

RESEARCH ARTICLE

Microbiome: An ally to plant breeding

K. Murugan, M. Vengadesan, L. Soukoumar, P. Adhimoolam

Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal- 609 603 Puducherry, India

Corresponding authors email: prembreeder2107@gmail.com

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Abstract

Conventional plant breeding primarily focuses on genotype $\times$ environment ($G \times E$) interactions to select superior cultivars for commercial cultivation. However, plant-microbe interactions have remained largely underexplored despite their critical role in regulating plant growth, development and environmental adaptation. Plant-associated microbiomes enhance tolerance to biotic and abiotic stresses by modulating plant metabolism, nutrient acquisition, signaling pathways, and antimicrobial defense mechanisms. Host-specificity of beneficial microbes remains a major challenge limiting their successful application under field conditions. Therefore, further research is required to overcome these constraints and facilitate the effective integration of microbiomes into plant breeding programs. This review summarizes recent advances in microbiome-assisted crop improvement, discusses mechanisms underlying stress resilience and breeding applications, and outlines future directions for integrating beneficial microbiomes into sustainable plant breeding programs.

Keywords: Abiotic stress, biotic Stress, microbiome, nutrient acquisition, plant breeding

Introduction

In conventional plant breeding programs, breeders focus on the assessment of different genotypes across multi-location trials to identify elite genotypes with desirable agronomic traits, resistance to biotic and abiotic stresses and different grain quality parameters. From this breeding approach, breeders have consistently released improved genotypes for commercial cultivation that contributed significantly to food security, while the contribution of plant microbes to plant breeding remains insufficiently investigated. Recent studies have suggested that plant microbiomes play a pivotal role in nutrient acquisition, resistance to biotic and abiotic stresses suggesting their potential to the development of climate-resilient varieties (Shi *et al.*, 2026, Gopal and Gupta, 2016). Therefore, this article highlights the role of plant-associated microbiomes in enhancing plant growth, stress resistance and their prospective role in future crop improvement programs.

Plant microbiome habitats

The plant microbiome inhabits diverse niches, including the rhizosphere (root-associated soil), rhizoplane (root surface), endosphere (internal plant tissues), phyllosphere (above-ground plant surfaces), and spermosphere (seed-associated environment), where they interact each other.

In natural ecosystems, plants coexist with a diversity of microbes that colonize habitats both above and under the soil and interact with plants throughout the life cycle. These associations are beneficial interactions with the host as it enhances plant resilience even under stress conditions. Plant microbiomes comprise diverse groups of microorganisms such as bacteria, fungi, archaea and microalgae that facilitate nutrient acquisition, disease suppression and tolerance to biotic and abiotic stresses. Thus, microbiomes influence plant growth, development and resilience through phytohormone production and synthesis of bioactive metabolites that enhance plant adaptation to environmental stresses. Microbial communities can be classified into distinct habitats depending on the location such as seed microbiome, rhizosphere microbiome, endosphere microbiome and phyllosphere microbiome. Each microbial compartment interacts with its host plant, and it enhances plant performance even under stress conditions (Chauhan *et al.*, 2023; McNear, 2013).

Integration of plant microbiomes into crop improvement programs

In biotic/abiotic stress conditions, plants secrete root exudate to attract beneficial microorganisms in rhizosphere. These microbes facilitate stress mitigation through osmotic adjustment, pathogen suppression and secretion of secondary metabolites. By this mechanism, plants improve adaption even under extreme conditions (Afridi *et al.*, 2023, Halshoy *et al.*, 2025) and the diversity of microbes with different stress conditions are depicted in Fig 1. Breeders need to understand the interaction between plant genotypes, microbes and environment to incorporate microbes into future crop improvement programs. These new strategies improve the precision of conventional crop improvement programs through Genotype x Environment x Microbiome and accelerate the development of stress-resilient cultivars (Macro *et al.*, 2023; Shelake *et al.*, 2025).

Harnessing the microbiome for salinity tolerance in crops

Salinity is one of the major abiotic constraints limiting crop productivity, especially in regions affected by inland salinity and coastal salinity. Excessive accumulation of Na⁺ (sodium) and chloride (Cl⁻) ions in the soil affect plant growth and development by affecting physiological, biochemical and molecular processes. Elevated level of accumulation of Na⁺ ions interferes with the uptake of essential nutrients such as potassium (K⁺), Calcium (Ca²⁺), Magnesium (Mg²⁺) ions. This nutrient imbalance impairs metabolic activities, protein synthesis and enzyme activity. Salinity stress induces the formation of Reactive Oxygen Species (ROS) which causes oxidative damage to protein and nucleic acids (Atta *et al.*, 2023; Tripathi *et al.*, 2025). Salt-tolerant microbes such as *Halomonas* and *Arthrobacter* mitigate salinity stress through production of glycine betaine, and trehalose. These compound help maintain cellular osmotic balance and protect plants from dehydration. In addition, plant growth-promoting rhizobacteria synthesize ACC deaminase which decreases ethylene precursor of 1-aminocyclopropane-1-carboxylate (ACC) level. This reduces ethylene accumulation thereby promoting root elongation under saline stress conditions. Based on experimental studies, beneficial microbial communities enhance osmotic adjustment, ion homeostasis, and antioxidant regulation, thereby developing tolerance to saline conditions. Thus, integrating microbiomes with plant breeding could accelerate development of saline tolerant crop varieties (Kumar *et al.*, 2023; AbuQamar *et al.*, 2024, Orozco-Mosqueda *et al.*, 2020).

Microbiome-mediated tolerance to heat and cold stress

Globally, temperature stress including heat and cold stress poses a significant challenge to plant growth, development and productivity. Heat stress disrupts cellular homeostasis through protein denaturation, membrane destabilization and inhibition of enzymatic activities. Cold stress impairs cellular metabolism through membrane

rigidification and intracellular ice formation. Under low-temperature stress conditions, *Pseudomonas putida* and *Sinorhizobium meliloti* produce cold shock proteins (CSPs) that stabilize the structure of mRNA and maintain ribosomal function. In a similar fashion, *Bacillus subtilis* and *Trichoderma spp.* synthesize compatible solutes such as trehalose and glycerol which protect cellular membranes from damage against temperature stress conditions (Hasanuzzaman *et al.*, 2013; Reva *et al.*, 2006, Ullah *et al.*, 2025; Hoffmann and Breme, 2011). Thus, plant-associated microbes improve plant resilience against extreme temperature stress under changing climatic conditions.

Microbiome-assisted protection against biotic stress

Biotic stress imposed by pathogens, insects, nematodes, and other harmful organisms adversely affects plant growth, development, and productivity and may ultimately lead to plant death under severe conditions. One of the unique features of beneficial microorganisms is their ability to regulate pattern-triggered immunity (PTI), which enables successful root colonization and promotes beneficial plant-microbe associations. These microorganisms produce elicitors, signaling molecules, and secondary metabolites that modulate immune signaling pathways and enhancing plant defense mechanisms (Nishad *et al.*, 2020; Tsai *et al.*, 2023). Plants possess pre-existing structural defense mechanisms, including cuticles, wax layers, and trichomes, which function as physical barriers that limit pathogen attachment, penetration, and subsequent infection. Plant receptors function as critical components of the surveillance system by recognizing microbe-associated molecular signals and differentiating between beneficial and pathogenic microorganisms, leading to the establishment of mutualistic associations with beneficial microbes and defense responses against invading pathogens. Beneficial microorganisms establish successful associations with plants by either evading plant immune recognition or suppressing immune

signaling pathways (Adedayo *et al.*, 2025; Ji *et al.*, 2022; Bittel and Robatzek, 2007) and representative examples are presented in Table 1.

Microbial enhancement of nutrient availability

Plant growth development and productivity depend on an adequate supply of essential nutrients and nutrient deficiency remains a major limitation to crop performance across agricultural ecosystems. Plant Growth-Promoting Rhizobacteria (PGPR) enhance nutrient acquisition through nutrient cycling, improve nutrient uptake, and increase nutrient availability in the rhizosphere. For instance, *Rhizobium spp.* establish symbiotic associations with host plants and convert atmospheric nitrogen into biologically available forms that support plant growth. Similarly, *Gluconacetobacter diazotrophicus* enhances plant nutrition under nitrogen-deficient conditions through biological nitrogen fixation and contributes to improved plant growth and productivity.

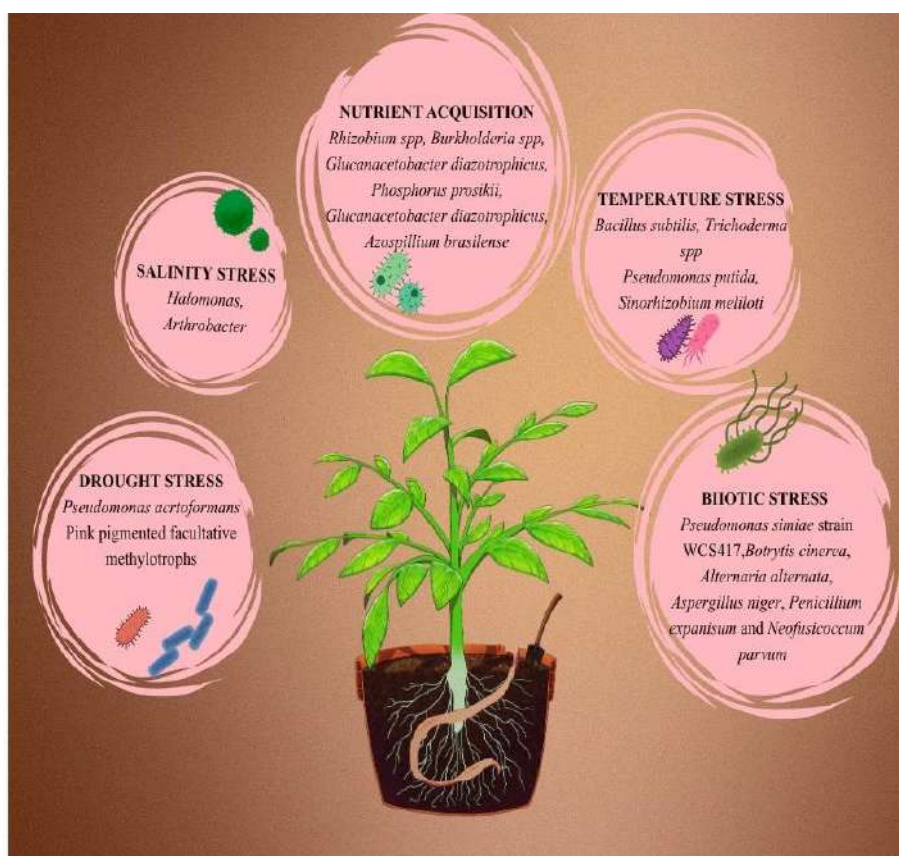
The secretion of organic acids such as acetate, succinate, citrate, and gluconate enables phosphate-solubilizing bacteria to transform insoluble phosphorus into plant-accessible forms. In addition, *Pseudomonas protekii* promotes phosphate solubilization through rhizosphere acidification and organic acid production, increasing phosphorus mobilization from insoluble sources and enhancing its availability to plants. Siderophores and other iron-chelating compounds produced by PGPR facilitate the mobilization of iron and essential micronutrients and promote nutrient uptake and plant growth under nutrient-limited conditions (Zhang *et al.*, 2024., Goyal *et al.*, 2021, Ceballos-Aguirre *et al.*, 2025, Bakki *et al.*, 2024, Praženicová *et al.*, 2026).

Challenges of microbial communities in natural ecosystems

In natural ecosystems, the application of microbial communities is limited by several factors that restrict large scale adoption. One of the major constraints is that specificity of microbial strains which limits broader applicability to the many

microbial communities are effective only in specific plant species or genotypes. The complexity of microbe–microbe interactions poses a major challenge to microbial applications because introduced beneficial microorganisms encounter competition to indigenous microbial populations for nutrients, space, and ecological niches, thereby reducing their establishment and effectiveness. In addition to that, the performance of microbial communities is often inconsistent across environments because environmental factors such as soil pH, moisture, temperature and nutrient availability significantly influence microbial survival, colonization and activity. Another major impediment to large-scale adaption is the lack of cost-effective production, formulation and delivery system to farmers. (Etesami, 2025; Brockett *et al.*, 2012, Ehinmitan *et al.*, 2024).

Fig 1: Major abiotic/biotic stresses, beneficial microorganisms involved in enhancing plant stress tolerance



These challenges can be addressed through advanced microbial screening, formulation technologies and precision agriculture thereby promoting sustainable utilization of microbes in natural ecosystems.

Conclusion

Numerous studies have demonstrated the potential of microbial communities to enhance plant growth, improve stress resilience, and increase agricultural

productivity. However, the dynamic and complex nature of plant–microbe interactions which is influenced by soil properties, host plants, and environmental conditions and it often limits the successful translation of microbial technologies from laboratory research to field applications. Further research is required to develop innovative strategies for integrating beneficial microbes into plant breeding programs to develop sustainable and climate-resilient agricultural production systems.

Table 1: Beneficial microorganisms involved in the suppression of plant pests and pathogens through antimicrobial metabolites and induced defense responses

Crop	Beneficial microorganism	Target pest/pathogen	Reported mechanism	Reference
<i>Triticum aestivum</i>	<i>Bacillus</i>	<i>Pyricularia oryzae</i> (wheat blast)	Production of volatile organic compounds (hexanoic acid, 2-methyl butanoic acid and phenylethyl alcohol)	Surovy <i>et al.</i> , 2023
<i>Oryza sativa</i>	<i>Streptomyces arisarensis</i>	<i>Rhizoctonia solani</i> (sheath blight)	Production of the antimicrobial metabolite 6-amino-5-nitrosopyrimidine-2,4-diol	Oyedoh <i>et al.</i> , 2024
<i>Oryza sativa</i>	<i>Bacillus subtilis</i>	<i>Magnaporthe oryzae</i> (rice blast)	Inhibition of conidial germination and appressorium formation	Lei <i>et al.</i> , 2023
<i>Zea mays</i>	<i>Bacillus.</i> , <i>Enterobacter</i> , <i>Pseudomonas</i> . <i>Microbacterium oleovorans</i>	<i>Fusarium verticillioides</i>	Suppression of fumonisin production and inhibition of fungal growth	Omotayo <i>et al.</i> , 2023
<i>Solanum lycopersicum</i>	<i>Metarhizium brunneum</i>	<i>Tetranychus urticae</i> (two-spotted spider mite)	Induction of chlorogenic acid (CGA) biosynthesis, enhancing plant defense against herbivory	Rasool <i>et al.</i> , 2023
<i>Solanum lycopersicum</i>	<i>Pseudomonas putida</i> , <i>Aspergillus tubingensis</i>	<i>Alternaria</i> rot, bacterial canker and root rot	Production of antimicrobial compounds and suppression of phytopathogens	Benaissa <i>et al.</i> , 2025
<i>Saccharum officinarum</i>	<i>Bacillus velezensis</i>	<i>Colletotrichum falcatum</i> (red rot)	Recruitment of beneficial rhizosphere microorganisms and induction of systemic resistance	Xie <i>et al.</i> , 2024
<i>Musa spp.</i>	<i>Pseudomonas aeruginosa</i>	<i>Fusarium oxysporum</i> f. sp. <i>cubense</i> (Panama disease)	Production of antifungal metabolites including phenazine and phenazine-1-carboxylic acid	Lu <i>et al.</i> , 2024
<i>Stevia rebaudiana</i>	<i>Streptomyces antibioticus</i>	<i>Meloidogyne incognita</i> (root-knot nematode)	Production of actinomycins V and X ₂ , resulting in nematocidal activity	Sharma <i>et al.</i> , 2019

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