Chapter 2
Microbial Consortium: A Boon for a Sustainable Agriculture

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Abstract Rhizosphere is a highly activated region in the soil where microbial number and diversity is huge. These belowground microbes are interacted with each other as well as with the plant roots and some of these interactions are beneficial for plant growth. The plant signalling molecules (like root exudates) produced by plants shapes the microbial diversity in the rhizospheric region. Some of the rhizosphere microbes are useful for the plant development and are known as plant growth promoting rhizomicrobes (PGPR). These PGPR exerted various plant growth promoting effects by various mechanisms like phosphate solubilisation, nitrogen fixation, plant growth hormones production, secretion of antimicrobial compounds etc. These PGPR are excellent substitute for chemical inputs used for increasing crop production as chemical inputs disrupt the soil biological as well as chemical property. The PGPR formulation used as biofertilizer and are generally use single microbial strain. But the application of single microbial strain biofertilizer in soil showed inconsistency in the results. Research studies have showed that application of biofertilizer containing two or more microbial strains also known as co-inoculation or consortium is more beneficial as compared to single microbial strain application. Therefore, in the present chapter the importance of biofertilizer containing microbial consortium for the application in sustainable agriculture is discussed.

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Introduction

With increase in human population there is demand of increasing crop production to main the food supply at equilibrium. Initially usage of chemical fertilizers achieve this target but continuous and increased usage of these chemical fertilizers have adverse affect on soil biological health which degrades the soil physico-chemical properties as well as these chemicals enter into the food chain and cause diseases in human [1]. Microorganisms are marvellous alternate for sustainable agriculture to overcome the issues encountered by the usage of chemical fertilizers. Plant associated microbiome is found to promote plant health therefore worldwide scientists trying to explore these useful microorganisms [2]. The huge diversity of these useful microbes is persisting mainly in the rhizospheric region (soil surrounding the plant root) because of exudation from plant roots which serve as nutrients for the microbes [2, 3]. These rhizospheric microbes reported to exert beneficial effect on plant growth by various mechanisms like helping in absorbing nutrients, conversion of non-usable form of nutrients to available form, protect plant from pathogens by secreting antimicrobial compounds, improve stress tolerance capacity of plants under adverse growth conditions etc. [4]. So, utilizing these beneficial microbes in agriculture not only decrease our dependence on chemical inputs but also improve soil health along with improved crop production.

The plant roots and rhizopsheric microbiome are not only connected physically but also chemically. The microbiome composition in the rhizopshere is influenced by signal molecules produced by the plant roots like root exudates. The root exudates shape the microbial composition in the rhizospheric region and microbial diversity varies with the plant species [5]. In the same harmony, rhizospheric microbes also influence the plant growth and perform other ecological cycles. These diverse rhizospheric microbes communicate in the rhizosphere using various mechanisms like quorum sensing to maintain homeostasis in this region [6].

These rhizosphere associated microbes which exerted positive effect on plant growth are known as Plant Growth Promoting Rhizomicrobes (PGPR) which includes bacteria as well as fungi. These PGPR colonize the root zone soil or may be present intracellularly within plant cell and exert positive growth affect on plant growth when applied to soil or surface of plant or seed [4]. The application of these PGPR not only improves the crop production under sustainable agriculture but also after continues use of these PGPR for 3–4 years there is no need to apply inocula of these beneficial strains as they naturally build up in sufficient quantity within soil ecosystem [7]. These PGPR are used as biofertilizers which may be phosphate solubilizers or nitrogen fixers etc. using bacteria or cyanobacteria or fungi or their combination.

Generally, biofertilizers containing single PGPR strain is applied in the agricultural soil but due to inconsistent performance of single microbial strain it is always beneficial to use mixed microbial culture or co-inoculation or consortium for the application in agriculture. This application of microbial consortium is helpful in exploiting the synergistic interaction of microbes or complimentary benefits for plant growth [8, 9]. The biofertilizer consortium basically consists of different compatible microbial strains (allochthonous) with diverse plant growth promoting attributes. The genetically different microbes in the consortium have different ability to adapt to various adverse soil conditions like pH, moisture, temperature etc. [10]. After application in the soil, these different consortium microbial strains can be activated by the root exudates or other plant physiological response in the rhizosphere region. The production of single biofertilizer strain in industry is costly as compared to the production of biofertilizer consortium [8, 10]. Also, with the application of biofertilizer consortium in the soil multiple plant growth promoting traits are activated simultaneously in the rhizospheric region. So, overall usage of microbial consortium is broad spectrum as compared to the application of single microbial strain. Therefore, to achieve improved plant growth the microbial consortium with multifarious plant growth traits are excellent tool over single microbial strain application in sustainable agriculture.

Multifarious PGP Attributes

The growth and development of plants are influenced by PGPR through a variety of direct and indirect mechanisms [5], which may be active concurrently or sequentially at diverse phases of plant growth and development (Table 2.1). Figure 2.1 depicts each of these mechanisms, which are then detailed in depth below for a better understanding.

Direct Mechanisms

The most vital nutrient in terms of plant growth and yield is nitrogen. Notwithstanding that there is over 78 percent of N_2 in the atmosphere, plants cannot use it. The process of biological nitrogen fixation (BNF) converts atmospheric N_2 into plant-available forms, with N_2 being converted to NH_3 by nitrogen-fixing microorganisms [27]. An enzyme called nitrogenase complex catalyses the N_2-fixation process [28]. The dinitrogenase reductase offers electrons with strong reducing power, which are then utilized by dinitrogenase for reducing N_2 to NH_3. The N_2-fixing mechanism differs structurally among different bacterial taxa. The enzyme, molybdenum nitrogenase that found in almost all diazotrophs, catalyses the majority of BNF [29]. Examples of diazotrophic bacteria that freely fix and supply nitrogen to a variety of plants include *Bacillus, Azospirillum, Anabaena, Azotobacter, Nostoc, Clostridium, Klebsiella, Rhodobacter*, and *Paenibacillus* [30]. Some diazotrophs, like *Herbaspirillum* spp., *Azospirillum* spp., *and*, *Azoarcus* spp., form endophytic and/or associative relationships with an array of plant roots, including cereal roots. The main *Azospirillum* species researched worldwide are *A. lipoferum* and *A. brasilense*, which are commonly used for inoculating maize, sugarcane, and rice.*A. brasilense* exhibit the potential to change the root architecture of plants by stimulating the growth and

Table 2.1 Mechanisms of plant growth by different microbes isolated from the rhizosphere

Biological role	Type of association	Organism involved	Mechanism	References
Nitrogen fixation	Free living	*Anabaena, Azotobacter,, Nostoc, Clostridium, Klebsiella*	Convert non-usable form of nitrogen into usable form and make available to plant roots	[11]
	Associative symbiotic	*Azospirillum, Herbaspirillum, Azoarcus, Enterobacter, Pantoea*		[12, 13]
	Symbiotic	*Azolla, Anabaena, Frankia, Rhizobium*		[14, 15]
Phosphate solubilisation & mobilization	Fungi	*Aspergillus, Arbuscular mycorrhiza, Glomus, Penicillium, Talaromyces, Trichoderma*	Solubilize insoluble form of phosphorus into souluble form that is absorbed by the plant roots	[16–20]
	Bacteria	*Bacillus, Burkholderia, Pseudomonas, Ralstonia*		[19, 21, 22]
Production of plant growth promoting hormones		*Azorhizobium, Azotobacter, Bacillus, Bradyrhizobium, Pseudomona, Rhizobium, Streptomyces*	Various plant growth hormones produced which improve the plant growth and yield	[23, 24]
Antifungal activity		*Bacillus, Pseudomonas, Streptomyces*	Some microbes produce metabolites which have antifungal activity against plant pathogens	[25, 26]

proliferation of lateral and adventitious roots, as well as root hairs [31] besides synthesizing NO via a variety of pathways. Root organogenesis, formation of root hairs along with lateral and adventitious roots, all require NO [32].

Rhizobia are the most well-known group of bacteria that exhibit the potential to fix nitrogen (>200 kg N/ha/ year) symbiotically with the plant species of *Fabaceae /Leguminosae* family in both temperate [33] and tropical [34] regions. However, two other bacterial genera, *Cyanobacteria* and *Frankia*, can also fix

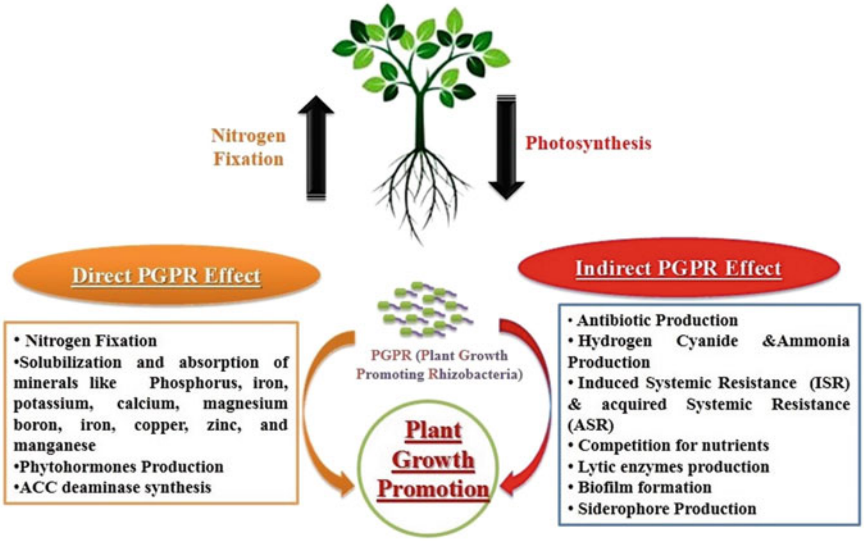

Fig. 2.1 Direct and indirect mechanisms of plant growth-promotion

nitrogen in a symbiotic relationship with plants. For nitrogen fixation, cyanobacteria can develop a symbiotic relationship with an array of plants viz., bryophytes, gymnosperms, and angiosperms, while *Frankia* fix nitrogen by nodulating the actinorhizal plants Chang et al. [35].

Cyanobacteria serve as the main source of fixed nitrogen in the Arctic as well as terrestrial ecosystems [36]. For instance, in northern boreal forests, a high copiousness of cyanobacterial—feather moss associations contribute around 1.5–2.0 kg N/ha/year [37]. Species of the genera viz., *Anabaena, Tolypothrix, Nostoc, Aulosira, Scytonema*, and *Cylindrospermum* are found in abundance in the rice fields, all of which contribute significantly to rice fertility. Cyanobacteria have been documented to contribute approximately 20–30 kg N/ha every season, plus organic matter, which is significant for economically disadvantaged farmers who cannot afford to invest in expensive chemical nitrogen fertilizers. The amalgam of *Anabaena* (a free-living N_2- fixing diazotroph) with *Azolla* provides a natural way to provide nitrogen to rice plants growing under waterlogged conditions [38]. Rice biofertilization with *Anabaena* provides high nitrogen levels (up to 50 kg/ha), minimizes nitrogen loss through ammonia volatilization, and promotes the growth and development of plant [39].

The genus, *Frankia,* is comprised of aerobic, free-living, and symbiotic soil actinomycetes (family: *Frankiaceae*) that fixes nitrogen in the range of 2–300 kg N/ha/year, in harsh environments including mines, reclaimed, and degraded lands [40]. Around 200 *Frankia* strains, belonging to the genera viz., *Agromyces, Arthrobacter,* *Corynebacterium, Micromonospora, Mycobacterium, Streptomyces* and *Propionibacteria* have been recovered from anarray of actinorhizal plant species, but not all, exhibiting N_2 fixing potential [41].

Phytohormone biosynthesis is also documented to encourage plant growth directly. Several species of genera *Azotobacter, Alcaligenes, Azospirillum, Bradyrhizobium, Bacillus, Brevibacillus, Enterobacter, Burkholderia, Klebsiella, Pseudomonas, Mycobacterium, Serratia,* and *Rhizobium* produce and release phytohormones viz., auxin, gibberellin, cytokinin, ethylene, and abscisic acid [42–44]. Indole-3-acetic acid (IAA) is the most commonly researched auxin in the world. Growth stimulation plus a transitory increase in IAA levels was observed in wheat seedlings upon treatment with *Bacillus subtilis* 11BM spores [45]. *Pseudomonas aeruginosa* and/or *Mesorhizobium* sp. produced IAA, which enhanced potassium and phosphate uptake in chickpea inoculated with these bacteria [46]. Species of genera viz., *Bacillus* spp., *Burkholderia cepacia, Promicromonospora* spp., and *Herbaspirillum seropedicae* are potential gibberellins (GAs) producers. *B. siamensis* is reported to enhance growth in banana plants via GA production [47]. GA3, produced by *Azospirillum* was verified to be imperative in increasing plant growth while, co-inoculation of *Pseudomonas fluorescens* plus *Azospirillum brasilense* boosted wheat biomass and yield [48].

Roots are accountable for the synthesis of 1-aminocyclopropane-1-carboxylate (ACC), which is a direct ethylene precursor. PGPR with ACC deaminase, an enzyme that converts ACC to α-ketobutyrate and ammonium and thereby decreases ethylene levels, can metabolize ACC. Ethylene promotes the elongation process of plant root under normal and stressed environments at low concentrations. Because ACC deaminase lowers ethylene levels, modifying ACC levels in hosts may assist in alleviating the negative impacts of abiotic and biotic stressors. Besides ethylene, Abscisic acid (ABA) also regulates plant growth in stressful environments. PGPR exhibiting ABA-producing activities include *Bacillus licheniformis, Achromobacter xylosoxidans, Bacillus pumilus, Brevibacterium halotolerans, Bacillus subtilis, Pseudomonas putida*, and *Lysinibacillus fusiformis* [49].

PGPR also provide nutrients like phosphorus, and potassium to plants under nutrient-limited environs [50, 51]. Phosphorus is typically present in soil as hydroxyapatite, rock phosphate and/or calcium phosphate, and is mostly found in the form of either phytate (organic form), or insoluble phosphate (inorganic form). PGPR exhibit the potential to solubilize phosphate either via organic acid production or phytase activity [52]. Phytase producing bacteria belong to the genera viz., *Bacillus, Enterobacter, Klebsiella,* and *Pseudomonas* while, *Bacillus, Burkholderia, Erwinia, Paenibacillus, Pseudomonas, Rhizobium,* and *Serratia* genera have all been documented to solubilize phosphate- via release of organic acids like oxalate, citrate, and acetate [53, 54].

Besides phosphorus and, nitrogen, PGPR can efficiently stimulate plant growth via solubilization and absorption of other nutrients [49, 51]. For instance, a noteworthy upsurge in the uptake of potassium, calcium, and magnesium via their solubilization was observed by Ogut et al. [53] after inoculating wheat with *Bacillus* sp. or *Pseudomonas* sp. in calcareous soil without applying fertilizers. Under water-stressed conditions, *Bacillus megaterium* boosted phosphorus, calcium, boron, iron, copper, zinc, and manganese absorption as well as biomass in trefoil plants [55].

Iron is another micronutrient that plays an indispensable role in an array of metabolic activities, and its deficiency impairs key plant metabolic activities like respiration and photosynthesis. Rhizobacteria like *Pseudomonas, Bacillus, Klebsiella, Enterobacter, Rhodococcus* are known to produce siderophores which are tiny iron—chelating molecules that allow iron to be transported to root cells under iron-limiting conditions. This mechanism aids plant growth while also creating an unfavourable environment for phytopathogens that cannot thrive in iron-deficient environments [32, 56]. To demolish soilborne pathogen's cell walls, *Paenibacillus, Bacillus, Serratia, Pantoea*, and *Enterobacter* secrete lytic enzymes such amylase, chitinase, β-1, 3-glucanase, and protease [56].

Indirect Mechanisms

Numerous literature sources reveal that PGPR serve the function of protective agents against soil-inhabiting pathogens [57]. Rhizobacteria can limit disease development via multiple ways, for instance, antagonistic effect of pseudomonads via synthesizing a multitude of antibiotics viz., pyoluteorin, phenazine, pyrrolnitrin, tropolone, tensin, amphisin etc. [58]; competition for nutritional substrates and ecological niches with phytopathogens plus other detrimental microbes proliferating in the rhizosphere [59]; production of cell wall degrading molecules like chitinases, β-1,3-glucanase, and biosurfactants [60], production of ammonia and hydrogen cyanide like volatile organic inhibitory molecules [61]; and induced resistance [62].

Recent scientific findings have reported that biofilm production in the rhizosphere plays a significant role in rhizobacteria's mode of action on root pathogens. The high population density of bacteria in biofilms is ascribed for the production of diverse metabolites like toxins and antibiotics in their periphery, which suppress phytopathogens in the soil. For instance, in case of *Bacillus subtilis,* biofilm is made up of surfactins, which are cyclic molecules containing lipids and amino acids that operate as potent biosurfactants with antimicrobial (antibacterial and antifungal) properties besides inducing resistance in plants [63]. The particulars of antagonist effect of *B. subtilis* strain SG6 on *Fusarium* hyphae as discerned by electron microscopic studies reveal the evident anomaly in mycelial growth that can be allied with the influence of chitinase like cell wall degrading enzymes [60]. Other toxic compounds obtained from *B. subtilis* include lipopeptide antibiotics, belong to the surfactin and iturin group that are accountable for plant disease suppression. In the rhizospheric region, antagonism encompassing competition for nutrients and space within an ecological niche is also crucial. This was demonstrated in on *B. megaterium*, a bacterium that can competently colonize roots and diminish *Rhizoctonia solani* [64].

Rhizobacteria produce siderophores as a secondary byproduct of their metabolism. These compounds exhibit the potential of sequestering Fe^{3+} ions, which are mandatory for cell growth and metabolism. In this context, plant root's colonizing bacteria might display competition for the iron available in the soil, inhibiting the growth of other rhizospheric microbes. Siderophore-producing PGPR can inhibit harmful microbes from proliferating around the root [65].

To combat phytopathogens, plants possess a basal natural defensive system, but additional systems can be activated or induced to boost plant resistance [66]. Induced systemic resistance (ISR) and acquired systemic resistance (ASR) are two types of resistance induction that have been researched extensively. ISR is commenced by non-pathogenic rhizospheric microbes and does not entail the salicylic acid signalling route or synthesis of plant pathogenesis related proteins (PRPs); instead, ethylene and jasmonic acid-mediated—resistance-signaling pathway is activated [67]. In ASR, on plant's exposure to a pathogen that act as an inducing agent, defence mechanisms are activated both at the induction site that exhibits necrosis like changes as well as another distant sites, providing systematic protection to plant against subsequent infections caused by an array of pathogens [68]. ASR is followed by a rise in salicylic acid content and the build up of PRPs, which are plant defense mechanisms [69].

In nutshell, growing usage of PGPR could be envisaged amongst major avenues to maintain or enhance yield while reducing environmental imprint via explanation of many mechanisms that will assist to make these plant-beneficial rhizobacteria a valued partner in agriculture to generate future insights.

Microbial Consortium in Agriculture (Bacteria-Bacteria and Bacteria-Fungi Consortium)

Microbes possess functional attributes that regulates the plant growth, improve the availability soil nutrients, and provides protection against stress conditions. These traits led to vast exploration of microbial strains followed by commercialization. However, in any niche area, composition and structure of microbes played crucial role in overall beneficial functions enhancement. Microbial consortia that have synergistic interactions among themselves can exhibit high level performance compared to single strains due to the diverse set of plant growth promotion attributes and biocontrol mechanisms [8]. These microbial consortia are equipped with RIDER mechanism that helps in higher nutrient uptake and ameliorating drought and salinity under extreme environments [70]. Others are crucial for maintaining soil health by nutrient assimilation, N-fixations excluding the conventional methods of agricultural production. Before developing a microbial consortium, first steps are needed. This means that the compatibility of the microorganisms used in the host plant in question, and the co-occlusion of these microorganisms, directly or indirectly affect the host. Inoculation in combination with beneficial microorganisms showed improved plant growth and yield characteristics as well as germination, nutrient absorption, plant height, number of branches, tuber formation, yield, and total crop biomass. The consortium's proposals improve the efficiency, consistency, and reliability of microorganisms in a variety of soil conditions [71]. The combination of biocontrol agents in the consortium is said to provide a higher level of protection and have the potential to control multiple plant diseases.

Bacteria–Bacteria Interactions

Bacterial consortiums are usually referred to as groups of different strains of bacteria that can live together in the community. Rhizobacteria that promote plant growth (PGPR) can inhabit the soil or rhizosphere zone along with other bacterial strains [72]. Bacterial diversity has properties that promote plant growth and development, as well as general benefits that contribute to one health approach. There are many factors that influence the bacterial consortium, and interactions between consortium members are important for long-term stability. The interaction of these bacteria can be positive, negative, or neutral [73]. Positive associations include mutualism, protocooperation, and commensalism. Biocontrol mechanisms are the example of positive associations which employs various biological control bacterial strains having growth promoting traits to achieve desired results. These types of positive interactions require compatibility of consortium strains in soil and/ or rhizosphere zones and devoid of any kind of competition within the group. Evaluation is likely the maximum critical section for the duration of improvement of microbial consortium as it gives a know-how of its contribution in reducing stress and growing plant boom. Attempts are being made to expand microbial consortium for pests and diseases suppression and plant growth promotion. The important concept at the back of using bacterial consortiums is that an unmarried microorganism does now no longer always offer safety in opposition to a couple of pathogens, so the use of a set of microorganisms guarantees that safety in opposition to a couple of goal pathogens is provided [71, 74].

On the other hand, negative interactions bring about suppression of bacterial individuals of the consortium, disrupting network shape and characteristic. These consist of amensalism, predation, parasitoids, and competition. Competition arises whilst individuals of the bacterial consortium want the equal resources. It‘s nutrients, water, or even the space. Therefore, fast-developing strains dominate over time. Neutral interaction happens whilst the two bacterial species devour distinctive materials (nutritional differences) and do now no longer produce compounds that inhibit individuals of the consortium. In agriculture, individuals of the consortium actively have interaction whilst symbiotic associations are preferred to attain solid overall performance in long-time period cultivation for you to attain the useful outcomes anticipated whilst carried out to producing crops.

In this regard, bacterial consortium is presently most effective superficially understood. The interaction among consortium relies upon at the generation, recognition, and reaction of extracellular signaling molecules that adjust and shape bacterial populations within the consortium. In the consortium, most effective compatible bacterial strains are worried in changing plant protection responses that have an effect on plant health and production [75]. Bacterial consortium interactions are based closely on molecular signals. Among them, quorum sensing performs a critical function in bacterial compatibility in consortium formulations [76]. Of the numerous signaling molecules, the acylhomoserine lactone (AHL) signaling molecule is the maximum outstanding identified in bacterial strains [77]. On the alternative hand, AHL produced through bacterial consortium of *S. liquefaciens* and *S. phymuthica* help in root improvement and plant biomass. Other bacterial strains including *S. fredii* and *P. aananatis* form biofilm within the roots of *Oryza sativa* and *Phaseolus vulgaris* [78].

Other vital signaling compounds stated in bacterial consortia are unstable compounds called volatile organic compounds (VOCs), which are identified with bacteria–bacteria and plant–bacteria communications [79]. These compounds encompass terpenoids, alkanes, alkenes, ketones, sulfur-containing compounds, and alcohols that act as low-molecular-weight compounds. Individual and bacterial consortium of *A. brasilense* Sp7, *P. putida* KT2440, *Acinetobacter* sp. EMM02, and *Sphingomonas* sp. OF178A are the crucial examples of bacterium- maize seed interactions [80]. It was also observed that the inoculation of the bacterial consortium also improves the bacterial colonization. Bacterial colonization is predicated upon on the plant variety. The colonization of a consortium formulated with *G. diazotrophicus*, *H. seropedicae*, *H. rubrisubalbicans*, *A. amazonense*, and *B. tropica* differ in different forms of sugar cane (SP70-1143 and SP 813,250) [81].

It is essential to confirm the protection of bacterial consortium earlier than theyŕe used as biofertilizers, especially if theyŕe carefully associated with pathogenic bacterial traces. For instance, *Bacillus* sp. (RZ2MS9) and *B. ambifaria* (RZ2MS16) gift a cap potential threat because of their taxonomic proximity to pathogenic groups [82]. The coinoculation of maize with *A. brasilense* and *B. subtillis* has additionally proven more advantages than individual inoculation [83]. The maize inoculation with a consortium with *A. chrococcum* and *A. liporefum* ended in increments in shoot and seed dry weight, plant height, and yield as compared to the individual inoculation of bacterium and the control [84]. Nitrogen fertilization at 100% and the consortium plus 50% urea resulted the best increments in height, diameter, dry root weight, and grain weight compared to non-inoculated plants. These results confirmed that the bacterial consortium stimulates the growth of maize whilst a 1/2 of dose of mineral nitrogen utilized in conventional agricultural practices. In another study, the rice inoculation with a consortium (blended *Pseudomonas* culture in addition to *A. Chroococcum* and *A. brasilense*), the benefits of 50% mineral phosphorus were like the total dose of phosphorus and consortium [85, 86]. In sunflowers, the bacterial consortium (*Azotobacter* sp. and *Azospirillum* sp.), 50% nitrogen fertilization was identified in addition to the highest grain production, oil and protein levels. Most studies in which plants were inoculated with bacterial consortium found spikes in yield and biomass [87, 88].

Plants interact with indole generating and phosphate solubilizing bacteria at low nutrient situations. However, in a mild nutrient scheme, plants selectively partner with bacteria with a better potential for phosphate solubilization [89, 90]. Better plant growth and productivity with 50% urea plus the bacterial consortium could be because of the excessive phosphate solubilization functionality and indole manufacturing by few members of bacterial consortium [91]. However, it‘s miles important to do extra research addressing this topic, possibly the use of bacterial consortium in those mechanisms to confirm their roles in nutrient solubilization and plant growth. More research is also needed to outline the function of bacterial consortium on plant inoculation that provides an opportunity to implement sustainable agricultural practices without compromising crop yields.

Bacteria-Fungal Interactions

It is now feasible to behavior studies on the character and composition of microbial interactions with plants using next-technology sequencing (NGS) techniques. Many bacterial and fungal interactions play role in plant improvement through nutrient mobilization and to cope up with numerous biotic and abiotic stresses [92]. For instance, phosphate may be solubilized through phytases secreted by soil-borne bacteria or fungi, thus favoring its uptake. Another low-molecular-weight molecule of microbial consortium are called siderophores that are the starting place with an excessive affinity for iron and contribute to solubilize iron within the rhizosphere. Biological nitrogen fixation is the most important form of symbiotic association with a microbial consortium that resolves N_2. The exchange of nutrients between plants, fungi (rootstock fungi) and bacteria help improve plant nutrition, including nitrogen uptake. Plant N uptake can be increased in the presence of symbiotic persistent and binding N_2 bacteria and mycorrhizal fungi (AMF). The minerals are taken up from the soil by mycorrhizal fungi and contribute to higher plant uptake. The minerals are then secreted by the fungal cells at the dendritic interface and picked up by the plant cells. Apart from N, the phosphatase released by bacteria associated with fungi, inorganic phosphate is absorbed by fungi and plant cells via the phosphate vector (PT). Phosphate polymers can be stored inside and outside the radical fungi at the plant roots. Polyphosphate is decomposed and inorganic phosphates are then transported to the ambient interface [93, 94].

Rhizobium is an alphaproteobacteria that usually causes persistent N_2 symbiosis with leguminous plants. This is the most characteristic process of endosymbiosis in plants containing N_2 bacteria. Some root species are able to induce the formation of N_2-fixing root nodules in the non-vegetative plant *Parasponia* sp. [95, 96]. Other blue bacteria (cyanobacteria) that dissolve N_2 can be associated with plants and offer NH_4^+ hosts without forming specialized nodules. In general, those blue bacteria that solve N_2 symbiotics belong to the Nostoc species. They can distinguish between specialized cells referred to as heterocysts that fix nitrogen in plants. In symbiotic rhizobia-legumes, plants benefit from reduced N_2 doubling even when microbes utilize carbohydrates provided by host plants [97, 98]. When there is an interaction between plants and nitrogen-fixing microorganisms, the location of the roots is rich in carbohydrates, in root exudates. In a few cases, AMF is associated with various microbes within the root area. Although these triangular interactions have not yet been accurately classified, they appear to rely heavily on food exchanges between the plant host and microbes. These exchanges include the exudate secretions with the help of fungi to facilitate access to plants [99, 100]. For example, microorganisms can be larger without problems in melting phosphates more than fungi, thus reinforcing all fungi and plants. In addition, some species of *Paenibacillus* are N_2 stabilizers able to dissolve phosphate and iron and secrete phytohormones [50]. Many plant-related fungi are colonized with the help of the use of endogenous diazotrophs that can present N to fungi [101–103].

Many of these tripartites may want a symbiotic status that dissolves larger green fungi and N_2, and there is no doubt that the use of plants will increase N acquisition. Therefore, additional studies to discover microorganisms that support the current state of symbiotic affiliation between plant life, bacterial and fungal consortium show that these three affiliations enhance plant N acquisition, especially under reduced fertilization conditions. Linking plant life to a more complex bacterial-fungal consortium is all other approaches that have the potential to improve overall plant performance. This is because fungal inoculation mixed with a bacterial consortium away from unfertilized soil promotes nutrient (N and P) uptake [104].

Conclusions and Future Prospects

In the agricultural sector, the concern for sustainable food production that satisfies the demands of the global human population has become a critical problem. To meet present and future food demand, the development of innovative sustainable solutions to boost crop yields and quality while also restoring soil fertility is critical. Microbial consortiahave the potential to be a long-term and successful strategy for various abiotic and biotic stress conditions. Microbial consortia offer a long-term and cost-effective solution to plant productivity losses caused by changing climate variables, as well as help in the optimization of human inputs in the agro-ecosystem. The use of microbial consortium may also aid in the maintenance of agro-ecosystem ecological balance by minimizing the use of pesticides and/or heavy metals in agricultural activities. Furthermore, microbial consortium efficiency varied greatly depending on the crop and ambient circumstances. Future study should concentrate on generating more precise products, such as diving further into the interactions of the microbial strains with indigenous plant-associated microbiomes.

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