



Rhizosphere-microbes interaction with plants

Poonam, Prabhavathi*, Kiran Bamel

Department of Botany, Shivaji College, University of Delhi, Delhi, India

*Corresponding Author: prabha.udsc@gmail.com

Abstract

Lorenz Hiltner, in 1904, described the term rhizosphere for the first time, hence the rhizosphere is the area of soil, that is to say, immediately near the root surface, in which the microbial population of soil is influenced by the chemical events of plant roots that exude substances that aid as nutrients for rhizosphere microbial growth. In this way, the rhizosphere is considered a very vital zone for plant growth and development, disease resistance, and nutrient recycling. Billions of microbes are present in a handful of soil, which comprises fungi, bacteria, viruses, nematodes, archaea etc., which differ according to plant species, root zone, growth stage of the plant, along with the incidence of stress and occurrence of disease. The root exudates released from the roots create a different environment for microbial growth in the rhizosphere than in the bulk soil. The plant-microbial association in the rhizosphere has a positive impact on the development of the rhizosphere-microbiota population, inducing production of auxins and cytokinin (the growth-promoting hormones), increasing accessibility of nutrients, stimulating host defence criteria, sustaining agriculture, inducing tolerance to stress, and controlling pathogenesis through antagonism. Hence, biofertilizers and biocontrol agents can be formulated from these beneficial plant growth-promoting (PGP) microbes. Along with this, several microbes are also violent towards plants and, therefore, show pathogenic activity. Hence, this review summarizes the natural associations between plants and microbes in the rhizosphere and discusses how their relationship affects plants both beneficially and negatively.

Keywords: rhizosphere, microorganisms, biofertilizers, biocontrol agents

Introduction

The area of a root that extends a few millimetres from the root surface where the microbial population of soil is affected by the root exudates of plants is known as the rhizosphere. The plants' roots and immediate surrounding soil are collectively called the rhizosphere. The rhizosphere, which is considered to be one of the most active interfaces on earth, is a narrow zone of soil that is surrounded and influenced by plant roots. A very significant and rigorous association of rhizosphere microfauna takes place with the plant and soil in that certain environment. Broadly, there are three separate zones that describe the complete rhizosphere system; first, the rhizosphere per se (soil), second, the rhizoplane, and third, the root itself. Hence, first, the zone of soil influenced by root exudates that influence microbial diversity is the rhizosphere. Second, the rhizoplane represents the strongly adhering root particles at the root surface. And third, the root has certain endophytic microorganisms that are capable of inhabiting inner root tissues, thus, root itself is part of the rhizospheric system. In this environment, the interactions between plant roots, soil, and microbes significantly modify soil physical and chemical aspects, which in turn change the microbial population in the rhizosphere [1].

The rhizosphere is considered the supreme position for ecosystem facilities, for example, nutrition uptake, carbon utilization and storage, crop proffering, carbon and water cycling, etc. [2], because rhizosphere microbial diversity can affect directly or indirectly the configuration and biomass of plant communities in natural ecosystems [3,4]. A number of research works have been done on plants on the microbial diversity of the rhizosphere region and on plant-microbe interactions. Several microbial populations are beneficial for

plants that promote growth and development of plants known as plant growth promoting bacteria (PGPR). They accomplish vital roles for plant growth and health in several ways. Some microorganisms produce beneficial hormones in large numbers that encourage plant growth, but some rhizospheric microbes are pathogenic and attack living plant roots. The diversity and function of rhizospheric soil's presented numerous bacteria, viruses, fungi, nematodes, and protozoa are determined by the respiration activity of the plant-microbe system, release of root exudates, and biogeochemical reactions of the rhizosphere [5, 6]. It is reported that about 2-5% of rhizo-bacteria show PGP (Plant growth promoting) activity. *Pseudomonas* and *Bacillus* are the maximum reported PGPR species out of all other bacteria [7].

Several external biotic and abiotic aspects also regulate the rhizospheric microbial diversity of plants, along with the soil type [8]. Only because of these soil rhizospheric microbial populations, there is association and communication between the plants and the soil. Therefore, in the present review, we focus on this micro-ecosystem, which is made up of several biota (mainly microorganisms) that reside in the soil and can manifest complex communities that interact in beneficial, harmful, or neutral ways with plants [9].

The rhizosphere microbial diversity

Numerous bacteria, fungi, viruses, protozoa, and nematodes etc., collectively form the rhizosphere microbiota. Plants have established complex interactions with the microbes present in the rhizosphere. Root exudates, which are a wide range of organic compounds, secreted to increase microbial diversity and other functions in the rhizosphere zone

compared to bulk soil (the soil area away from the rhizosphere is recognized as bulk soil), are the main food source for the microbial population. Along with root exudates, types and properties of soil, also affect the population and the configuration of rhizospheric microbial diversity^[10, 11]. Plant-specificity is always shown by the rhizosphere microbial population in relation to both organizational and functional diversities. The abundant bacterial phyla in the rhizosphere of the plant *Boswellia sacra* are *Bacteroidetes*, *Proteobacteria*, *Gemmatimonadetes*, *Actinobacteria*, *Acidobacteria*, and *Planctomycetes*^[12]. A large range of fungal populations are also accompanied by rhizospheric plants roots that depend upon the host plant, edaphic properties, climate, season, and abiotic and biotic factors. *Proteobacteria* (for example, bacteria from the *Pseudomonadaceae* or *Burkholderiaceae* family) are considered the dominant members of the rhizosphere microbiota by several independent findings^[13, 14, 15]. Because proteobacteria are generally fast-growing r-strategists, they have the ability to utilize a broad range of root-derived carbon substrates. Several studies have indicated that a number of biotic and abiotic factors are responsible for the generation and maintenance of rhizosphere diversity^[9]

Plant-Microbe interaction system

Rhizospheric Important microbial activities that are likely to occur in the rhizospheric zone include pathogenesis and its

counterpart, plant defence/growth promotion, in addition to the production of antibiotics, plant colonization and geochemical cycling of minerals. So, depending upon the microbial specificity, involved plant, and usual environmental conditions, the plant-microbe association may thus be measured as beneficial, neutral, or harmful to the plant. In this way, the rhizosphere explores a new and attractive area of research by separating the possible relationships of rhizospheric microbes with plants.

Beneficial plant-microbe interaction system

In order to recover and encourage the growth, development, and health of plants for numerous applications, as well as agricultural purposes, beneficial plant-microbe interactions are of particular interest^[16, 17].

Plant-microbe beneficial interactions can be roughly divided into three groups- first categories of microorganisms found in association with plants and are in control of their nutrition [i.e., a microbial population that can enhance the amount of mineral nutrients to the plant]. Second, a group of microbes are mentioned as bio control agents that promote plant development indirectly by stopping the growth or activity of pathogens.

Third, the group comprises those microorganisms accountable for the production of phytohormones for direct growth promotion.

Therefore, there are several examples of beneficial plant-microbe interaction systems (Table 1).

Table 1: Beneficial rhizosphere-microbes in plants

Sr. No.	Rhizosphere-Microbes	Functions	Host crop	References
1.	<i>Aeromonas veronii</i>	Produced IAA hormone	Rice	Mehnaz <i>et al</i> (2001)
2.	<i>Methylobacterium fujisawaense</i>	Promoted root elongation in canola	<i>Brassica campestris</i> L.	Madhaiyan <i>et al</i> (2006)
3.	<i>Pseudomonas fluorescens</i>	Induced serpentine metabolite in plant	<i>Catharanthus roseus</i> (L.) G. Don	Jaleel <i>et al</i> (2007)
4.	<i>Rhizobium leguminosarum</i> bv. <i>Viciae</i> 128C53 K	Enhanced nodulation in plants	<i>Pisum sativum</i> L.	Ma <i>et al</i> (2003)
5.	<i>Azospirillum</i> sp.	Fix atmospheric nitrogen	Maize	Garcia de Salamone <i>et al</i> (1996)
6.	<i>Bacillus</i> sp.	As a biocontrol agent against cotton aphids	Cucumber	Stout <i>et al</i> (2002)
7.	Fungus (<i>Trichoderma harzianum</i> TST h)	Beneficiary in nutrient-poor and petrochemical-contaminated soils	Tomato and Wheat	Repas <i>et al</i> (2017)
8.	Fugus (<i>Glomus clarum</i>)	Enhanced biomass production in salinity stress affected crops	Basil (<i>ocimum basilicum</i> var. <i>odoratus</i>)	Elhindi <i>et al</i> (2016)
9.	Virus- <i>Curvularia thermal tolerance virus</i> (CThTV)	Effective against heat stress	<i>Dichantheium lanuginosum</i>	Marquez <i>et al</i> (2007)
10.	Virus- <i>Brome mosaic virus</i> (BMV), <i>Cucumber mosaic virus</i> (CMV), <i>Tobacco mosaic virus</i> and <i>Tobacco rattle virus</i>	Effective against drought stress	Beet, pepper watermelon, cucumber, Tomato, rice and Zucchini	Xu <i>et al</i> (2008)

Improvement of plant growth and health

The germinated seed interacts with a wide variety of microorganisms present in the rhizospheric soil during seed germination and seedling growth. As the seeds germinate and develop roots through the soil, there is development of an active microbial zone that contains plant roots and adjacent soil of a few mm in thickness because of the release of organic material that provides the driving force for the development of microbial populations. This phenomenon is referred to as the rhizosphere effect. PGPR affect seed germination and seedling growth improvement

by synthesized Gibberellins. Various differentially expressed genes (DEGs) are upregulated by arbuscular mycorrhizal fungi (AMF) that are involved in auxin signalling. Root proliferation, development of root hair, and metabolism, etc. are modulated by the Indoleacetic acid (IAA) produced by PGP microbes. A number of rhizospheric bacteria like *Bacillus megaterium*, *Bradyrhizobium* sp., *Azospirillum* sp., *Jeotgalicoccus huakuii*, *Rhizobium* sp., *Klebsiella* sp., *Pseudomonas* sp., *Erwinia herbicola*, *Agrobacterium* sp., etc. are accomplished of producing IAA^[18, 19]. Bacteria such as

Azospirillum lipoferum, *Arthrobacter mysorens*, *Acetobacter*, *Agrobacterium radiobacter*, *Bacillus polymyxa*, *Azoarcus*, *Burkholderia*, *Diazotrophicus*, *Gluconacetobacter*, *Paenibacillus polymyxa*, *Pseudomonas putida*, *Rhodobacter capsulatus*, *Herbaspirillum*, etc. promote plant development through nitrogen fixation^[20]. A number of physical parameters, like increased in root length, number of leaves, leaf length and total gel volume in *Aloe vera* increased by the phosphate solubilizing microbes *Enterobacter hormaechei*, *Serratia marcescens*, *Burkholderia gladioli*, and *Pseudomonas synxantha*. Hence, the development, health, and survival of plants in unfavourable environments can be significantly influenced by the rhizospheric microbiome; in this manner, the rhizosphere biota can be measured as a kind of essential mechanism of plant survival, and has thus coevolved with plants.

Mineral Nutrition

Soil microbes decompose and recycle nutrients in organic matter, hence showing a very significant role in nourishing plant growth, going along in retrieving minerals in rocks, and making available nitrogen from the atmosphere for plant use. Therefore, based on the functions of microbes, they are classified into three groups, namely: Recyclers: These are the organisms which degrade dead plants and animal waste stuff into raw materials for plants, hence also known as 'decomposers'^[21, 22]. For example, *Bacillus subtilis*, *Pseudomonas* and *Frankia*^[23]. Miners: These microbes release exudates in the form of a sludge/slush through exertion on the rocks and minerals and not on living matter^[24]. For example, lithotrophic bacteria such as *Acidithiobacillus ferrooxidans*^[24]. Refiners: These are able to refine nitrogen from the atmosphere, process it, and change it into plant-obtainable form ammonia and also additional nitrogen organic compounds. Such as *Clostridium*, *Azospirillum*, *Azotobacter*, and *Rhizobium*^[23].

Plants growing in a nutrient poor environment can increase their nutrient uptake through various root microbe associations, such as symbiosis [eg. Mycorrhizal or Rhizobia] & specific association [Associative N₂ fixing bacteria with grasses etc. – *Azospirillum*]. Plant growth and development is known to be sustained by sufficient availability of iron, for example, a component of chlorophyll, sustains the structure and function of the chloroplast. Several nutrients, such as Fe, Cu, Ca, Zn, Na, Mn, Mg, etc., can be absorbed by rhizospheric microbes. AM fungal hyphae are also known to help in the consumption and assimilation of NH₄⁺ and NO₃ into amino acids. Hence, nutrient attainment such as phosphorus, nitrogen, and important micronutrients can regulate phytohormone concentration levels, enhanced auxins, gibberellins, and cytokinins, all these are facilitated by rhizospheric biota, while also regulating the special decline in ethylene through initiation of the 1-aminocyclopropane-1-carboxylate deaminase (1-ACCDC) enzyme action in the plants, by these microbes^[25].

The more efficient genera, including *Pseudomonas*, *Bacillus*, and *Mycobacterium*, stimulated the uptake of N, P, and K in corn plants, which are more likely to grow in nutrient-deficient soils compared to nutrient-rich soils^[9]. Therefore, the diversity and abundance of rhizospheric microbiomes have both direct and indirect effects on soil nutrients and their bioavailability.

Effects on physiology and metabolic processes

A number of rhizospheric PGPRs, like *Azospirillum*, *Bacillus*, *Rhizobium*, *Arthrobacter*, *Pseudomonas*, *Flavobacterium*, etc., promote plant metabolic activity, osmoregulation, and resistance to starvation to convey tolerance to drought and salinity. The plant physiology and root exudation process are affected by the complex physico-chemical characteristics of soils, which in order to impact the structure of the rhizosphere microbiota. The enormous physiological adaptability is exhibited by the rhizospheric population as they produce and secrete a number of enzymes like lignocellulase, lignase, cellulase, and hemicellulase, which are of great importance and dynamically reduce the lignocellulosic content of agri-waste. Hence, the microbial habitat inhabiting the rhizosphere has been recognized as an important factor for decades, influencing the physiology and development of plants. AMF altered mineral status and photosynthetic parameters in stressed plants through a mitigation strategy that also regulates carbohydrate metabolism in plants. In addition, plant-AMF interaction also controls carbon handling, which is a significant portion of the plant's photosynthates (sugars) is directed toward AMF and, hence, can regulate carbohydrate metabolism. In addition to this, as we study the effect of As (Arsenic) contamination with AMF inoculation on physiological parameters such as photosynthesis and carbohydrate metabolism, we have shown their effects at the seedling stage only^[26]. Therefore, microbial population of rhizosphere play a very vital role in regulation of important physiological and metabolic processes of plants.

Counteracting abiotic and biotic stress

A bundle of literature research has verified the important role of PGPR microbes in conferring resistance to different stresses, such as drought^[27], temperature^[28], salinity^[29], tolerance to heavy metals^[17] and biocontrol pathogens^[30, 31]. When plants are inoculated with non-pathogenic rhizospheric bacteria, they can offer "bioprotection" to stand against biotic stresses, and some root associating rhizobacteria enhance tolerance against abiotic stresses, for example, drought, salinity, and metal toxicity. Along with rhizospheric bacteria, AM fungi are also identified as increasing tolerance to numerous biotic and abiotic stresses. To tackle several abiotic stresses such as salinity and water deficit conditions, the microbes mainly involve managing the water status of the leaf mainly through regulating the stomatal conductance behaviour of the host plant, which is known as the prime defensive mode of action of rhizosphere biota is to convey water and salinity tolerance to the host plant and, hence, increase the photosynthetic efficiency of the plant elucidation in improved development^[32]. Plants show a number of variable root microbes which are grown in high salinity conditions and prevailed by halophytic microbes, mainly the salt-tolerant bacteria *Halococcus*, *Halomonas*, and *Halobacterium*, as well as fungal species which contain members of the phylum *Glomeromycota*^[33]. These microbes recover the nutritional rank of the plant, improve the antioxidant enzymatic procedures, and also increase the plant's phytohormone concentrations. Even a number of bacterial isolates can improve their resistance to low and freezing temperatures by having ice nucleation proteins (INPs)^[34]. In this way, we can say, the plant-

microbe interaction is very vital for the host plant to stand up to biotic and abiotic stress.

Role in conservation of endangered plants

Ecosystem biodiversity and species composition define the stability and functioning of an ecosystem. Recent bundle of literature studies has increased awareness of the rhizosphere ecology of non-cultivated plant species and the restoration of previous natural ecosystems to conserve biodiversity, which is mainly dependent upon the relationships between plants and soil biota of the rhizospheric region. Along with the conservation of endangered plants, the role of rhizosphere microbiota can also be observed in relation to other natural phenomena, such as natural succession. Hence, we can say, exotic plant species and also extinct species might have changed the community composition of soil biota and other soil characteristics of the rhizosphere. However, it is known that pathogenic and mutualistic-symbiotic organisms, and decomposers also in the rhizospheric biota, influence plant community diversity and succession and are also responsible for conserving important plant species from becoming extinct.

Many endangered species have shown association with AMF. The use of mixed association of AM fungi (*Glomus geosporum*, *G. microcarpum* and one crude consortium of AM fungal spores) over monospecific cultures for the sustainable cultivation and conservation of endangered medicinal plant such as *Curculigo orchioides*. However, the mechanism for conservation practices with AMF symbiosis has yet to be unravelled because studies pertaining to the role of AMF in conservation practices are diminutive. In this way, conservation of plants outside their natural habitat, i.e., ex-situ conservation, has become significant. Accompanying sustainable development goal 2 (SDG 2) is Goal 15, which is designed to prevent hesitant and retrogressive land degradation and habitat loss [35]. Its main aims are to take vital and important steps to diminish the loss of biodiversity, re-establish degraded land and protect and reduce the loss of soil endangered species.

For Sustainable Agriculture

A number of interactions processes in the rhizosphere region have emerged current understanding of agricultural or horticultural crop plants and also on model species such as *Arabidopsis thaliana* and *Medicago truncatula*. Because the index of agroecosystem productivity can be measured by the belowground soil microbial diversity and thus the plant-microbe interaction is perilous to regulating crop yield [36-39]. Identification and influence of rhizospheric microorganisms is another research strategy that influences several plant activities for enhancing agricultural sustainability. This information from rhizosphere microbes has the potential to alleviate the productions that can be used to breed or select new varieties of plant cultivars. The negative consequences of climate change, especially on agricultural productivity, can be improved by rhizosphere microbiota that can be used to improve plant growth to sustain agriculture, with a particular focus on agricultural crops. In agricultural soils, there are three main nutrients, such as nitrogen (N), carbon (C), and phosphorus (P), which are mainly responsible for soil fertility, made possible only because of the activities of plant-root associated rhizospheric microbes. PGPR isolated from the medicinal weed, *Cassia occidentalis*, are a striking eco-friendly substitute for chemicals in agriculture and dig

out opportunities for the utilisation of these in plant growth increase and succeeding increase of yield for agricultural crops. Many rhizospheric microbial genera are being used like *Pseudomonas*, *Azotobacter*, *Bacillus*, *Rhizobium*, *Klebsiella*, *Azospirillum*, *Enterobacter*, *Caulobacter*, *Micrococcous*, *Chromobacterium*, *Alcaligenes*, *Burkholderia*, *Serratia*, and *Arthrobacter* etc. for enhancement of plant strength and growth in agriculture.

As a Biofertilizer

"A biofertilizer is an inoculant which contains living microorganisms which when applied to seeds, plants, or soil, colonizes the rhizosphere or the interior of the plants and promotes plant growth by increasing the supply of nutrients to the host plant" [40]. These microbes have been encouraged to reap the naturally available biological system of nutrient mobilization, which enormously increases soil fertility and crop yield. The enormous use of chemical fertilizers to meet the increasing demand for food supply has unquestionably led to environmental pollution and ruthlessly damaged microbial habitats and beneficial insects. Hence, it is compulsorily required to review many of the present agricultural approaches, which comprise of using chemical fertilizers, pesticides, herbicides, fungicides, and insecticides [41]. Keeping in mind the harmful effects of chemical fertilizers, biofertilizers are supposed to be a safe substitute for chemical involvement and minimize ecological disturbance to a great extent. Biofertilizers are eco-friendly, low cost, and their insistent use enhances soil strength and fertility. Furthermore, the previous use of compost as an organic fertilizer (particularly in minor scale farming, which is most frequently associated with animal husbandry) is not successful and appropriate in current agricultural practices. This is the consequence of the shift and increase in agriculture to huge scale/commercial farming, thus making manure application less suitable and inadequate as it is not consistently dispersed by animals on farmlands [42]. Hence, to enhance crop productivity and avoid food scarcity worldwide, the use of chemical fertilizers is widespread, particularly among commercial and large-scale farmers [43, 44]. The continuing usage of chemical fertilizers is responsible for a decrease in the soil pH and a disintegration in the chemical properties of the rhizosphere [45]. Therefore, number of plants creating association with numerous microorganisms can be formulated as biofertilizer and biocontrol tools.

Diseases resistant

The huge microbial population is considered to be probable in both plant growth enhancement and disease resistance. PGPRs of the rhizosphere consult disease resistance in plants by displaying antipathy to infective microbes through chitinase secretion, beta-1, and 3-glucanase; antibiotic and hydrogen cyanide production; proteases, parasitism, competition for food and establishment, etc. [46]. A number of antibiotics, anti-fungal metabolites, enzymes, phenolic compounds, signalling compounds, and other determinants of defence are produced by the PGP directly or indirectly in response to pathogen attack. *Bacillus subtilis* Jdm2 from the rhizospheric region of *Trichosanthes kirilowii* is opposed to nematodes and encourages plant progress [47]. The AM colonization of *Glomus fasciculatum* and *Pseudomonas monteilii* controlled the root-rot diseases caused by *Ralstonia solanacearum* and *Fusarium chlamydosporum* in

C. forskohlii. Pathogenesis in plants can be controlled by some rhizospheric bacteria by using the pathogenic toxins as an energy source. For example, pathogens *Fusarium solani*, *F. oxysporum* and *F. verticillioides* produce fusaric acid which causes wilt diseases, and these pathogens are used as a carbon source by rhizospheric microbes such as *Klebsiella oxytoca*, *Burkholderia ambifaria*, *B. cepacia*, etc., hence, reducing their pathogenic impact [48]. Viruses require nematodes or fungi to penetrate the root tissue to infect plants via the roots. *Streptomyces lydicus* was found to successfully diminish root and seed deterioration in tomatoes [49, 50] and also in regulation of *Pythium* and *Fusarium* challenges in spinach [50].

The beneficial organism degrades the pathogenicity factors of the pathogen such as toxins, hence, considered as a protective mechanism. In this way, along with increasing root colonization densities by PGPR microbes, they also function as the delivery system of antagonistic metabolites which are involved in direct inhibition of plant pathogens. *Streptomyces* is the major bioactive source of natural products to date. About two-thirds of natural antibiotics are produced by *actinomycetes*, out of which 75% are produced by the *Streptomyces* genus. *Streptomyces* is the most studied and reported genus and has grabbed a lot of attention because of its ability to sustain in harsh soil conditions.

Harmful Plant-microbe interaction

Along with the beneficial organisms, pathogenic populations are also equally attractive through the release of root exudates, that express their pathogenicity to only a small number of host species (Table 2). In nature, situations that are favourable for plant growth may not be appropriate for pathogens, because plant diseases are the exception rather than the rule. According to the bundle of research, plants are not defenceless. Actually, it is predicted that only about 2% of the known fungal species are able to occupy plants and cause disease. Even though plants are in permanent assemble with hidden pathogens such as bacteria

or viruses, fungi, successful infections are rarely found, this type of general resistance has been referred to as "horizontal resistance" or "non-host-resistance". This indicates that plants are not an appropriate target for infection because of the inactive resistance method which results in "basic-incompatibility". Hence, some structural barriers and a number of toxic compounds are known as resistance mechanisms that exist in unaffected and healthy plants, but in some cases, pathogens that have the capacity to overcome these factors cause successful infection called "basic compatibility". If pathogens are not able to make successful connections with the plant tissue, then a type of chemical component known as phytoanticipins is able to fight against the pathogen. In this way, several mechanisms are present which cause harmful infection in plants.

There is a huge loss in productivity because of the pathogenic activity of microbes, hence, natural agricultural resources are destroyed by plant diseases. Among them, fungi are measured as more violent, therefore causing imperative losses. Pathogenic possessions range from minor symptoms to disasters, therefore, huge implanted fields with agricultural productivity are demolished. Hence, we can also say, these pathogenic microbes are the main and ongoing pressures on agricultural productivity and ecosystem steadiness globally. Usually well studied bacterial agents include some gram-negative bacteria like *Erwinia carotovora*, *Pseudomonas*, *Ralstonia spp*, and some gram-positive bacterium such as *Streptomyces scabies*, along with the fungal and oomycete phytopathogens including members of *Fusarium*, *Phytophthora*, *Pythium*, *Rhizopus*, *Rhizoctonia* and *Verticillium* and also from the forest pathogens, among the most important are the filamentous fungi *Heterobasidion* and *Armillariella* and *Phytophthora spp*. which are pathogenic and attack living plant roots. However, in some cases, along with the beneficial results, the plant-associated PGPRs, can overcome the pre-formed barriers and cause pathogenic infection and lead to harmful plant disease.

Table 2: Harmful rhizosphere-microbes in plants

Sr. No.	Harmful Rhizosphere-microbes	Effects	Host Crops	References
1.	<i>Fusarium</i>	production of mycotoxin	potent against animal and human health	Summerell <i>et al</i> (2001)
2.	<i>Meloidogyne graminicola</i> (nematode)	infecting rice and causes up to 87% yield losses	Rice plant	Padgham <i>et al</i> (2004), Soriano <i>et al</i> (2000), Jabbar <i>et al</i> (2015)
3.	<i>Fusarium oxysporum</i>	caused systemic wilt pathogen	<i>Acacia koa</i>	Anderson <i>et al</i> (2002)
4.	<i>Phellinus weirii</i>	Effects not specified	<i>Pseudotsuga menziensis</i>	Hansen (2000)

Conclusion

Investigation about plant-microbe interactions in rhizosphere system has been of much interest in recent time because rhizospheric microbes are attracted to a large extent by high levels of exudates in the rhizosphere than anywhere else in the soil. These microbes show a broad variety of bacterial and fungal species which have high implications for plant nutrient attainment and for the production of secondary metabolites.

These rhizospheric microbial population benefits plant development by giving tolerance against abiotic and biotic stress, mineralization of phosphate and nitrogen fixation. The use of these PGPR is a supportable and eco-friendly way to improve the quantity and quality of plant productivity. However, much of the evidence presented in this review suggests that the natural associations between

plants, microbes and soil that collectively form the rhizosphere system and their inter-relation affects plants both beneficially and destructively. Research focusing on understanding the diversity and the effects of rhizospheric microbes associated with plants will be required in the future to well comprehend to fulfil requirement of the present time.

So, we can say the rhizospheric diversity of microbes shows both beneficial and pathogenic activity to regulate plant's functions.

Therefore, to untie the complex plant-microbial interactions in the rhizosphere, additional information on rhizosphere activities needs a multidisciplinary approach. This investigation suggest that more work need to be done in future to decipher the mechanism of action of the microbes-plant interaction at physiological and molecular level

emphasizing species-specific microbial community which may be beneficial for the agriculture sector.

Declarations

Acknowledgements

We thank the University of Delhi, Shivaji College (University of Delhi) for the excess of library resources.

Author Contributions

Poonam collected the relevant material, interpreted it and wrote the review. PV and KB proposed, developed and critically reviewed the idea. All authors read and approved the final review.

Funding

No funding was received to assist with the preparation of this manuscript.

Compliance with Ethical Standards

Conflict of interest

The authors declare no competing interests

Informed Consent

Not applicable

Ethics approval

Not applicable

References

- Nihorimbere V, Ongena M, Smargiassi M, Thonart P. Beneficial effect of the rhizosphere microbial community for plant growth and health. *Biotechnol Agron Soc*,2011:15:327-337.
- Adl S. Rhizosphere, food security, and climate change: a critical role for plant-soil research. *Rhizosphere*,2016:1:1-3
- Kardol P, Cornips NJ, van Kempen MM, Bakx-Schotman JT, van der Putten WH. Microbe-mediated plant-soil feedback causes historical contingency effects in plant community assembly. *Ecol monogr*,2007:77(2):147-162
- Schnitzer SA, Klironomos JN, HilleRisLambers *et al.* Soil microbes drive the classic plant diversity-productivity pattern. *Ecology*,2011:92(2):296-303
- Narula N, Kothe E, Behl RK. Role of root exudates in plant-microbe interactions. *J Appl Bot Food Qual*,2009:82:122-130
- Shrivastava S, Prasad R, Varma A. Anatomy of root from eyes of a microbiologist. In: *Root engineering*, Springer, Berlin, Heidelberg, 2014, 3-22.
- Kumar P, Dubey RC, Maheshwari DK. *Bacillus* strains isolated from rhizosphere showed plant growth promoting and antagonistic activity against phytopathogens. *Microbiol Res*,2012:167(8):493-499.
- Vacheron J, Renoud S, Muller D, Babalola OO, Prigent-Combaret C. Alleviation of abiotic and biotic stresses in plants by *Azospirillum*. In: *Handbook for Azospirillum*. Springer, Berlin, 2015, 333-365.
- Santoyo G, Pacheco CH, Salmerón JH, Leon RH. The role of abiotic factors modulating the plant-microbe-soil interactions: toward sustainable agriculture. A review. *Span J Agric Res*,2017:15(1):13
- Lakshmanan V, Selvaraj G, Bais HP. Functional soil microbiome: belowground solutions to an aboveground problem. *Plant Physiol*,2014:166:689-700
- Bulgarelli D, Rott M, Schlaeppi K *et al.* Revealing structure and assembly cues for *Arabidopsis* root-inhabiting bacterial microbiota. *Nature*,2012:488:91-95
- Khan AL, Asaf S, Al-Rawahi A, Lee IJ, Al-Harrasi A. Rhizospheric microbial communities associated with wild and cultivated frankincense producing *Boswellia sacra* tree. *PloS one*,2017:12(10):e0186939
- DeAngelis KM, Brodie EL, DeSantis TZ, Andersen GL, Lindow SE, Firestone MK. Selective progressive response of soil microbial community to wild oat roots. *The ISME journal*,2009:3(2):168-178
- Peiffer JA, Spor A, Koren O, Jin Z, Tringe SG, Dangl JL *et al.* Diversity and heritability of the maize rhizosphere microbiome under field conditions. *Proc Natl Acad Sci USA*,2013:110(16):6548-6553
- Uroz S, Buee M, Murat C, Frey-Klett P, Martin F. Pyrosequencing reveals a contrasted bacterial diversity between oak rhizosphere and surrounding soil. *Environ Microbiol Rep*,2010:2(2):281-288.
- Santoyo G, Orozco-Mosqueda MC, Govindappa M. Mechanisms of biocontrol and plant growth-promoting activity in soil bacterial species of *Bacillus* and *Pseudomonas*: A review. *Biocon Sci Technol*,2012:22:855-872.
- Glick BR. Bacteria with ACC deaminase can promote plant growth and help to feed the world. *Microbiol Res*,2014:169:30-39
- Misra S, Dixit VK, Khan MH, Kumar Mishra S, Dwiwedi G, Yadav S *et al.* Exploitation of agro-climatic environment for selection of 1-aminocyclopropane-1-carboxylic acid (ACC) deaminase producing salt tolerant indigenous plant growth promoting rhizobacteria. *Microbiol Res*,2017:205:25-34
- Katiyar D, Hemantaranjan A, Singh B. Plant growth promoting rhizobacteria-an efficient tool for agriculture promotion. *Adv Plants Agric Res*,2016:4:426-434.
- Backer R, Rokem JS, Ilangumaran G, Lamont J, Praslickova D, Ricci E, Subramanian S *et al* Plant growth-promoting rhizobacteria: context, mechanisms of action, and roadmap to commercialization of biostimulants for sustainable agriculture. *Front Plant Sci*,2018:9:1473
- Caitlin H. How do soil microbes influence nutrient availability. Pennsylvania State University, 2018.
- Buchan A, LeClerc GR, Gulvik CA, Gonzalez JM. Master recyclers: features and functions of bacteria associated with phytoplankton blooms. *Nat Rev Microbiol*,2014:12:686-698
- Omotayo OP, Babalola OO. Resident rhizosphere microbiome's ecological dynamics and conservation: Towards achieving the envisioned Sustainable Development Goals, a review. *International Soil and Water Conservation Research*, 2020.
- Jon E. Microbial miners. *Chemistry World*, 2014. <https://www.chemistryworld.com/features/microbial-miners/7879>
- Orozco-Mosqueda MDC, Rocha-Granados MDC, Glick BR, Santoyo G. Microbiome engineering to improve biocontrol and plant growth-promoting mechanisms. *Microbiol Res*,2018:208:25-31

26. Sil P, Das P, Biswas S, Mazumdar A, Biswas AK. Modulation of photosynthetic parameters, sugar metabolism, polyamine and ion contents by silicon amendments in wheat (*Triticum aestivum* L.) seedlings exposed to arsenic. *Environ Sci Pollut Res*,2019;26:13630-13648
27. Rolli E, Marasco R, Vigani G *et al.* Improved plant resistance to drought is promoted by the root-associated microbiome as a water stress-dependent trait. *Environ Microbiol*,2014;17:316-331
28. Alexandre A, Oliveira S. Response to temperature stress in rhizobia. *Crit Rev Microbiol*,2013;39:219-228.
29. Kang SM, Khan AL, Waqas M, You YH, Kim JH, Kim JG *et al.* Plant growth-promoting rhizobacteria reduce adverse effects of salinity and osmotic stress by regulating phytohormones and antioxidants in *Cucumis sativus*. *J Plant Interact*,2014;9(1):673-682.
30. Martinez-Absalon S, Rojas-Solis D, Orozco-Mosqueda MC *et al.* Potential use and mode of action of the new strain *Bacillus thuringiensis* UM96 for the biological control of the grey mould phytopathogen *Botrytis cinerea*. *Biocon Sci Technol*,2014;24:1349-1362.
31. Hernandez-Leon R, Rojas-Solis D, Contreras-Perez M *et al.* Characterization of the antifungal and plant growth-promoting effects of diffusible and volatile organic compounds produced by *Pseudomonas fluorescens* strains. *Biol Cont*,2015;81:83-92
32. Vejan P, Abdullah R, Khadiran T, Ismail S, Nasrulhaq Boyce A. Role of plant growth promoting rhizobacteria in agricultural sustainability-a review. *Molecules*,2016;21:1-17
33. Ruppel S, Franken P, Witzel K. Properties of the halophyte microbiome and their implications for plant salt tolerance. *Funct Plant Biol*,2013;40(9):940-951
34. Chialva M, Bonfante P. Plant microbiota: from model plants to Mediterranean crops. *Phytopathol Mediterr*, 2018;57:123-145
35. Omer MA, Noguchi T. A conceptual framework for understanding the contribution of building materials in the achievement of Sustainable Development Goals (SDGs). *Sustain Cities Soc*,2020;52:101869
36. Singh D, Raina TK, Kumar A, Singh J, Prasad R. Plant microbiome: a reservoir of novel genes and metabolites. *Plant Gene*,2019;18:100177
37. Varma A, Swati T, Prasad R. *Plant microbe interface*. Springer International Publishing, Switzerland, 2019. ISBN 978-3-030-19831-2
38. Varma A, Swati T, Prasad R. *Plant biotic interactions: state of art*. Springer International Publishing, Switzerland, 2019. ISBN 978-3-030-26657-8
39. Varma A, Swati T, Prasad R. *Plant microbe symbiosis*. Springer International Publishing, Switzerland. ISBN 978-3-030-36247-8
40. Malusa E, Vassilev N. A contribution to set a legal framework for biofertilizers. *Appl Microbiol Biotechnol*,2014;98(15):6599–6607
41. Pretty J, Bharucha ZP. Integrated Pest Management for Sustainable Intensification of Agriculture in Asia and Africa. *Insects*,2015;6:152-182
42. Kantikowati E, Yusdian Y, Suryani C. Chicken manure and biofertilizer for increasing growth and yield of potato (*Solanum tuberosum* L.) of Granola varieties. *Enviro Earth Sci*,2019;393(1):01-20.
43. Nkoa R. Agricultural benefits and environmental risks of soil fertilization with anaerobic digestates: A review. *Agron sustain Dev*,2014;34(2):473-492.
44. Sun R, Zhang XX, Guo X, Wang D, Chu H. Bacterial diversity in soils subjected to long-term chemical fertilization can be more stably maintained with the addition of livestock manure than wheat straw. *Soil Biol Biochem*,2015;88:9-18
45. Lin W, Lin M, Zhou H, Wu H, Li Z, Lin W. The effects of chemical and organic fertilizer usage on rhizosphere soil in tea orchards. *PLoS one*,2019;14(5):e0217018.
46. Ahmed EA, Hassan EA, El Tobgy KM, Ramadan EM. Evaluation of rhizobacteria of some medicinal plants for plant growth promotion and biological control. *Ann Agric Sci*,2014;59:273-280.
47. Wei L, Shao Y, Wan J, Feng H, Zhu H, Huang H *et al.* Isolation and characterization of a rhizobacterial antagonist of root-knot nematodes. *PLoS one*,2014;9(1): e85988
48. Simonetti E, Roberts IN, Montecchia MS, Gutierrez-Boem FH, Gomez FM, Ruiz JA. A novel *Burkholderia ambifaria* strain able to degrade the mycotoxin fusaric acid and to inhibit *Fusarium* spp. growth. *Microbiol Res*,2018;206:50-59
49. Goudjal Y, Zamoum M, Sabaou N, Mathieu F, Zitouni A. Potential of endophytic *Streptomyces* spp. for biocontrol of *Fusarium* root rot disease and growth promotion of tomato seedlings. *Biocontrol Sci Technol*,2016;26(12):1691-1705
50. Weiland JE. *Pythium* species and isolate diversity influence inhibition by the biological control agent *Streptomyces lydicus*. *Plant Dis*,2014;98(5):653-659.
51. Mehnaz S, Mirza MS, Haurat J, Bally R, Normand P, Bano A *et al.* Isolation and 16S rRNA sequence analysis of the beneficial bacteria from the rhizosphere of rice. *Can J Microbiol*,2001;47:110-117.
52. Madhaiyan M, Poonguzhali S, Ryu J, Sa T. Regulation of ethylene levels in canola (*Brassica campestris*) by 1-aminocyclopropane-1-carboxylate deaminase-containing *Methylobacterium fujisawaense*. *Planta*,2006;224:2
53. Jaleel CA, Manivannan P, Sankar B, Kishorekumar A, Gopi R, Somasundaram R *et al.* *Pseudomonas fluorescens* enhances biomass yield and ajmalicine production in *Catharanthus roseus* under water deficit stress. *Colloids Surf B*,2007;60(1):7-11
54. Ma W, Guinel FC, Glick BR. *Rhizobium leguminosarum* *Bovver viciae* 1-aminocyclopropane-1-carboxylate deaminase promotes nodulation of pea plants. *Appl Environ Microbiol*,2003;69:4396-4402.
55. Garcia de Salamone IE, Dobereiner J, Urquiaga S, Boddey RM. Biological nitrogen fixation in *Azospirillum* strain-maize genotype associations as evaluated by the 15N isotope dilution technique. *Biol Fertil Soils*,1996;23:249-256.
56. Stout MJ, Zehnder GW, Baur ME. Potential for the use of elicitors of plant defence in arthropod management programs. *Arch Insect Biochem Physiol*,2002;51:222–235
57. Repas TS, Gillis DM, Boubakir Z, Bao X, Samuels GJ, Kaminskyj SG. Growing plants on oily, nutrient-poor soil using a native symbiotic fungus. *PLoS One*,2017;12(10):e0186704.

58. Elhindi K, Sharaf El Din A, Abdel-Salam E, Elgorban A. Amelioration of salinity stress in different basil (*Ocimum basilicum* L.) varieties by vesicular-arbuscular mycorrhizal fungi. *Acta Agric Scand B-S P*,2016;66(7):583-592.
59. Marquez LM, Redman RS, Rodriguez RJ, Roossinck MJ. A virus in a fungus in a plant: three-way symbiosis required for thermal tolerance. *Sci*,2007;315(5135):513–515
60. Xu P, Chen F, Mannas JP, Feldman T, Sumner LW, Roossinck MJ. Virus infection improves drought tolerance. *New Phytol*,2008;180(4):911-921.
61. Summerell BA, Leslie JF, Backhouse D, Bryden WL, Burgess LW. *Fusarium: paul E. Nelson memorial symposium*. APS Press. The American Phytopathology Society, St Paul, 2001, 392.
62. Padgham JL, Duxbury JM, Mazid AM, Abawi GS, Hossain M. Yield loss caused by *Meloidogyne Graminicola* on lowland rainfed rice in Bangladesh. *J Nematol*,2004;36(1):42-48.
63. Soriano IR, Prot JC, Matias DM. Expression of tolerance for *Meloidogyne Graminicola* in rice cultivars as affected by soil type and flooding. *J Nematol*,2000;32(3):309-317
64. Jabbar A, Javed N, Khan SA, Ali MA. *Meloidogyne graminicola* an emerging threat to rice and wheat in Punjab province in Pakistan. *Pak J Nematol*,2015;33:227-228.
65. Anderson RC, DE Gardner, CC Daehler, FC Meinzer. Dieback of *Acacia koa* in Hawaii: ecological and pathological characteristics of affected stands. *For Ecol Manag*,2002;5576:1-14
66. Hansen EM. *Phellinus weirii* and other native root pathogens as determinants of forest structure and process in western North America. *Annu Rev Phytopathol*,2000;38:515-539.