



International Journal of Research in Agronomy

E-ISSN: 2618-0618
P-ISSN: 2618-060X
© Agronomy
NAAS Rating (2026): 5.20
www.agronomyjournals.com
2026; 9(8): 1266-1272
Received: 20-05-2026
Accepted: 22-06-2026

Suman Jayakumar Kankanwadi
Department of Microbiology,
Chaudhary Charan Singh Haryana
Agricultural University, Hisar,
Haryana, India

Crop-associated microbiomes in rice, wheat and legumes: Roles in plant growth and stress tolerance

Suman Jayakumar Kankanwadi

DOI: <https://www.doi.org/10.33545/2618060X.2026.v9.i8p.6414>

Abstract

Plant associated microbiomes play a vital role in plant growth, nutrient acquisition, stress tolerance and crop productivity. This review highlights the significance of plant-microbe interactions in major crops, particularly rice, wheat and legumes. Beneficial microorganisms inhabiting the rhizosphere, phyllosphere, endosphere and spermosphere promote plant performance through direct mechanisms such as nitrogen fixation, nutrient solubilization and phytohormone production, and indirect mechanisms including pathogen antagonism, siderophore production and induction of systemic resistance. Recent studies demonstrate that plant growth-promoting bacteria, endophytes, rhizobia and microbial consortia can effectively alleviate drought, salinity, cold and heavy-metal stresses by improving plant growth, nutrient uptake, osmolyte accumulation, chlorophyll content and antioxidant defence. The integration of beneficial microorganisms with advanced omics approaches provides opportunities for understanding complex plant-microbe interactions and developing climate-resilient agricultural systems. Overall, effective management of crop-associated microbiomes offers a sustainable strategy for enhancing crop productivity, stress resilience and long-term agricultural sustainability.

Keywords: Crop-associated microbiomes, rice, wheat, legumes, plant-microbe interactions

Introduction

Global variations due to change in climatic conditions and extreme weather conditions like alteration in temperature, cold and characterized by the change in the precipitation patterns has made a significant challenge to the agricultural systems, which in turn affecting the global food security (Olanrewaju *et al.*, 2024) ^[22].

The global population from 2009 to 2050, is projected to grow by more than a third, equivalent to 2.3 billion people. By 2050, due to the rapid expansion of the global population the total global food demand is expected to increase by 35% to 56% between 2010 and 2050. Annual cereal production, for instance, would have to grow by almost one billion tonnes. Among cereals, rice, wheat, maize, and millets are majority grown in India. In that year, worldwide wheat and rice production came to about 793.24 and 532.87 million metric tons, respectively. As rice and wheat is top first and second most important crop grown in India, it accounts for about the 214.2 million tonnes and 113.3 million tonnes of production in India with 3.6 and 2.5%, respectively increase in the production (Fao.org/giews/countrybrief/country.jsp?code=IND). Apart from the cereals, the legumes also play the important role in the sustainable agricultural development and ensures nutritional security across the globe with annual production of 242.46 LMT. Among several legumes cultivated in the world, common bean, chickpea, cowpea, groundnut, lentil, pigeon pea, and soybean are the major seven legumes highly preferred across the globe.

Synergy in Nature: Exploring Plant-Microbe Interactions

To survive and adapt to changes in global climatic conditions, plants have evolved multiple, protective mechanisms to tackle these changes. One such mechanism is plant microbe interaction. Plant-microbe interactions constitute an evolutionarily favoured dynamic association forming an integral component of the ecosystem and helps to meet the urgent demand of food production due to population growth and urbanization (Tiwari *et al.*, 2024) ^[37]. In turn it increases the economic development of the country (Kimotho and Maina, 2024) ^[18]

Corresponding Author:
Suman Jayakumar Kankanwadi
Department of Microbiology,
Chaudhary Charan Singh Haryana
Agricultural University, Hisar,
Haryana, India

Plant provides the niche for growth of diverse microorganisms where, they live in and around plants, forming a complex microbial ecosystem. It has been suggested that plants, together with their associated microbiota, constitute a "holobiont." (Trivedi *et al.*, 2020) ^[38]. These microbiomes *i.e.*, community of microorganisms associated with plants include bacteria, fungi, nematodes, archaea and viruses that inhabit different parts of plants. These microbial communities interact with plants, both externally and internally, and shape their behaviour and health (Compant *et al.*, 2019) ^[19]. These parts include the phyllosphere (above-ground parts like leaves and stems), rhizosphere (soil surrounding roots), endosphere (internal tissue) and spermosphere (seed surfaces) (Shelake *et al.*, 2019; Rochefort *et al.*, 2021) ^[29, 30]. They play a crucial role in regulating the mechanisms underlying plant growth and development by

facilitating nutrient absorption, enhancing stress resilience and conferring resistance to pathogens. These microorganisms exhibit the beneficial, pathogenic and neutral behaviour of interaction with the plants. Relationship between plants and microbes plays a vital role in ecosystem is based on various factors *i.e.*, environmental factors, host factors, edaphic conditions and anthropogenic factors. In order to analyse the interaction among the various factors recent advances in omics have developed in order to eliminate the challenges faced by these factors (Olanrewaju *et al.*, 2024) ^[22]. Omics techniques help to study the molecular aspects of plant microbe interaction at various levels and thus accelerate the deeper understanding of processes in plant microbe interaction. Omics includes metabolomics, genomics and transcriptomics (Tiwari *et al.*, 2024) ^[37].

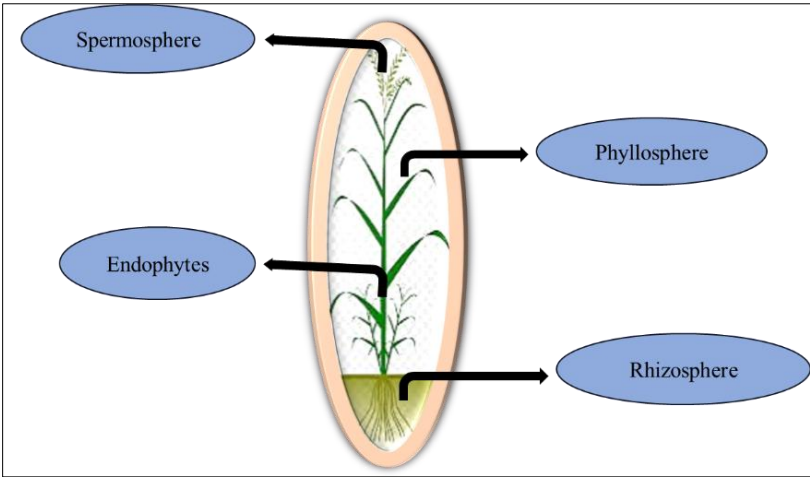


Fig 1: Representation of microbiome associated with plant

Mechanisms in plant microbe interaction

The mechanisms in plant microbe interaction includes the direct and indirect mechanisms. It includes the transformation and translocation of essential nutrients in the soil to make them available to plants (for example, nitrogen fixation), mitigation of

environmental stresses (such as drought) and protection from plant pathogens through competition, antibiosis and the production of hydrolytic enzymes, enhancement of a plant’s resistance responses.

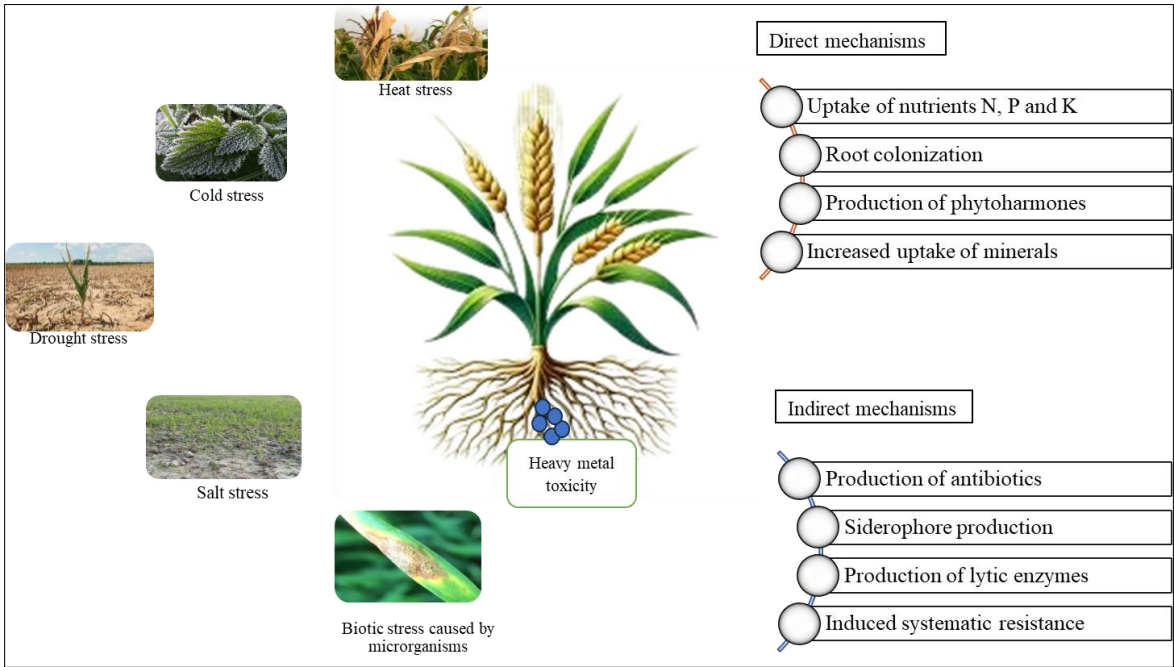


Fig 2: Diagram representing the mechanisms involved in plant microbe interaction

Direct effects are mediated through nitrogen fixation, through unlocking of essential nutrients from minerals by solubilizing, oxidizing and chelating minerals through the production of organic acid *etc* thus improving the plant's ability to absorb the nutrients. In addition, other direct effects include the production of plant hormones that include auxins, gibberellins, cytokinin and phytohormone mimics and detoxification enzymes. Benefits can also be indirect, as the plant-associated microbiome protects the plant against pathogens or pests through antagonism or through inducing systemic resistance in plants. The plant-associated microbiome defends plants against pathogens through antagonism by the production of antibiotics, lytic enzymes, volatile compounds, and siderophores or by inducing systemic resistance in plants (Trivedi *et al.*, 2020; Singh *et al.*, 2021) ^[38, 33]

Soil Microbiome Balance of crop - microbes in rice, wheat and legumes

Rice: Rice is one of the most important crops, as it serves as a primary food source for over 3.5 billion people worldwide. The growth of rice crop can be increased by the use of microorganisms as they help to mitigate the various biotic and abiotic stresses in crop.

The consortium of endophyte *Serendipita indica* and an actinobacterium *Zhihengliuella* sp. ISTPL4 were found to be efficient microorganisms in elimination arsenic metal toxicity by increasing the activity of antioxidant enzymes such as SOD, CAT, PAL, PPO and POD. Thus, helps to grow the rice crop efficiently under arsenic metal toxicity (Sharma *et al.*, 2024) ^[28]. Its well proven that *Bacillus* strains NMTD17, GBSW22, and FZB42 were tolerated the salt stress at various concentration up to 16% and showed the various growth-promoting ability and antioxidant activities at various concentrations. *Bacillus* strains NMTD17 had shown the significant effect in rice crop under salt stress by increasing rhizobacterial community (Ali *et al.*, 2022) ^[2]. Seed biopriming employing SH-9 strain with rice plants helps to mitigate the drought stress in rice crop by enhancing the germination of rice crop and protecting the rice crop by the production of antioxidants and phytohormones. SH-9 was found to be belongs Bacillaceae family after molecular identification. SH-9 is one of the efficient drought-tolerant microorganisms as it could tolerate drought up to 35% PEG 6000, thus helps to mitigate the drought stress in rice crop (Shaffique *et al.*, 2024) ^[27].

Seed-borne endophytes are integral to the establishment and development of the plant microbiome, exhibiting persistence across multiple tissues—including foliar, stem, and root compartments—and exerting significant influence on host plant health, growth, and productivity. Members of the Microbacteriaceae family—a taxonomically diverse group of Gram-positive bacteria within the class Actinobacteria—are frequently identified as common endophytic inhabitants of plant tissues (Tarlachkov *et al.*, 2020) ^[36]. Thus, one such cold-tolerant seed endophyte, *Microbacterium testaceum* M15 was inoculated in the cold sensitive CB9 and the cold-tolerant JG117 rice variety which increases the germination rate from 40% to 56.67% at 14°C and doubled a survival rate from 22.67% to 66.67% under cold stress (4°C). M15 significantly increased the chlorophyll content, catalase activity, protein content and reduced malondialdehyde (Zhao *et al.*, 2024) ^[40]. The effect of inoculation of nitrogen-fixing bacterium R3 (*Herbaspirillum*) at the rhizosphere during seedling stage, significantly increasing α -diversity of the communities thus increasing the group of nitrogen-fixing genera such as *Ralstonia*, *Azotobacter*, *Geobacter*, *Streptomyces*, and *Pseudomonas*. Inoculation with the R3 strain increased the amounts of nitrate nitrogen, ammonium nitrogen, and available phosphorus in the

rhizosphere thus increasing the uptake of nutrients to plants. The expression levels of the nitrogen absorption and transport-related genes *OsNRT1* and *OsPTR9* in rice roots were upregulated by inoculation with the R3 strain. Thereby the yield of rice plant was increased by increasing the number of rice panicles and seed setting rate (Li *et al.*, 2024) ^[20]. Nag *et al.*, 2024 ^[21], Determined the beneficial effect of *Rhodotorula mucilaginosa* JGTA-S1 is a yeast strain exhibits the nitrogen fixing ability through its association with the endobacteria *Stutzerimonas* (*Pseudomonas*) *stutzeri* and *Bradyrhizobium* sp. To gain deeper insights into the endosymbiotic community within the yeast *Rhodotorula mucilaginosa* JGTA-S1, they performed whole-genome shotgun metagenomic sequencing of JGTA-S1 cells cultivated under both nitrogen-sufficient and nitrogen-deficient conditions. They isolated the culturable form under nitrogen-replete conditions viz. *Bacillus velezensis* and *Staphylococcus* sp. and unculturable forms *Lysinibacillus telephonicus*., *Brevibacillus* sp., and *Niallia circulans* under nitrogen-depleted conditions. The culturable endosymbionts *Staphylococcus* sp. and *Bacillus velezensis* appear to harbour genes associated with dissimilatory nitrate reduction to ammonium (DNRA), an alternative nitrogen transformation pathway that facilitates ammonia synthesis. Inoculation of Cyanobacteria modulated the plant growth by enhancing the nutrient availability, induce systemic resistance, by synthesizing the bioactive metabolites which shows antagonistic activities against *Rhizoctonia solani*. *Rhizoctonia solani* causes the rice sheath blight which is major disease in rice crop. The researchers carried out a systematic investigation to screen and evaluate the biocontrol potential of nitrogen-fixing cyanobacterial strains against the target disease, employing microchamber and microarea experimental methodologies. Three strains (SCAU04, SCAU15, and SCAU26) showed significant inhibition i.e., > 80% of disease. Observing this results, micro area experiment was conducted to for two seasons where SCAU26 treatment showed the highest disease control efficacy (54.5%) thus significantly promoted root length, underground biomass, and number of grains per panicle. The cell extracts of algal strains SCAU04, SCAU15, and SCAU26 demonstrated strong inhibitory effects on the mycelial growth of *Rhizoctonia solani*, with inhibition rates of 90.12%, 78.33%, and 89.87%, respectively. Gas chromatography analysis showed that about eight bioactive compounds was responsible for this antifungal activity. Among the compounds identified, diisooctyl adipate exhibited the strongest inhibitory effect against *Rhizoctonia solani*, suggesting its potential role as a key bioactive agent in the algal extract (Zhou *et al.*, 2020) ^[41].

Wheat: Wheat (*Triticum aestivum* L.) is among the top three major cereal crops worldwide and serves as a vital element in ensuring global food security (Bentley *et al.*, 2022) ^[5]. Demand for crop is increasing due to the increase in the population. During the growth of wheat crop it is subjected to various biotic and abiotic stress which decreases the yield and quality of the crop (Saleh *et al.*, 2020, Berger *et al.*, 2022, Singh *et al.*, 2021) ^[25, 6, 32]. In order to mitigate this, the farmers are depending on more of agrochemicals and fertilizers. But these introduce the harmful effects on the soil and plant. Now, utilization of the beneficial microorganisms found as an effective approach for enhancing crop performance, including yield and resilience to biotic and abiotic stressors, thus helps to maintain environmental balance (Chen *et al.*, 2022) ^[8].

Abiotic stress

Drought stress: Drought stress is a significant factor bestowing huge losses to agriculture worldwide. As water accounts for about 80-90% of the total biomass in plants and it plays a vital role in physiological processes, for transporting nutrients and metabolites.

One of the promising approaches for mitigation of drought stress is by the use of microorganisms. Yadav *et al.*, 2022 determined the beneficial effect of two isolates DT-85 and DT-97 on wheat crop, which showed tolerance to high osmotic stress (10-30% polyethylene glycol 6000), salinity (5-15%), and temperature (45°C). These were identified as *Bacillus paramycoides* and *Bacillus paranthracis* using 16S rRNA gene sequencing. They increased the activity of ROS-scavenging enzymes like superoxide dismutase, peroxidase, catalase, and proline. Among both, strain DT-97 exhibited efficient plant growth promoting traits such as production of phosphate, siderophores (SPI 2.93), exopolysaccharide (216-244%), indole-3-acetic acid (49-59%), ammonia and gibberellic acid (110.5%) in comparison to strain DT-85 under both normal watered and drought stress conditions. Hence, *B. paranthracis* DT-97 is considered as the best strain for mitigation of drought stress in wheat crop. Adverse effect of drought stress was also reduced by treating the *Triticum aestivum* HD-2967 cultivar with *Piriformospora indica*, arbuscular mycorrhiza fungi (AMF), and plant growth-promoting bacteria (PGPB) by improving growth and physio-biochemical parameters showing better adaptation to the stress by accumulating the higher content of compatible solutes and antioxidant activity to protect it from osmotic stress and regulate cellular processes. Microbial inoculation helped wheat plants to overcome water stress-induced deficiency of macro- (Ca^{2+} , Mg^{2+} , and K^{+}) and micronutrient (Cu, Mn^{2+} , Fe, and Zn^{2+}), and reduced damage to the cell ultrastructure (plasma membrane and chloroplasts) (Singh *et al.*, 2023) [34]. Khan, A., & Singh, A. V. (2021) [17] isolated *Serratia marcescens* and *Pseudomonas* sp. is potential drought tolerant plant growth-promoting rhizobacteria (PGPR) exhibit the production of ACC deaminase, exo-polysaccharide, siderophore, ammonia, HCN, IAA. As ACC deaminase prevents ethylene production, EPS helps to form soil aggregates and retain moisture due to its glutting property, IAA contribute to plant growth and development, Siderophore production helps to chelate Fe^{3+} essential for plant growth and has the biocontrol potential, production of HCN provides antibiosis activity. Apart from this, *Serratia marcescens* and *Pseudomonas* sp. helps to ameliorate drought stress tolerance by improving water status, reactive oxygen species, osmolyte accumulation, chlorophyll and carotenoids content in plant leaves confirmed the excellent drought tolerance. Out of 24 isolated strains, two bacterial strains, *Bacillus subtilis* (Accession No. MT742976) and *Azospirillum brasilense* (Accession No. MT742977), were chosen for their capacity to produce EPS and tolerate drought stress in wheat. Under osmotic stress (20% polyethylene glycol, PEG6000) consortium of these strains improved seed germination, seedling vigor index, and promptness index. In a pot experiment, these strains also enhanced plant growth, resulting in an increase in shoot length, root length, and expansion in leaf area. Likewise, the physiological attributes (chlorophyll a, chlorophyll b, and carotenoid content), osmolytes (proline, amino acid, sugar and protein) and antioxidant enzymes such as superoxide dismutase (SOD), catalase (CAT), and peroxidase (POD) was enhanced respectively (Ilyas *et al.*, 2020) [14]. Priming of wheat inoculated with isolates from these targeted genera, including *Curtobacterium flaccumfaciens* (Cf D3-25) and *Arthrobacter* sp. (Ar sp. D4-14) by seed priming, exhibited drought stress

resistance. Metagenomic and culture-based approaches have been employed to analyze and characterize the seed microbiome in drought-tolerant and susceptible wheat cultivars, revealing that *Curtobacterium flaccumfaciens* and *Arthrobacter* sp. contribute to wheat growth promotion under drought conditions (Hone *et al.*, 2021) [12].

Cold stress: To mitigate cold stress, Dasila *et al.*, 2023 [10] with the aim to develop psychrotroph-based Phosphate solubilizing biofertilizers (PSB) isolated the four PSB strains (*Pseudomonas* sp. L3, *Pseudomonas* sp. P2, *Streptomyces* sp. T3, and *Streptococcus* sp. T4) from agroforestry systems which helps to overcome deficiency problem phosphorous to crop which increases the alkaline phosphatase (AP) and soil acid phosphatase (AcP) activity. Inoculation of this improved the grain NPK%. A cold-adapted indole acetic acid (IAA)-producing bacterial consortium isolated from Ghulkin glacier, Hunza Valley, Pakistan enhanced the root length, shoot length, root and shoot fresh, dry weight and chlorophyll content in pot trials in both garden soil and the glacial flour by showing efficient plant growth promoting parameters such as, siderophore production, zinc-solubilizing activity, phosphate solubilizing activity, ability to utilize L-aminocyclopropane-1-carboxylate and for nitrogen fixation. All these helps for the wheat crop stand in cold stress (Irfan *et al.*, 2025) [15]. The diverse effects of cold stress is mitigated by the phosphorus solubilizing *Acinetobacter rhizosphaerae* EU-KL44 isolated from wheat cultivars in the Keylong region of Himachal Pradesh (Kour and Yadav, 2023) [19].

Salt Stress: Two salt-tolerant PGPEs, *Kocuria rhizophila*: KF875448 (14ASP) and *Cronobacter sakazakii*: KM042090 (OF115), with ACC deaminase activity were investigated for their potential to ameliorate plant salinity stress. The wheat varieties Pasban 90 and Khirman were subjected to two levels of salt stress (80 and 160 mM NaCl) under greenhouse conditions by using a completely randomized design. Analyses of plant growth parameters, antioxidant enzyme activities, chlorophyll and plant mineral contents were conducted to investigate the stress tolerance induced by the PGPEs. The ACC utilization by the PGPEs directly relates to the promotion of plant growth due to the lowering of excess ethylene production under salt stress. High levels of NaCl exhibited negative effects in both varieties. However, inoculation with PGPEs increased the morphological traits and antioxidant activities of the plants while decreasing the Na^{+} contents in all treatments compared to uninoculated treatment. Adverse effects of salt stress are diluted by the inoculation of *Bacillus* sp. (KF719179), *Azospirillum brasilense* (KJ194586), *Azospirillum lipoferum* (KJ434039), and *Pseudomonas stutzeri* (KJ685889) singly or in consortium which improved the production of compatible solute and phytohormones, including indole acetic acid (IAA), gibberellic acid (GA), cytokinin (CK), and abscisic acid (ABA). Inoculated plants reduced electrolyte leakage and increased production of total chlorophyll and chlorophyll a, b, osmolytes, including soluble sugar, proline, amino acids, and antioxidant enzymes (superoxide dismutase, catalase, peroxidase) thus showing sustainability to salt stress (Ilyas *et al.*, 2020) [13].

Biotic stress: Araujo *et al.*, 2020 [3] showed that *Paenibacillus* and *Streptomyces* strains were the efficient biocontrol agents against the *Pythium*-infested soils in wheat. Wheat root and rhizosphere soil microbiome was compared to check the stability of biocontrol agent. These biocontrol agents enhanced the growth of wheat.

Legumes: Leguminous species play a vital role in both ecological

sustainability and agricultural productivity owing to their capacity for biological nitrogen fixation through symbiotic associations with rhizobia. Among leguminous species, *Medicago truncatula* has gained prominence as a widely accepted model organism for legume research, particularly in the domains of breeding, genomics, and genetics. This is primarily due to its relatively small and well-annotated genome, autogenous reproductive nature, and robust symbiotic nitrogen fixation efficiency. Irshad *et al.*, (2021) ^[16], combined the use of *Rhizobium* inoculation (RI) and melatonin (MT) pretreatment to mitigate the cold stress in *Medicago truncatula* plants. This significantly improved root activity and plant biomass production when pretreated with RI and MT alone or combined by increasing the chlorophyll contents, antioxidative ability, osmolyte accumulation, nitrate reductase activity and drastically decreasing the MDA levels. The synergistic application of arbuscular mycorrhizal fungi (AMF) and plant growth-promoting rhizobacteria (PGPR) significantly enhances plant performance under abiotic stress conditions by modulating phytohormonal signalling pathways, improving nutrient bioavailability and uptake, facilitating the biosynthesis of plant growth regulators, and promoting nutrient solubilization processes (Abd-Alla *et al.*, 2014) ^[1]

It is found that in order to maximize the efficacy of legumes in the rehabilitation of salt-affected soils requires the successful establishment of symbiotic interactions with compatible rhizobial strains (Borges, *et al.*, 2012). Transcriptome analysis was employed in a recent study to explore the molecular responses of 12 *Medicago sativa* genotypes (G01-G12) subjected to salt stress. Among the evaluated genotypes, G03 exhibited upregulation of *Salt Overly Sensitive* (SOS1, SOS2, and SOS3) genes, which facilitate Na⁺ efflux from roots into the soil. This genotype also demonstrated minimal accumulation of Na⁺ in shoots and achieved the highest biomass under salt stress conditions (Sandhu *et al.*, 2017) ^[26]. Soumare *et al.* (2015) ^[35] examined the influence of arbuscular mycorrhizal fungi and nitrogen-fixing bacteria in enhancement of legume crop growth under different stress conditions. Till today, there are around 13,000 legume species comprising about 700 genera and 98 species of legume-nodulating bacteria, classified into 13 bacterial genera, have been identified (Rajwar *et al.*, 2013) ^[23]. 1-Aminocyclopropane-1-carboxylate (ACC) deaminase represents an important plant growth promoting trait in bacteria but limited among some rhizobial species. Ben Gaied *et al.* (2024) ^[4] investigated the effects of a co-inoculation strategy involving selected plant growth-promoting bacteria (PGPB) in combination with compatible rhizobial strains, particularly those deficient in ACC deaminase activity. The study was aimed to evaluate the potential of three non-rhizobial endophytes—*Phyllobacterium salinisoli* (PH), *Starkeya* sp. (ST), and *Pseudomonas turukhanskensis* (PS) isolated from native legumes in arid regions of Tunisia, to enhance the growth of a cool-season legume and promote symbiotic efficiency with an ACC deaminase-deficient rhizobial strain under heat stress conditions. The detrimental effects of heat stress were effectively alleviated in plants co-inoculated with the Δ acdS mutant strain and selected consortia of non-rhizobial endophytes by altering the phenolic content in pea root exudates. The legume species *Lathyrus cicera* (red pea) is a valuable crop for enhancing soil fertility through biological nitrogen fixation in its root nodules Gritli *et al.* (2022) ^[11] determined the beneficial effect of different microbial inocula including arbuscular mycorrhizal fungus (AMF) *Rhizophagus irregularis*, nitrogen-fixing *Rhizobium laguerreae*, a complex mixed inoculum of AMF isolated from rhizospheric soil in “Al Aitha. The study was further investigated the efficacy of several plant growth-promoting

bacterial (PGPB) strains—including *Bacillus subtilis*, *Bacillus simplex*, and *Bacillus megaterium*—applied alone or in combination with *Rhizobium*, an arbuscular mycorrhizal fungi (AMF) consortium, or *Rhizophagus irregularis*, in alleviating salt-induced stress (100mM) in legume species. The significant dilution of effect of salt stress was mitigated by the combined use of PGPB and AMF on *L. cicera* by upregulating the expression of two marker genes (LcHKT1 and LcNHX7). Rotaru (2016) ^[24] evaluated the effectiveness of *Bradyrhizobium japonicum*, either as a sole inoculant or inoculated with *Pseudomonas putida*, in combination with phosphorus fertilization or organic manure application at two soil moisture regimes with one at the 35% WHC as moderate water stress. Inoculated plants showed that the combined application of rhizobacteria enhanced the N and P contents than the single inoculation irrespective of soil water conditions thus proving its potentially to improve the growth of plant. Similarly, three bio-inoculants, namely arbuscular mycorrhiza (AM) fungi, rhizobial (Rhi) and phosphate-solubilizing bacteria (PSB), effectively enhanced the yield of *Phaseolus mungo* and *Vigna radiata* (Shukla *et al.*, 2022) ^[31].

Conclusion

Plant-microbe interactions are fundamental to maintaining crop growth, productivity and resilience under changing environmental conditions. Beneficial microorganisms associated with rice, wheat and legumes enhance plant performance through nutrient mobilization, nitrogen fixation, phytohormone production, pathogen suppression and activation of stress-responsive mechanisms. Recent studies demonstrate their potential to mitigate major abiotic stresses, including drought, salinity, cold and heavy-metal toxicity, while improving plant growth, nutrient uptake, antioxidant activity and physiological performance. Microbial consortia often provide broader benefits than individual inoculants through synergistic interactions and multiple plant growth-promoting mechanisms. Integration of beneficial microbes with omics-based approaches can further elucidate complex plant-microbe interactions and facilitate the development of efficient, crop-specific bioinoculants. Overall, effective management of crop-associated microbiomes offers a promising, sustainable and environmentally friendly strategy for improving crop productivity, stress resilience and agricultural sustainability under future climatic challenges.

References

1. Abd-Alla MH, El-Enany AWE, Nafady NA, Khalaf DM, Morsy FM. Synergistic interaction of *Rhizobium leguminosarum* bv. *viciae* and arbuscular mycorrhizal fungi as a plant growth promoting biofertilizers for faba bean (*Vicia faba* L.) in alkaline soil. Microbiological Research. 2014;169(1):49-58.
2. Ali Q, Ayaz M, Mu G, Hussain A, Yuanyuan Q, Yu C, *et al.* Revealing plant growth-promoting mechanisms of *Bacillus* strains in elevating rice growth and its interaction with salt stress. Frontiers in Plant Science. 2022;13:994902.
3. Araujo R, Dunlap C, Franco CM. Analogous wheat root rhizosphere microbial successions in field and greenhouse trials in the presence of biocontrol agents *Paenibacillus peoriae* SP9 and *Streptomyces fulvissimus* FU14. Molecular Plant Pathology. 2020;21(5):622-635.
4. Ben Gaied R, Sbissi I, Tarhouni M, Brígido C. Enhancing *Pisum sativum* growth and symbiosis under heat stress: the synergistic impact of co-inoculated bacterial consortia and ACC deaminase-lacking *Rhizobium*. Archives of Microbiology. 2024;206(5):203.

5. Bentley AR, Donovan J, Sonder K, Baudron F, Lewis JM, Voss R, *et al.* Near-to long-term measures to stabilize global wheat supplies and food security. *Nature Food*. 2022;3(7):483-486. doi:10.1038/s43016-022-00559-y.
6. Berger K, Machwitz M, Kycko M, Kefauver SC, Van Wittenberghe S, Gerhards M, *et al.* Multi-sensor spectral synergies for crop stress detection and monitoring in the optical domain: a review. *Remote Sensing of Environment*. 2022;280:113198. doi:10.1016/j.rse.2022.113198.
7. Borges WL, Prin Y, Ducouso M, Le Roux C, de Faria SM. Rhizobial characterization in revegetated areas after bauxite mining. *Brazilian Journal of Microbiology*. 2016;47:314-321. doi:10.1016/j.bjm.2016.01.009.
8. Chen J, Sharifi R, Khan MSS, Islam F, Bhat JA, Kui L, *et al.* Wheat microbiome: structure, dynamics, and role in improving performance under stress environments. *Frontiers in Microbiology*. 2022;12:821546.
9. Compant S, Samad A, Faist H, Sessitsch A. A review on the plant microbiome: ecology, functions, and emerging trends in microbial application. *Journal of Advanced Research*. 2019;19:29-37.
10. Dasila H, Sah VK, Jaggi V, Kumar A, Tewari L, Taj G, *et al.* Cold-tolerant phosphate-solubilizing *Pseudomonas* strains promote wheat growth and yield by improving soil phosphorous (P) nutrition status. *Frontiers in Microbiology*. 2023;14:1135693.
11. Gritli T, Boubakri H, Essahibi A, Hsouna J, Ilahi H, Reinhardt D, *et al.* Salt stress mitigation in *Lathyrus cicera* by combining different microbial inocula. *Physiology and Molecular Biology of Plants*. 2022;28(6):1191-1206.
12. Hone H, Mann R, Yang G, Kaur J, Tannenbaum I, Li T, *et al.* Profiling, isolation and characterisation of beneficial microbes from the seed microbiomes of drought tolerant wheat. *Scientific Reports*. 2021;11(1):11916.
13. Ilyas N, Mazhar R, Yasmin H, Khan W, Iqbal S, Enshasy HE, *et al.* Rhizobacteria isolated from saline soil induce systemic tolerance in wheat (*Triticum aestivum* L.) against salinity stress. *Agronomy*. 2020;10(7):989.
14. Ilyas N, Mumtaz K, Akhtar N, Yasmin H, Sayyed RZ, Khan W, *et al.* Exopolysaccharides producing bacteria for the amelioration of drought stress in wheat. *Sustainability*. 2020;12(21):8876.
15. Irfan M, Ahmad N, Rafiq M, Wadham JL, Williamson CJ, Haleem A, *et al.* Bioprospecting cold-adapted indole acetic acid-producing bacteria with multifaceted plant growth promoting traits for wheat growth from Ghulkin Glacier, Pakistan. *Journal of Basic Microbiology*. 2025:e70017.
16. Irshad A, Rehman RNU, Kareem HA, Yang P, Hu T. Addressing the challenge of cold stress resilience with the synergistic effect of *Rhizobium* inoculation and exogenous melatonin application in *Medicago truncatula*. *Ecotoxicology and Environmental Safety*. 2021;226:112816.
17. Khan A, Singh AV. Multifarious effect of ACC deaminase and EPS producing *Pseudomonas* sp. and *Serratia marcescens* to augment drought stress tolerance and nutrient status of wheat. *World Journal of Microbiology and Biotechnology*. 2021;37(12):198.
18. Kimotho RN, Maina S. Unraveling plant-microbe interactions: can integrated omics approaches offer concrete answers? *Journal of Experimental Botany*. 2024;75:1289-1313. doi:10.1093/jxb/erad448.
19. Kour D, Yadav AN. Alleviation of cold stress in wheat with psychrotrophic phosphorus solubilizing *Acinetobacter rhizosphaerae* EU-KL44. *Brazilian Journal of Microbiology*. 2023;54(1):371-383.
20. Li P, Tian Y, Yang K, Tian M, Zhu Y, Chen X, *et al.* Mechanism of microbial action of the inoculated nitrogen-fixing bacterium for growth promotion and yield enhancement in rice (*Oryza sativa* L.). *Advanced Biotechnology*. 2024;2(4):32.
21. Nag M, Pallavi J, Chakraborty S, Roychoudhury T, Mondal S, Ghosh A, *et al.* Bacterial endosymbionts of a nitrogen-fixing yeast *Rhodotorula mucilaginosa* JGTA-S1-insights into a yet unknown micro-ecosystem. *Molecular Omics*. 2024;20(10):630-641.
22. Olanrewaju OS, Glick BR, Babalola OO. Metabolomics-guided utilization of beneficial microbes for climate-resilient crops. *Current Opinion in Chemical Biology*. 2024;79:102427. doi:10.1016/j.cbpa.2024.102427.
23. Rajwar A, Sahgal M, Johri BN. Legume-rhizobia symbiosis and interactions in agroecosystems. *Plant Microbe Symbiosis: Fundamentals and Advances*. 2013:233-265.
24. Rotaru V. Effects of combined application of *Bradyrhizobium japonicum* and *Pseudomonas putida* on nutrients and water. 2016.
25. Saleh SR, Kandeel MM, Ghareeb D, Ghoneim TM, Talha NI, Alaoui-Sossé B, *et al.* Wheat biological responses to stress caused by cadmium, nickel and lead. *Science of the Total Environment*. 2020;706:136013. doi:10.1016/j.scitotenv.2019.136013.
26. Sandhu D, Cornacchione MV, Ferreira JFS, Suarez DL. Variable salinity responses of 12 alfalfa genotypes and comparative expression analyses of salt-response genes. *Scientific Reports*. 2017;7:42958. doi:10.1038/srep42958.
27. Shaffique S, Imran M, Injamum-Ul-Hoque M, Zainurin N, Peter O, Alomrani SO, *et al.* Unraveling the new member *Bacillus pumilus* SH-9 of Bacillaceae family and its potential role in seed biopriming to mitigate drought stress in *Oryza sativa*. *Plant Stress*. 2024;11:100318.
28. Sharma N, Yadav G, Tyagi J, Kumar A, Koul M, Joshi NC, *et al.* Synergistic impact of *Serendipita indica* and *Zhihengliuella* sp. ISTPL4 on the mitigation of arsenic stress in rice. *Frontiers in Microbiology*. 2024;15:1374303.
29. Shelake RM, Pramanik D, Kim JY. Exploration of plant-microbe interactions for sustainable agriculture in CRISPR era. *Microorganisms*. 2019;7:269.
30. Rochefort A, Simonin M, Marais C, Guillerme-Erckelboudt AY, Barret M, Sarniguet A. Transmission of seed and soil microbiota to seedling. *mSystems*. 2021;6:e0044621.
31. Shukla A, Kumar A, Prasad R, Kumar N, Dhyani SK, Chaturvedi OP, *et al.* Efficacy of arbuscular mycorrhizal fungi and bacterial inoculants in enhancing yield of *Phaseolus mungo* L. and *Vigna radiata* (L.) R. Wilczek under central Indian conditions. *Journal of Soil Science and Plant Nutrition*. 2022;22(2):1559-1571.
32. Singh A, Jones S, Ganapathysubramanian B, Sarkar S, Mueller D, Sandhu K, *et al.* Challenges and opportunities in machine-augmented plant stress phenotyping. *Trends in Plant Science*. 2021;26(1):53-69. doi:10.1016/j.tplants.2020.07.010.
33. Singh J, Singh P, Vaishnav A, Ray S, Rajput RS, Singh SM, *et al.* Belowground fungal volatiles perception in okra (*Abelmoschus esculentus*) facilitates plant growth under biotic stress. *Microbiological Research*. 2021;246:126721. doi:10.1016/j.micres.2021.126721.
34. Singh M, Sharma JG, Giri B. Microbial inoculants alter resilience towards drought stress in wheat plants. *Plant Growth Regulation*. 2023;101(3):823-843.

35. Soumare A, Diop T, Manga A, Ndoeye I. Role of arbuscular mycorrhizal fungi and nitrogen fixing bacteria on legume growth under various environmental stresses. *International Journal of Biosciences*. 2015;7(4):31-46.
36. Tarlachkov SV, Starodumova IP, Dorofeeva LV, Prisyazhnaya NV, Leyn SA, Zlamal JE, *et al*. Draft genome sequences of 13 plant-associated Actinobacteria of the family Microbacteriaceae. *Microbiology Resource Announcements*. 2020;9(38). doi:10.1128/mra.00795-20.
37. Tiwari P, Bose SK, Park KI, Dufossé L, Fouillaud M. Plant-microbe interactions under the extreme habitats and their potential applications. *Microorganisms*. 2024;12(3):448.
38. Trivedi P, Leach JE, Tringe SG, Sa T, Singh BK. Plant-microbiome interactions: from community assembly to plant health. *Nature Reviews Microbiology*. 2020;18(11):607-621.
39. Van Dijk M, Morley T, Rau ML, Saghai Y. A meta-analysis of projected global food demand and population at risk of hunger for the period 2010-2050. *Nature Food*. 2021;2(7):494-501.
40. Zhao J, Liu X, Hou L, Xu G, Guan F, Zhang W, *et al*. The seed endophytic microbe *Microbacterium testaceum* M15 enhances the cold tolerance and growth of rice (*Oryza sativa* L.). *Microbiological Research*. 2024;289:127908.
41. Zhou Y, Bao J, Zhang D, Li Y, Li H, He H. Effect of heterocystous nitrogen-fixing cyanobacteria against rice sheath blight and the underlying mechanism. *Applied Soil Ecology*. 2020;153:103580.