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Rhizospheric microbiomes for agricultural sustainability

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EDITORIAL

Agricultural sustainability rests on a foundation of microbial diversity and activity. Soil consists of a rich biodiversity of microorganisms belongs to all three domains of life, i.e., *archaea*, bacteria, and eukarya. The rhizosphere is the plenty of extensively colonized zone of the soil due to the availability of nutrients to the microorganisms. The rhizospheric zone is one of the largest ecosystems, with the bacterial population being predominant. Bacteria in the rhizospheric region benefit the plants by stimulating their growth and productivity through diverse mechanisms, including the production of plant growth regulators and siderophores, the fixation of atmospheric nitrogen, and the solubilization of unavailable and insoluble macro- and micro-nutrients. Plant growth-promoting (PGP) rhizomicrobiomes protect the plants against phytopathogens by producing antibiotics, extra-cellular hydrolytic enzymes, prussic acid, and ammonia. Furthermore, PGP rhizomicrobiomes also help the plants under abiotic stress from cold, salinity, drought, and heavy metals by lowering the levels of inhibitory ethylene, increasing the accumulation of osmolytes in the plants, and production of the reactive oxygen species scavengers. PGP rhizomicrobiomes belong to diverse phyla of the domain *archaea*, bacteria, and eukarya, in which the predominant members are *Actinobacteria*, *Bacteroidetes*, *Firmicutes,* and *Proteobacteria*. These beneficial rhizomicrobiomes could be used as bioinculants for agricultural sustainability.

Bacterial diversity in the rhizospheric region can be examined by various methodologies. A range of culture media have been designed for the isolation of culturable rhizobacteria [1]. In addition to traditional methods of isolation, bacterial diversity can be characterized at the molecular level by polymerase chain reaction amplification, followed by sequencing. There are different methods for characterization of unculturable microbiomes [2]. PGP rhizopsheric microbiomes with multifunctional attributes could be sorted out with standard proctocols and methods of screening microbes under *in vitro* conditions. The selected microbes could be utilized to check their potential role in soil health and plant growth promotion under controlled and natural environmental conditions. The selected microbes could be commercialized as biofertilizers, biopesticides, and biostumulants for sustainability [3]. There are different communication strategies utilized by plants, fungi, and bacteria in the rhizosphere [Figure 1].

Nitrogen (N) is an important nutrient required by plants in substantial proportion, and its accessibility is a major significant aspect of expansion and growth [4]. One of the most effective and environmentally friendly ways to meet the nitrogen needs of plants while minimizing the usage of chemical nitrogen fertilizers is through the use of N_2-fixing rhizobacteria [5]. Nitrogen fixers belong to different categories, viz., symbiotic, free-living, and associative symbiotic [6]. Nitrogen fixers reported and well characterized include *Pseudomonas*, *Rhizobium, Herbaspirillum*, *Bacillus*, *Azotobacter*, *Azospirillum,* and *Azoarcus* [7].

Phosphorus (P) is another major nutrient requisite by plants for their development and metabolic processes. The management of phosphorus in soil is severely critical to secure sustainable and lucrative agriculture with negligible consequences for the environment [8]. In this regard, rhizobacteria with the ability to solubilize phosphorus are emerging bioresources and are known as phosphorus solubilizing bacteria (PSB). PSB employs a diverse perspective to make phosphorus accessible to plants in a way that assists efficient absorption by plants, which includes the evacuation of compounds that dissolve the mineral and the production of extracellular enzymes for solubilization of the phosphorus [9]. PSBs reported belong to different genera, including *Serratia*, *Rhodococcus*, *Pseudomonas*, *Microbacterium*, *Flavobacterium*, *Burkholderia*,

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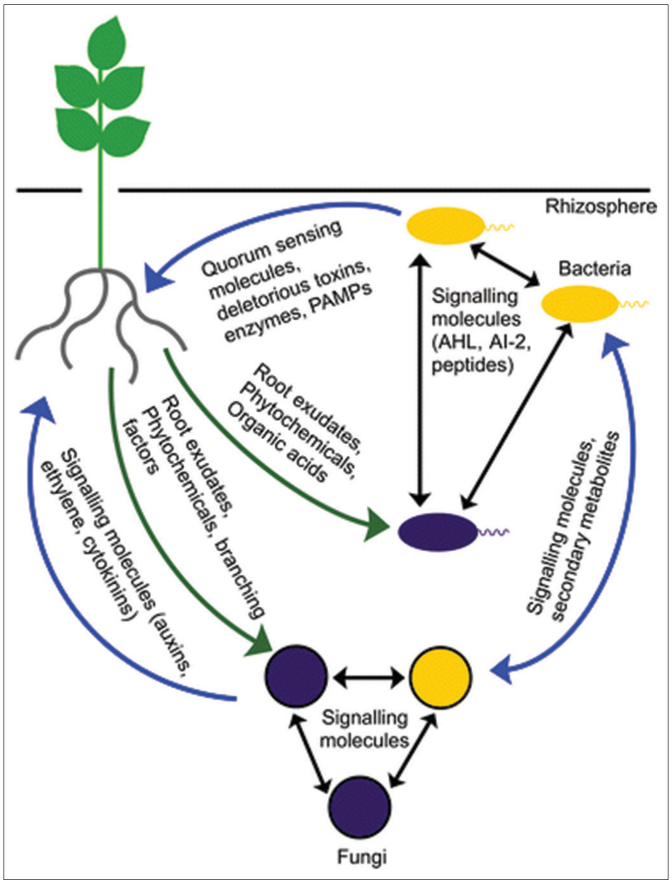

Figure 1: Schematic overview of interactions between plants, fungi and bacteria in the rhizosphere. Adapted from Lareen *et al.* [31].

Bacillus, and *Arthrobacter* [9]. PSB has attracted greater anticipation from agriculturists as bioinoculants for boosting the growth and productivity of plants.

Potassium (K) is a crucial macronutrient that plants need for optimal operation; however, its solubilization is a significant detriment for reducing agricultural production [10]. The present outline of K deficiency in soil is gradually increasing due to the unobtainable form of K in soil. Currently, agriculturalists are facing the obstacle of chemical potash fertilizer due to its high costs [11]. The fulfilling of the plant demands for potassium requires alternative and sustainable approaches. In this regard, the use of potassium-solubilizing bacteria could be a beneficial strategy. K-solubilization has been reported in *Arthrobacter* spp., *Acinetobacter* spp., *Achromobacter* spp., *Bacillus* spp., *Kocuria* spp., *Paenibacillus* spp., *Sphingomonas* spp., and *Staphylococcus* spp. [12,13].

A variety of plant growth and development, for instance, tissue differentiation, apical dominance, cell division, and cell elongation, are controlled by the phytohormones [14]. Phytohormone production has been well known in plant growth-promoting rhizobacteria (PGPR). Indole acetic acid (IAA) is the foremost energetic auxin with roles in cell division, seed germination, vegetative growth, root development, and pigment production. This has been reported in species of *Acinetobacter*, *Arthrobacter*, *Bacillus*, *Pseudomonas,* and *Xanthomonas* [12,15]. Gibberellins, another important plant growth regulator, have been produced by *Bacillus licheniformis* and *Bacillus pumilus* [16]. Cytokinins mediate many essential phases of plant expansion in aerial and subsurface organs. Cytokinins control the shoot's interaction with light conditions and the root's access to nutrients and water. It also has a role in responding to biotic and abiotic stress [17]. A study concluded that *Arthrobacter*, *Azospirillium*, *Azotobacter*, *Bacillus*, *Pseudomonas,* and *Rhizobium* have been reported for cytokinin production [18].

Recently, the usage of PGPR in disease management has been rising. PGPR, through different mechanistic approaches, protects the plants from the devastating impacts of the phytopathogens. PGPR produces antibiotics such as kanosamine, pantocin, pyoluteorin, 2,4-diacetyl phloroglucinol, phenazine-1-carboxylic acid, and zwittermycin-A. The synthesis of antibiotics is mediated by a cascade of endogenous signals such as sigma factors, N-acyl homoserine lactones, and sensor kinases [19]. PGPR releases various volatile organic compounds (VOCs), which are biocontrol specialists against phytopathogens [20]. VOCs of *Bacillus* sp. are successful inhibitors of fungi. HCN is an important VOC with biocontrol potential. The exhibition of hydrolytic enzymes such as proteases, chitinases, dehydrogenases, β-glucanases, lipases, and phosphatases by PGPR is another major mechanism of biocontrol against Pythium ultimum, Botrytis cinerea, Fusarium oxysporum, Phytophthora spp., Rhizoctonia solani, and Sclerotium rolfsii [21]. *Bacillus subtilis* has been reported to have biocontrol activity due to cellulases against C*olletotrichum gloeosporioides* [22]. Actinomycetes have also been reported to have biocontrol activity due to cellulases [23].

Draft genome sequencing has a significant role in studies of PGP microbes. A draft genome of diverse PGPRs has been reported. The draft genome of PGPR, *Serratia fonticola* AU-P3(3), revealed a 5.02-Mb genome sequence and genes of plant growth development and biocontrol action [24]. The draft genome of *Bacillus* sp. strain RZ2MS9 revealed genes related to PGP mechanisms, including IAA production, nitrogen fixation, and P-solubilization [25]. The draft genome sequencing of *Citrobacter braakii* AN-PRR1 by Nawaz *et al*. [26] revealed genes for PGP activites. The draft genome sequencing of *Lysinibacillus xylanilyticus* t26 by Phazna *et al*. [27] revealed siderophore production pathways and plant growth response bioassays. The draft genome sequences of the novel strains, Devosia rhizoryzae LEGU1^T and Devosia oryziradicis G19^T, revealed the biosynthesis of Fe-chelating, auxin-accessible, and tryptophan biosynthetic genes [28].

However, a number of biofertilizer restrictions prevented their wide application as well as commercialization. When inoculants are manufactured and introduced to soil, a variety of factors have an impact on their quality and effectiveness [29]. The qualities of the growing medium and the incubation conditions (temperature, pH, and time) affect the growth of a certain strain. They only have a limited shelf life, and if they are not used promptly or stored correctly, they could lose their efficacy [30]. In order to provide compositions a longer shelf life, new biotechnological approaches need to be invented.

PGPR has been used in agricultural production systems for a very long period. The research into the development of microbe-based biofertilizer is proving to be a significant replacement for the chemicals that have been used for plant growth development for an extended period of time. In spite of the rising demand for their application in both the industrial and agricultural sectors, rhizospheric microorganisms have a bright future. Several PGPR strains are commercially available as biofertilizers and biocontrol agents. In the last 40 years, PGPR has shown promise to support sustainable agriculture. Despite all the extensive study done so far, much more work needs to be done to reveal the PGPR's hidden attributes so that they can be an effective strategy for sustainable agriculture.

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