbes regulate the rhizosphere osmolality and promote adaptation through counteracting saline shock (Bharti et al. 2016; Sarma et al. 2012). Halotolerant rhizobacteria such as Achromobacter sp., Serratia sp., and Enterobacter sp., which presented ACC deaminase activity and IAA production, were found to increase the length of the shoot and root system in avocado plants exposed to saline stress conditions. The consortium intensified the superoxide dismutase activity and diminished lipoperoxidation (Barra et al. 2017). Halotolerant Aeromonas spp. mixture protected wheat plants from saline stress improving the root and leaf biomass and increasing the grain yield under half chemical fertilization (Rajput et al. 2018).

11.4.3 Drought

Comparable to salt toxicity, drought increases osmotic stress. The main physiological processes altered by drought are photosynthesis and the uptake and transport of nutrients (Farooq et al. 2012). Therefore, the germination, growth, and development of plants are drastically disrupted under this adverse condition (Asrar and Elhindi 2011; Liu et al. 2011; Samarah and Alqudah 2011). Under drought, plants raise the synthesis of abscisic acid, a phytohormone that induces stomatal closure and prevents water loss through transpiration (Tombesi et al. 2015). Rhizobacteria may support plant growth in water-deficient conditions via decreasing stomatal aperture and reducing ethylene levels (Chiappero et al. 2019; Cho et al. 2008; Mayak et al. 2004). Rhizobacterial consortia alleviated the growth repression of common bean and mung bean triggered by drought stress (Figueiredo et al. 2008; Silambarasan et al. 2019). Crops exposed to drought and grown under pretreatments with bacteria showed more superoxide dismutase, peroxidase, and catalase activity (Barra et al. 2017; Kohler et al. 2008). The mixture of *Ochrobactrum* sp., *Pseudomonas* sp., and *Bacillus* sp. had a synergic effect on the growth of different plant species exposed to drought. Also, they reduce the ACC levels in plants (Saikia et al. 2018).

11.4.4 Temperature

Extreme temperatures either heat or cold affect crop productivity. Production of ROS, heat shock proteins, and abscisic acid and the activation of mitogen-activated protein kinases (MAPKs) are part of the signaling mechanisms triggered by heat stress (Andrási et al. 2019; Evrard et al. 2013; Guo et al. 2016; Link et al. 2002; Yu et al. 2019). Elevated temperatures impair water content, photosynthesis, and membrane stability (Liu and Huang 2000; Mathur et al. 2011; Wassie et al. 2019). Thermotolerant rhizobacteria can enhance plant mechanisms associated with tolerance to heat stress, such as the production of osmolytes, activation of antioxidant enzymes, and reduction of ethylene levels (Ali et al. 2011; Khan et al. 2020; Mukhtar et al. 2020; Sarkar et al. 2018).

The foliage is very sensitive to cold stress and is one of the organs more impacted by chilling, exhibiting wilting, necrosis, chlorosis, and deformation, which affect early leaf growth and flowering (Kumar et al. 2010; Rymen et al. 2007; Yadav 2010). Acclimation to low temperatures is regulated positively by abscisic acid since mutants altered in the signaling of this phytohormone are hypersensitive to cold stress (Shi and Yang 2014). Adverse effects of cold stress can be attenuated by an overproduction of solutes such as sugars and amino acids, whose accumulation is stimulated through interaction with rhizobacteria (Ait Barka et al. 2006; Fernandez et al. 2012; Mishra et al. 2011). Tomato plants grown in soil inoculated with B. cereus, B. subtilis, and Serratia sp. were exposed to cold stress and showed a high level of hydrogen peroxide (H_2O_2) than non-inoculated plants. After days, the consortium moderated the oxidative stress caused by low temperatures mainly through the activation of superoxide dismutase and peroxidase activities. Besides, rhizobacteria increased the production of osmoprotectants such as proline and sugars. These effects helped to reach almost 100% plant survival (Wang et al. 2016). Kakar et al. (2016) applied a combination of *Bacillus* sp. and *Brevibacillus* sp. in rice seedlings and then applied cold stress treatment. The bacteria improved cold tolerance, upregulated the activity of antioxidant enzymes, and increased the proline content of plants, stimulating their growth and survival.

11.5 Biotic Challenges

Considerable crop losses occur due to nematode, viral, bacterial, oomycete, and fungal pathogens, which cause damage at each developmental stage (Savary et al. 2019). The control of plant diseases has been possible in the last decades by applying biocides that pollute air, water, and soil, damage pollinators, and ultimately enter the food chain (Popp et al. 2013; He et al. 2016). Thus, an important goal to achieving sustainable productivity is to develop new alternatives based on understanding plantmicrobe interactions in an ecological context (Fig. 11.2).

Plants manifest constitutive and inducible defenses to protect themselves from pathogens. The properties of their immune system can be further modulated by abiotic and biotic stresses (Jain et al. 2016; Miura and Tada 2014). Detailed

information on how plant defense is mounted has been gathered in leaves, and until recently little was known about how roots react under attack. It has become evident that damaged roots unlock a protective mechanism in coordination with probiotic bacteria surrounding them that boosts the defense reaction (Berendsen et al. 2012; Hematy et al. 2009).

11.5.1 Disease Suppressive Soils

Some soils have the property to suppress plant diseases because their microbiomes inhibit the spread of phytopathogens. On the other hand, the so-called conducive soils favor the incidence of plant diseases (Schlatter et al. 2017). Abiotic factors and certain farming practices can influence the growth of microorganisms related to the balance required for plants to survive and thrive (Jansson and Hofmockel 2020; Mehta et al. 2014). Continuous cropping is a practice that diminishes rhizobacterial diversity, generating a higher vulnerability to the root rot disease (Tan et al. 2017). In contrast, monocropping systems triggered the reduction of take-all disease, a phenomenon linked to the rising of P. fluorescens (Sanguin et al. 2009). The release of root exudates attracts specific groups of bacteria, causing changes in the soil microbial composition that reinforces defensive barriers (Berendsen et al. 2012). Proteobacteria, Firmicutes, Acidobacteria, and Actinobacteria strains predominate in the bacterial community of suppressive soils associated with tolerance to distinct crop diseases (Cha et al. 2016; Kyselkova et al. 2009; Sanguin et al. 2009). Mendes et al. (2011) dissected the rhizobacterial microbiome of sugar beet cultivated in suppressive soils of damping-off disease, concluding that the bacterial taxa contribute to disease mitigation. Seven rhizobacterial strains delayed the Fusarium verticillioides mycelial growth on maize seeds and decreased the blight disease incidence in seedlings. Each bacterial strain had a biocontrol effect on spreading the fungus and disease incidence, but not to the same degree as the consortium did (Niu et al. 2017). Other rhizobacteria showed a synergistic biocontrol on the blast disease in rice and collar rot disease in betelvine (Lucas et al. 2009; Singh et al. 2003). This protective capacity could persist for more than one season (Zhang et al. 2019). Therefore, multiple mechanisms depending on the composition of the microbial consortia account for the natural root antagonism to soilborne pathogens.

11.5.2 Fighting Plant Diseases

The production of antibiotics such as 2,4-diacetylphloroglucinol (2,4-DAPG), phenazine-1-carboxylic acid, pyrrolnitrin, oomycin, aerugine, and kanosamine is an important mechanism used by rhizobacteria to suppress the growth of phytopathogens (Kenawy et al. 2019). These compounds damage cell membranes, interfere with the electron transport chain, and affect enzymatic activity (Janiak and Milewski 2001; Raaijmakers et al. 2009; Troppens et al. 2013). Santhanam et al. (2019) evaluated biofilm development during the colonization of tobacco roots by *Bacillus* sp., *Pseudomonas* sp., and *Arthrobacter* sp. This consortium increased plant survival against the sudden wilt disease, and one of the factors associated with the resistance was the production of surfactin, an antifungal compound. A single antibiotic can control diverse phytopathogens; for example, 2,4-DAPG, produced by several *Pseudomonas* strains, suppressed take-all, root rot, and damping-off fungal diseases and crown gall caused by *Agrobacterium tumefaciens* (Weller et al. 2007).

Cell wall degrading enzymes can be secreted by rhizobacteria that affect fungal phytopathogens. Chitinase and glucanase production is one of the desirable determinants to select rhizobacteria for biocontrol (Pliego et al. 2011). In this manner, the attenuation of *F. oxysporum* in maize was made possible, and at the same time plant growth and yield increases were obtained upon applying a quadruple bacterial inoculum composed of *B. megaterium*, *P. aeruginosa*, *Serratia* sp., and *P. fluorescens* (Akhtar et al. 2018).

Micronutrient availability is an ecological determinant for plant-microbe interactions. Under deficiency of Fe, an essential micronutrient, specific bacteria produce and secrete siderophores to chelate the available iron, rendering it unavailable for phytopathogens (Kramer et al. 2020). Treatments of *Pseudomonas* sp. or its siderophores protected plants against *Gaeumannomyces graminis* and *F. oxysporum* (Kloepper et al. 1980). Besides, some consortia had suppressive effects related to the activity of siderophores (Akhtar et al. 2018; Estevez de Jensen et al. 2002; Santhanam et al. 2019).

11.5.3 Plant Defensive Reactions

The plant immune system is reinforced by gene expression related to lytic enzymes and the production of antimicrobial compounds (Jain et al. 2016). Two main pathways control the defense reactions, the first involves systemic acquired resistance (SAR), stimulated after an attack of pathogens and dependent on the phytohormone salicylic acid. SAR induces pathogenesis-related (PR) genes, and it is initially manifested in the damaged site but later spreads systemically to distant tissues (Klessig et al. 2018). In the second pathway, the so-called induced systemic resistance (ISR) involves plant interactions with nonpathogenic rhizobacteria, which promote defense-related gene expression through signaling of the phytohormones ethylene and jasmonic acid. ISR has been reported to occur in the aerial and root system and also in leaves, keeping the plant defense machinery ready and alert to respond quickly to single and multiple biotic stimuli (Pieterse et al. 2014).

Berendsen et al. (2018) isolated three bacterial strains from the *Arabidopsis thaliana* rhizosphere, which prevailed during foliage infection caused by the oomycete *Hyaloperonospora arabidopsidis*. The plants grown in soil previously inoculated with these rhizobacteria showed less incidence of the oomycete in leaves. Besides, a combination of rhizobacteria and plant growth-promoting fungi (PGPF) protected cucumber plants against *F. oxysporum* infection in stems, enhancing the expression of genes encoding chitinases, glucanases, and enzymes involved in the

synthesis of antifungal compounds (Alizadeh et al. 2013). Peroxidase is another defense component of plants that limits the pathogen spread as it mediates the establishment of physical barriers such as lignin and suberin in cells (Passardi et al. 2005). Adjusting the levels of reactive oxygen species, both peroxidase and superoxide dismutase, can create a toxic environment for pathogens in plant cells (Torres et al. 2006). *Bacillus* spp. diminished the bacterial and fungal infection in tomato and pepper apparently by induction of the peroxidase and superoxide dismutase activity (Jetiyanon 2007).

The plant phenylpropanoid pathway directs the production of phenolic compounds with antimicrobial properties. Phenylalanine ammonia-lyase converts L-phenylalanine into *trans*-cinnamic acid, a precursor for the synthesis of phenolics (Cheynier et al. 2013). Indeed, polyphenol oxidase oxidizes phenols to generate quinones, which also inhibit phytopathogen growth (Jukanti 2017). *Pseudomonas* sp., *Rhizobium* sp., and *Trichoderma* sp. reduced the mortality in chickpea plants infected by *Sclerotium rolfsii*. The triple microbial consortium enhanced the gene expression of peroxidase and superoxide dismutase and increased phenylalanine ammonia-lyase, polyphenol oxidase activity, and lignin deposition (Singh et al. 2013).

11.5.4 Quorum-Sensing-Mediated Antagonistic Activity

Colonization of roots, either by beneficial microorganisms or by plant pathogens, initiates a complex interrelationship where root exudates and mineral nutrients play an essential role. The formation of biofilms mainly composed of bacteria is a biological barrier that extends beyond the root epidermis. This process is under the control of a cell-to-cell chemical communication program termed quorum sensing (QS). In Gram-negative bacteria, QS controls the transcription of genes by producing small molecules, mainly the *N*-acyl-L-homoserine lactones (AHL) (Dwivedi et al. 2017). These compounds have strong activity not only in bacteria but also in roots, which suggests that they modulate the inter-kingdom plant-bacteria language (Ortíz-Castro et al. 2008).

Mutants of *P. chlororaphis* deficient in QS regulation lost their ability to inhibit the growth of plant pathogens. These variants exhibited low expression of *phzA/ prnA* genes related to the production of two broad-spectrum antibiotics phenazine-1carboxylic acid and pyrrolnitrin. AHL supplements induced the *prnA* expression, indicating that the QS compounds directly trigger pyrrolnitrin synthesis (Selin et al. 2012; Shah et al. 2020). Kim et al. (2017) concluded that the QS in *Chromobacterium* sp. supports its capacity to suppress fungal diseases in plants since the mutation of the gene encoding homoserine lactone synthetase reduced its chitinolytic activity. Other rhizobacterial enzymes attenuated the virulence of phytopathogenic bacteria by degrading QS molecules. For instance, Actinobacteria releases lactonases, which degrade AHLs in *Pectobacterium carotovorum* and affect its virulence (Vesuna and Nerurkar 2020). The interaction between bacterial communities also upregulated or downregulated the production of siderophores via QS signals (Shah et al. 2020; Stintzi et al. 1998; Whiteley et al. 1999).

11.6 Perspectives

Plants and microorganisms have developed inter-kingdom relations, which have been gaining special attention in agriculture since they improve crop yields and may reduce fertilization and pest control costs. The combination of selected traits from two or more bacteria further intensifies the probiotic effects on crops. Competition for energy and nutrient sources from exudates has led rhizobacteria to influence the host defense responses against bacteria and fungi that could be a threat. Therefore, it is crucial to identify and understand the mechanisms that define rhizobacteria compatibility and antagonism to develop successful inoculants.

Exploration of natural ecosystems has proven to be a valuable strategy to identify novel traits in both bacteria and plants useful to resist stress. The search for halophyte bacteria in a largely untouched sink hole termed the "Poza Salada," located in the Chihuahua Desert, enabled the identification of a group of plant beneficial bacteria living in association with roots of well-adapted plant species, which grow healthy despite the very high salt concentrations. Three bacterial isolates typified molecularly as Bacillus sp., P. lini, and Achromobacter sp. promoted the growth of A. thaliana, Cucumis sativus, and Citrullus lanatus in vitro and in soil under standard and saline growth conditions (Jiménez-Vázquez et al. 2020; Palacio-Rodríguez et al. 2017). Noteworthy, Achromobacter sp. interfered with the root gravity response and caused the formation of waves and circles called coils, which primed roots for enhanced branching through the proliferation of lateral roots (Jiménez-Vázquez et al. 2020). The mechanisms underlying the beneficial properties of halophytes to plants are far from being understood; however, their protection from salinity in different plant species opens new avenues for agriculture. Regardless of the plant growth-promoting traits that rhizobacteria have in their natural niche, their survival should be tested under different environmental conditions to warrant their prevalence on crops. Generating more knowledge about the ways rhizobacteria interact with plants will facilitate access to biological tools for more productive and sustainable agriculture.

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