

Review Paper

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Rhizosphere Microbial Community Structure: A Review

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Abstract

Microbial communities play an essential role in the functioning of plants by influencing their physiology and development. While many members of the rhizosphere microbiome are beneficial to plant growth, also plant pathogenic microorganisms colonize the rhizosphere striving to break through the protective microbial shield and to overcome the innate plant defence mechanisms in order to cause disease. Although the importance of the microbial community associated with rhizosphere has been widely recognized to enhance plant growth including soil structure formation; decomposition of organic matter; toxin removal; and the cycling of carbon, nitrogen, phosphorus, potassium, ion chelation and sulphur. Thus these rhizospheric microbial community can be exploited for commercial application as Biofertilizer and Biocontrol agents.

Introduction

Microorganisms may comprise of mixed populations of naturally occurring microbes in soil that can be applied as inoculants to increase soil microbial diversity. Investigations have shown that the inoculation of efficient microbial community to the soil ecosystem improves soil quality, soil health, growth, yield and quality of crops. These microbial populations may consist of selected species of microorganisms including plant growth promoting rhizobacteria, cyanobacteria, plant disease suppressive bacteria and fungi, soil toxicant degrading microbes, actinomycetes and other useful microbes (Kavino et al. 2007) Efficient and potential soil microbial biota is required for sustainable agriculture practices and some of them have other potential applications. It is an added dimension to optimizing soil and crop management practices such as crop rotation, organic

amendments, conservation tillage, crop residue recycling, soil fertility restoration, maintenance of soil quality and the biocontrol of plant diseases. If used adequately, microbial communities can significantly benefit the agriculture practices. In this review Microbial diversity with relation to plant and its role in agro ecosystem would be discussed (Pandey et al. 2012).

A fundamental shift is taking place worldwide in agricultural practices and food production. Today, the drive for productivity is increasingly combined with the desire and even the demand for sustainability. Sustainable agriculture involves successful management of agricultural resources to satisfy human needs while maintaining environmental quality and also conserving natural resources for future. Improvement in agricultural sustainability requires the optimal use and management of soil fertility and its physico-chemical properties. Both rely on soil biological process and soil biodiversity. This implies management practices that enhance soil biological activity and thereby buildup long term soil productivity and crop health. Such practices are of major concern in almost all lands to avoid degradation and in restoration of degraded lands and in regions where high external input agriculture is not feasible (Lavania, et al. 2006).

Plants are always in immediate contact with microorganisms including different tissues of leaves and roots and also as endophytes presents within plant tissues. These microorganisms are actively associated with plant in their development, nutrient supply, plant growth promotion and protection against pathogens. There exist multiple diversity of microorganisms including bacteria, fungi, mycorrhiza, symbiotic and non-symbiotic nitrogen fixers. Here we have described some of the microbial diversity based on their significant role in plant growth (Goh et al. 2013).

Role Of Microbes In Soil

Microorganisms in soil are critical to the maintenance of soil function in both natural and managed agricultural soils because of their involvement in such key processes as soil structure formation; decomposition of organic matter; toxin removal; and the cycling of carbon, nitrogen, phosphorus, potassium, ion chelation and sulphur (Massol et al. 1995). In addition, microorganisms play key roles in suppressing soil borne plant diseases and in promoting plant growth (Doran et al. 1996). Soil microbial communities are often difficult to fully characterize because of their immense phenotypic and genotypic diversity, heterogeneity, and crypt city. With respect to the latter, bacterial populations in soil top layers can go up to more than 10^9 cells/g of soil (Cockell et al. 2009), and most of these cells are generally unculturable. The fraction of the cells making up the soil microbial biomass that have been cultured and studied in any detail are often less than 5% (Borneman and Triplett. 1997). As direct DNA-based methods offer the possibility to assess the total microbial diversity present, thus bypassing the limitations of cultivation-based studies, recent years have seen the rapid development of such cultivation-independent methods for analyzing the microbial communities in soil (Massol et al. 1995). The direct methods have become indispensable in such studies; however, one needs to be caution about what information they are giving (VonWintzingerode et al. 1997). Functional diversity is an aspect of the overall microbial diversity in soil, and encompasses a range of activities. The relationship between microbial diversity and function in soil is largely unknown, but biodiversity has been assumed to influence ecosystem stability, productivity and resilience towards stress and disturbance in plant.

Bacterial Diversity

Bacteria an important portion of the microbial diversity, represent one of the three domains in the phylogenetic tree (Archaea, Bacteria and Eukarya) (Olsen et al. 1994). Though bacteria are found almost everywhere, Rhizosphere is a region of soil which is in immediate contact with plants portion directly influenced by root exudates and considered as the most active region of soil where maximum microbial community resides. Rhizospheric region of soil plays a very important role in growth and development of plants. Bacteria are the major portion of biomass in the soil and are responsible for some essential nutrient cycling processes of carbon, nitrogen and sulfur. In addition to the bacterial diversity, intra specific diversity also persists. The bacterial diversity is not static, due to the high reproduction capacity associated with the short life cycle and high cell multiplication rates, which leads to the high adaptation value, and fast responses to environmental change (Konstantinidis et. al 2006).

A broad diversity of bacteria can interact with plants, composing bacterial communities with important roles in plant growth and development (Hallmann et al. 1997). There are various interactions associated with bacteria and plant which can vary according to the host plant in a process (Salvaudon et al. 2008). Bacterial populations are distributed in the rhizosphere, within epiphytic and endophytic communities.

Classification of bacteria as Epiphytic and endophytic depends on their colonization on plant surface and inner tissues of plants, respectively. Endophytes are those microbes which are isolated from the internal tissues of plant after disinfecting the outer surface (Hallmann et al. 1997). However, in addition to these definitions according to their essentiality in niche endophytes can be characterized into types one “passenger” endophytes, bacteria that eventually invade internal plant tissues by stochastic events and second “true” endophytes, those with adaptive traits enabling them to strictly live in association with the plants (Hardoim et al. 2008). The microbial cells in the rhizosphere, plant-surface or endophyte communities are variable. The analysis of these communities could lead to the conclusion that there is a strict specificity for their habitation and niche colonization. However, a more realistic situation is represented by the gradient of bacterial population distribution along and within the plants. If a didactic approach is applied to explain bacterial communities associated with plants and plant tissues, it would divide these bacteria into distinct communities, with separation between epiphytic and endophytic communities in accordance with plant organs, such as roots, stems and leaves.

All these bacterial diversities present in soil have distinct role, such as supplying nutrient to the plant, enhancing plant growth by producing plant growth hormones, inhibition of plant pathogens, and all such bacteria are referred as plant growth promoting bacteria which can have symbiotic association or non-symbiotic association with plant some examples are listed in Table 1

Plant growth promoting rhizobacteria (PGPR) enhancing growth and development of crop/ fruit plants (Singh et al. 2011)

PGPR	Plant Growth Parameters
<i>Rhizobium leguminosarum</i>	Growth promotion of canola and lettuce
<i>Pseudomonas putida</i>	Early developments of canola seedlings
<i>Azospirillum brasilense</i> and <i>A. irakense</i> strains	Growth of wheat and maize plants
<i>P. fluorescens</i> strain	Growth of pearl millet
<i>P. putida</i> strain	Growth and development of tomato plant
<i>Azotobacter</i> and <i>Azospirillum</i> strains	Growth and productivity of canola
<i>P. alcaligenes</i> PsA15, <i>Bacillus polymyxa</i> BcP26, and <i>Mycobacterium phlei</i> MbP18	Enhance uptake of N, P and K by crop in nutrient deficient
<i>Pseudomonas</i> , <i>Azotobacter</i> and <i>Azospirillum</i> strains	Stimulates growth and yield of chick pea (<i>Cicer arietinum</i>)
<i>R. leguminosarum</i> (Thal-8/SK8) and <i>Pseudomonas</i> sp. strain 54RB	Improve the yield and phosphorus uptake in wheat Plant
<i>P. putida</i> strains R-168 and DSM-291 and	Improves seed germination, seedling growth yield of maize Plant
<i>P. fluorescens</i> strains R-98 and DSM-50090 <i>A. brasilense</i> DSM-1691 <i>A. lipoferum</i> DSM-1690 and <i>P. putida</i> strain R-168	Seed germination, growth parameters of maize plant
<i>P. fluorescens</i> strain R-93, <i>P. fluorescens</i> DSM 50090, <i>P. putida</i> DSM291, <i>A. lipoferum</i> DSM 1691, <i>A. brasilense</i> DSM 1690 <i>P. fluorescens</i> strains, CHA0 and Pfl	Increase growth, leaf nutrient contents and yield of banana plants

Fungal Diversity

Fungi are an important component of the soil microbiota typically constituting more of the soil biomass than bacteria, depending on soil depth and nutrient conditions (Ainsworth and Bisby, 1995). Many important plant pathogens (e.g. smuts and rusts) and plant growth promoting microorganisms (e.g., ecto- and endo-mycorrhizae) are fungi. The saprobic fungi represent the largest proportion of fungal species in soil and they perform a crucial role in the decomposition of plant structural polymers, such as, cellulose, hemicellulose, and lignin, thus contributing to the maintenance of the global carbon cycle. In addition, these catabolic activities enable fungi to grow on inexpensive substrates.

Fungal diversity in soil plays a significant role such as water dynamics, nutrient cycling, disease

suppression and decomposition. Fungi usually have a symbiotic mutualistic association they are mainly member of Zygomycota, Ascomycota or Basidiomycota in these symbioses, the host plant receives mineral nutrients, while the fungus obtains photosynthetically derived carbon compounds (Fortin et al. 2002). At least seven different fungi – plants associations have been recognized, with distinct morphological patterns, involving different groups of organisms (Brundrett et al. 1996). The most common ones are: i) vesicular arbuscular mycorrhizas (VAM), in which Zygomycetes fungi produce arbuscules, hyphae and vesicles among root cortex cells, between cell wall and plasmatic membrane; ii) ectomycorrhizas (ECM), where Basidiomycetes and other fungi form a mantle around roots and a so called Hartig net among root cells; iii) orchid mycorrhizas, where fungi produce coils of hyphae within roots (or stems) of orchidaceous plants; (iv) ericoid mycorrhizas, developing hyphal coils in outer cells of Ericales hair roots (Stone et al. 2000). Factors that can influence the establishment and persistence of mycorrhizal associations are various, besides symbiont compatibility: external factors edaphic or microclimatic conditions, presence of further soil organisms, nutrient competition; and internal factors organism phenology. Infective propagules must be present when root growth activity occurs, since roots have a limited period of susceptibility.

Fungi and other microbes in the soil and are critical to decomposing organic residues and recycling soil nutrients. Most soil fungi decompose recalcitrant organic residues high in cellulose and lignin. Carbon use efficiency of fungi is about 40–55% so they store and recycle more C (10:1 C: N ratio) and less N (10%) in their cells than bacteria. Fungi are more specialized but need a constant food source and grow better under no-till conditions. Arbuscular Mycorrhizal (AM) fungi produce an amino polysaccharide called glomalin. Glomalin surrounds the soil particles and glues macroaggregate soil particles together and gives soil its structure. AM fungus store and recycle N and P in the soil and have a symbiotic relationship with most plants, greatly increasing the N and P extraction efficiency and improving soil structure and water retention (Fortin et al. 2002).

Mycorrhizal Diversity

Glomus forms largest genus of arbuscular mycorrhizal fungi (AMF). All species present in the species shows symbiotic relationships with plant roots. The establishment entire mechanism of symbiosis involves a sequence of recognition mechanism, following to the morphological and physiological integration of the two organisms (Logi et al. 1998). The life cycle of an AMF begins with spore germination, and follows with a pre-symbiotic mycelia growth phase, hyphal branching, appressorium formation, root colonisation, and finally arbuscule formation takes place (Giovannetti et al. 1994).

There are mainly of two types of mycorrhiza ecto- and endomycorrhizas. The ectomycorrhizas are characterized by an extracellular fungal growth associated with the root cortex and are more common in temperate and boreal forest trees, also found to be over 5000 species mainly within the Basidiomycetes (Covacevich et al. 2007). The tropical trees such as pine and eucalyptus plants, however, have also been found to appear ectomycorrhizal associations. The endomycorrhizas are characterized by inter-and intracellular fungal growth in root cortex, forming specific fungal growth, referred to as vesicles and arbuscules. This characteristic growth gives the endomycorrhiza the alternate name, vesicular arbuscular mycorrhiza. Mycorrhizal association in plants is widely distributed. About 80% of all terrestrial plant species form this type of symbiosis association and 95% of the world's present species of vascular plants belong to families that are characteristically

mycorrhizal (Quilambo et al. 2000). The arbuscular mycorrhizal fungi (AMF) belong to taxonomic order called Glomales.

Mycorrhiza shows symbiotic association between fungi and plant roots and is unlike either fungi or roots alone. Most trees and agricultural crops depend on or benefit substantially from mycorrhizae. The exceptions are many members of the Cruciferae family (e.g., broccoli, mustard), and the Chenopodiaceae family (e.g. lambsquarters, spinach, beets), which do not form mycorrhizal associations. The level of dependency on mycorrhizae varies greatly among varieties of some crops, including wheat and corn.

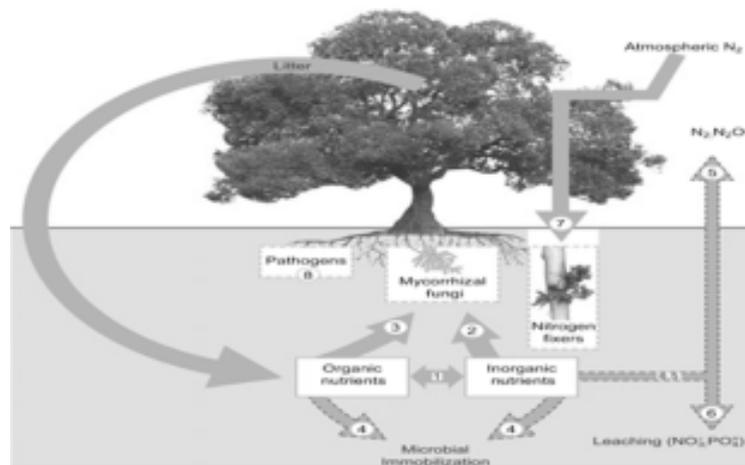
Land management practices affect the formation of mycorrhizae. The number of mycorrhizal fungi in soil will decline in fallowed fields or in those planted to crops that do not form mycorrhizae. Frequent tillage may reduce mycorrhizal associations, and broad spectrum fungicides are toxic to mycorrhizal fungi. Very high levels of nitrogen or phosphorus fertilizer may reduce inoculation of roots. Some inoculums of mycorrhizal fungi are commercially available and can be added to the soil at planting time (Banerjee et al. 2006). VAM fungi play crucial roles in both natural and agricultural situations, including Native ecosystems such as forests where fertilization of extensive land areas with large quantities of P is not practical, agricultural systems in which the high P-fixing capacities of soils and the unavailability or high cost of P fertilizer limits crop production, situations in which it is essential to reduce soil fertilizer application rates significantly because of environmental concerns, situations in which phosphate rock is readily available and used instead of superphosphate (Habte et al. 2000).

Beneficial Role Of Soil Microbes

Biological nitrogen fixation is considered as one of the major mechanisms by which plants get benefited from soil microorganisms. According to an estimate, global contribution of biological nitrogen fixation is 180×10^6 metric tons per year. Of this contribution, 83% comes from symbiotic associations of microbes, while the rest part of it is provided by free living or associative systems (Ashraf et al. 2013). Archaea and bacteria are the only living forms that are capable of fixing the atmospheric nitrogen and enrich the soil with this form of nitrogen (Robertson et al. 2009). These include symbiotic nitrogen fixers (Rhizobium in legumes, Frankia in non-leguminous trees) and non-symbiotic nitrogen fixers such as Azoarcus, Acetobacter diazotrophicus, Azotobacter, Azospirillum, cyanobacteria etc. Plants require an adequate supply of nutrients for their proper growth and development. Plants growing on the soils enriched with nutrients may still exhibit nutrient deficiencies due to unavailability of these mineral nutrients. However, plant growth promoting rhizobacteria are actively involved in the solubilization of important minerals such as phosphorous, iron, thereby enhancing the availability of these essential nutrients to plants (Glick et al. 1995). The positive role of PGPR in stimulating the plant growth by improving solubilization (releasing siderophores or organic acid) and nutrient uptake by the plants has been well documented in the literature (Glick et al. 1995).

Based on their activities Ahemad (2014) classified PGPR as biofertilizers (increasing the availability of nutrients to plant), phytostimulators (plant growth promoting, usually by the production of phytohormones), rhizoremediators (degrading organic pollutants) and biopesticides (controlling diseases, mainly by the production of antibiotics and antifungal metabolites). Bashan and Holguin (1998) proposed the division of PGPR into two classes: biocontrol-PGPB (plant-growth-promoting-

bacteria) and PGPB. This classification may include beneficial bacteria that are not rhizosphere bacteria but it does not seem to have been widely accepted. When studying beneficial rhizobacteria, the original definition of PGPR is generally used: it refers to the subset of soil and rhizosphere bacteria colonizing roots in a competitive environment, e.g. in non-sterilized or non-autoclaved field soils (García et al. 2003). Furthermore, in most studied cases, a single PGPR will often reveal multiple modes of action including biological control (García et al. 2003). Microorganisms like bacteria, fungi, actinomycetes, algae and protozoa exhibit various properties which are helpful in nutrient cyclin



Schematic

Nitrogen Cycling.

Among various important gases of Earth's atmosphere, N_2 is the most abundant gas which possesses the property of non-reactivity. Nitrogen (N_2) is one of the basic necessities of living world. It comprises the formation of amino acids and proteins. Various organic compounds are derived from nitrogen fixation process. Biological nitrogen fixation is an important part of the wide range of protective responses aimed at deterring microbial processes.

The conversion of molecular nitrogen to ammonia is an enzyme catalyzed reaction which is the base of nitrogen fixation process. This enzyme is nitrogenase, an oxygen labile enzyme complex and found produced by free living and symbiotic diazotrophs (Rubio and Ludden 2005). Diazotrophs are ubiquitous in earth's soils and waters and exhibit a range of metabolic life styles (Masepohl and Klipp 1996).

Non-Symbiotic Nitrogen Fixation

Free-living bacteria are found in soils that are free from the direct influence of plant roots and thus do not associate with plants. The amount of Nitrogen which is fixed by these microbe depends on their potential for accessibility to energy sources, i.e., substrates to generate adenosine triphosphate (ATP) and micronutrients required for the synthesis and functioning of nitrogenase (Reed et al. 2011). BNF by free-living diazotrophs is also limited by the severe oxygen sensitivity of nitrogenase (Postgate et al. 1998).

Due to their ability to fix N_2 , diazotrophs can have a competitive advantage over non- N_2 fixing bacteria in the rhizosphere and prevail in it particularly when soil N is limited (Dobereiner and Pedrosa, 1987). In addition to enhancing their own growth, rhizosphere diazotrophs like *Acetobacter*, *Azoarcus*, *Azospirillum*, *Azotobacter*, *Beijerinckia*, *Burkholderia*, *Enterobacter*, *Herbaspirillum*, *Klebsiella*, *Paenibacillus* and *Pseudomonas*) have been shown to enhance the growth of the plants. These include agriculturally-important species such as plants like rice, wheat, barley, potato and several vegetable crops (Chanway et al. 2014).

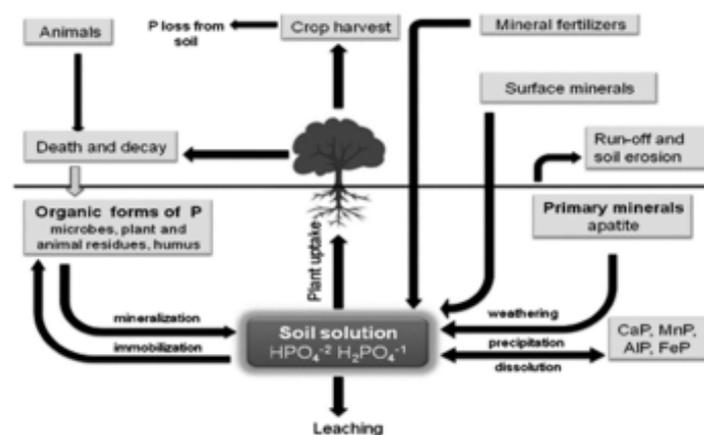
Symbiotic Nitrogen Fixation

The term symbiosis generally denotes the mutual beneficial partnership between two organisms. Bacteria known collectively as Rhizobia are famous for their abilities to induce nodules on the roots of legume plants. In legume root nodule symbiosis, the legume is the bigger partner while the rhizobium is the smaller partner, often referred as microsymbiont. Within these nodules, the differentiated ‘‘bacteroid’’ forms fix atmospheric nitrogen and the resultant ammonia being used as the source of fixed nitrogen (Kanthé et al. 2012). The genus rhizobium has been placed in bergey’s manual of determinative bacteriology in such diverse families as azotobacteriaceae, mycobacteriaceae, myxobacteriaceae and pseudomonadaceae.

Phosphorus Cycling

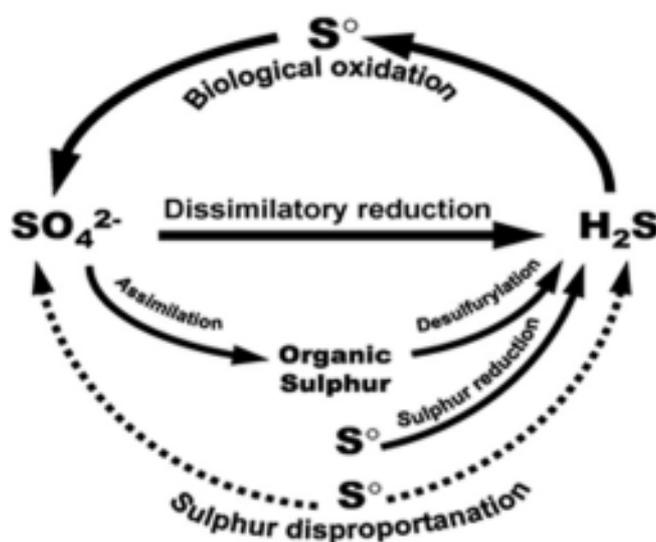
Phosphorus (P), being the second most important plant growth-limiting nutrient following nitrogen, is copiously available in both forms in soils, viz. organic and inorganic (Khan et al. 2009). Regardless of the large reservoir of P, the actual availability of its forms to the plant, is usually low. Richardson (2000) reported that most soils are poor in accessible phosphorus and phosphate compost signifies a high cost to the farmer; subsequently, it is intriguing to exploit soil microorganisms utilized as inoculum for the mobilization of phosphorus in poor soils. This low accessibility of phosphorous to plants is on the grounds that the dominant part of soil P is found in insoluble structures, while the plants assimilate it just in two solvent structures, the monobasic and the dibasic ions (Bhattacharyya and Jha 2012).

Use of phosphate solubilizing microorganisms assume imperative part in solubilizing the insoluble forms of phosphorus. Strains from genera *Pseudomonas*, *Bacillus* *Rhizobium*, *Aspergillus* and *Cephalosporium* are among the phosphate solubilizers.



Sulphur Cycling

Microorganisms assume an essential part in the worldwide cycle of different components, for example, sulfur, nitrogen, carbon and iron. Sulfur happens in mixed bag of oxidation states with three oxidation conditions of -2 (sulfide and decreased natural sulfur), 0 (essential sulfur) and +6 (sulfate) being the hugest in nature. Compound or natural operators help change of sulfur starting with one state then onto the next. A biogeochemical cycle which portrays these changes contains numerous oxidation-reduction responses. Hydrogen sulphide, a reduced type of sulfur, can be oxidized to sulfur or sulfate by a mixed population of microorganisms. Sulfate, can be again converted to sulfide by sulfate reducing microorganism (Ishimoto et al. 1954).



Sulphate reducing bacteria fall into three major branches: (i) the subclass of proteobacteria (more than 25 genera), (ii) the Gram positive bacteria (Desulfotomaculum, Desulfosporosinus), (iii) branches formed by Thermodesulfobacterium and Thermodesulfovibrio.

Pottassium Solubilization

Potassium uptake of plants can be increased by using potassium solubilizers as bio-inoculants further increasing the crop production. Also co inoculation with other bio inoculants like Phosphate solublizers has also shown positive co-relation with yields of crops. Muentz showed the first evidence of microbial involvement in solubilization of rock potassium (Muentz et al. 1890). Microorganisms like Aspergillus niger, Bacillus extroquens and Clostridium pasteurianum were found to grow on muscovite, biotite, orthoclase microclase and mica in vitro (Archana et al. 2013). Different bacterial species like silicate bacteria were found to dissolve potassium, silicates and aluminium from insoluble minerals produces acids like citric acid, formic acid, malic acid, oxalic acid. These organic acids produced, enhance the dissolution of potassium compounds by supplying protons and by complexing Ca²⁺ ions. Previous work has shown organic compounds produced by micro-organisms such as acetate, citrate and oxalate can increase mineral dissolution in soil (Sheng, 2003). Solubilization of potassium occurs by complex formation between organic acids and

metal ions such as Fe^{2+} , Al^{3+} and Ca^{2+} (Styriakova et al. 2003).

Ironchelation

Certain microbes oxidize ferrous iron to ferric state which hasten as ferric hydroxide around cells. These microorganisms usually known as iron microbes are typically non filamentous and round or bar molded like *Galionella*, *Siderophacus*, *Siderocapsa*, *Ferribacterium*, *Sideromonas* and so forth filamentous structures taking after green growth are likewise experienced like *Leptothrix* (Pringsheim et al. 1949), *toxothrix* etc. These microorganisms assume to play no critical part in cultivable soil.

Iron is an essential growth element for all living organisms. The scarcity of bioavailable iron in soil habitats and on plantsurfaces foments a furious competition (Loper and Henkels 1997). Under ironlimiting conditions PGPB produce low molecular weight compounds called siderophores to competitively acquire ferric ion (Whipps et al. 2001). Siderophores (Greek: "iron carrier") are small, high affinity iron chelating compounds secreted by microorganisms such as bacteria, fungi and grasses. Microbes release siderophores to scavenge iron from these mineral phases by formation of soluble Fe^{3+} complexes that can be taken up by active transport mechanisms. Many siderophores are non-ribosomal peptides, although several are biosynthesised independently (Challis et al. 2005). Siderophores are also important for some pathogenic bacteria for their acquisition of iron (Miethke and Marahiel 2007). Siderophores are amongst the strongest binders to Fe^{3+} known, with enterobactin being one of the strongest of these (Raymond, Dertz and Kim 2003). Distribution of siderophore producing isolates according to amplified ribosomal DNA restriction analysis (ARDRA) groups, reveals that most of the isolates belong to Gram negative bacteria corresponding to the *Pseudomonas* and *Enterobacter* genera, and *Bacillus* and *Rhodococcus* genera are the Gram positive bacteria found to produce siderophores

Other Trace Nutrients

Plants require trace nutrients like, iron, manganese, copper, zinc etc. Non availability of these trace metals in soil may result in the manifestation of specific symptoms on plant parts.

Manganese is obligated to oxidation in soil relying upon pH, oxygen supply and natural matter substance of soil. In acidic soils it is available in a bivalent state in which state it is effortlessly accessible for assimilation by plants. In unbiased and alkaline soils, manganese occurs in trivalent or tetravalent state when the component is not effortlessly accessible for retention by plants. The change of manganous to manganic particles may be a microbiological methodology including microscopic organisms, for example, *azotobacter*, *chroococcum*, *pseudomonas flourescens*, *P.trifolii*, *leptothrix* sp., *aerobacter* sp., *proteus* sp., *corynebacterium* sp., *flavobacterium* sp., *chromobacterium* sp., *metallogenium* sp., and a few other unidentified ones (Ghiorse et al. 1984).

Harmful Role Of Soil Microorganisms

Some soils are inhospitable to plant pathogens, by limiting either the survival or the growth of the pathogens. Such soils are known as pathogen- or disease-suppressive and are found throughout the world. Suppressiveness has been defined as either "general" or "specific," indicating either the absence or presence of information about the mechanisms involved. General suppression often reduces fungal and nematode attacks, whereas specific suppression is often effective against only one or a few pathogens.

Suppressive soils are further differentiated in accordance with their longevity in “long-standing suppression” and “induced suppression” (Chabrol et al. 1988). Long-standing suppression is a biological condition naturally associated with the soil, its origin is not known, and it appears to survive in the absence of plants. Induced suppression is initiated and sustained by crop monoculture or by the addition of inoculum of target pathogen.

Commercial Applications Of Plant Growth Promoting Rhizobacteria

Microbes as Biofertilizer

Plant growth promoting rhizobacteria as natural manures, a gathering of biofertilizers comprising helpful rhizobacteria recognized as PGPR, are strains from genera of *Pseudomonas*, *Azospirillum*, *Azotobacter*, *Bacillus*, *Burkholderia*, *Enterobacter*, *Rhizobium*, *Erwinia* and *Flavobacterium* (Rodriguez and Fraga, 1999). Free-living PGPR guarantee to act as biofertilizers (Podile and Kishore 2007). Secondary metabolites from PGPR upgrade root development, prompting a root framework with vast surface region and expanded number of root hairs (Mantelin and Touraine 2004). Numerous studies and overviews reported plant development advancement, expanded yield, uptake of N and some different components through PGPR immunizations (Glick et al. 2007).

Microbes as Biocontrol Agents

The PGPR is a gathering of rhizosphere colonizing microbes that creates substances to expand the development of plants and/or secure them against illnesses (Harish et al., 2009). PGPR may ensure plant safety against pathogens. These incorporate, the capacity to deliver siderophores to chelate iron, to combat against contagious metabolites, for example, anti-microbials, parasitic cell divider lysing proteins, or hydrogen cyanide that stifle the development of contagious pathogens (Persello Cartieaux et al., 2003).

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