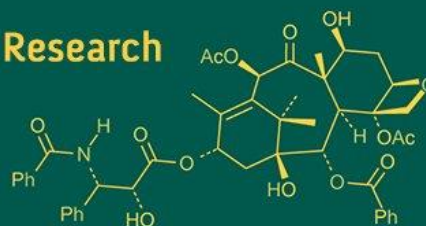


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AR Arsha

Department of Agricultural Microbiology, College of Agriculture, (Kerala Agriculture University), Vellayani, Thiruvananthapuram, Kerala, India

VI Soumya

Assistant Professor, Department of Agricultural Microbiology, College of Agriculture, Vellayani, Kerala Agriculture University, Vellayani, Thiruvananthapuram Kerala, India

S Anu Rajan

Assistant Professor, Department of Agricultural Microbiology, College of Agriculture, (Kerala Agriculture University), Vellayani, Thiruvananthapuram, Kerala, India

N Chitra

Assistant Professor and Head, Department of Agricultural Microbiology, College of Agriculture, (Kerala Agriculture University), Vellayani, Thiruvananthapuram, Kerala, India

KN Anith

Professor, Department of Agricultural Microbiology, College of Agriculture, (Kerala Agriculture University), Vellayani, Thiruvananthapuram, Kerala, India

R Beena

Associate Professor, Department of Plant Physiology, College of Agriculture, (Kerala Agriculture University), Vellayani, Thiruvananthapuram, Kerala, India

Corresponding Author:**VI Soumya**

Assistant Professor, Department of Agricultural Microbiology, College of Agriculture, Vellayani, Kerala Agriculture University, Vellayani, Thiruvananthapuram Kerala, India

The hidden allies in weeds: Plant growth-promoting and thermotolerant bacteria for heat-resilient rice production

AR Arsha, VI Soumya, S Anu Rajan, N Chitra, KN Anith and R Beena

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Abstract

Weeds, though often viewed as crop competitors, host diverse bacterial communities with remarkable plant growth-promoting and stress-mitigating potential. These weed-associated bacteria exhibit key functional traits such as nitrogen fixation, phosphate solubilization, phytohormone synthesis, and ACC deaminase activity, which collectively enhance rice growth and nutrient uptake. Many isolates also impart thermotolerance by boosting antioxidant defence, osmolyte accumulation, and membrane stability under heat stress. Harnessing these beneficial microbes offers a sustainable strategy to improve rice resilience while reducing dependence on chemical inputs. This review highlights the diversity, mechanisms, and applications of weed-associated bacteria in promoting growth and heat stress tolerance in rice under changing climatic conditions.

Keywords: Weed-associated bacteria, plant growth-promoting rhizobacteria, heat stress tolerance, climate resilience, sustainable agriculture

Introduction

Rice (*Oryza sativa* L.) is a staple food crop that feeds over half of the global population and plays a central role in ensuring food and nutritional security, particularly in Asia (FAO, 2021) [20]. However, the progressive rise in global temperatures poses a serious threat to rice productivity, as high temperature episodes impair photosynthetic efficiency, reduce pollen fertility, and accelerate grain filling, leading to considerable yield losses (Jagadish *et al.*, 2016) [29]. Moreover, prolonged or severe heat can disturb water balance and cellular hydration, leading to dehydration stress that further compromises membrane integrity, metabolic activity and cell survival (Ihsan *et al.*, 2019; Wahid *et al.*, 2007) [27, 58].

With climate projections indicating more frequent and intense heat episodes in major rice-growing regions, temperature stress poses a growing threat to global rice production (IPCC, 2021; Zhao *et al.*, 2017) [28, 62]. Strengthening rice resilience to such climatic extremes requires integrated approaches that complement genetic improvement with eco-friendly microbial interventions capable of maintaining physiological stability under heat stress (Grover *et al.*, 2022) [24].

In this context, weeds often perceived only as competitors are increasingly being recognised for their ecological value. Many weed species inhabit harsh environments where high temperatures, poor soils, and frequent disturbance are common. Consequently, their rhizospheres and internal tissues host diverse microbial communities that are naturally adapted to withstand thermal stress. Research indicates that these microorganisms exhibit traits that maintain cellular function under heat and may influence plant performance when transferred to agricultural crops (Qaisrani *et al.*, 2019; Afzal *et al.*, 2019) [42, 1]. Exploring these weed-associated, thermotolerant bacteria opens new possibilities for heat resilience in rice cultivation. Although considerable research has focused on the rhizosphere microbiome of cultivated crops, the microbial communities associated with weeds plants typically regarded as competitors in agroecosystems have been comparatively underinvestigated.

Weeds as Ecological Reservoirs of Beneficial Microbes

Weeds act as dynamic ecological niches that sustain a wide range of microorganisms in their rhizosphere and internal tissues, often more diverse than those found in cultivated plants.

Their rhizosphere and endophytic microbiota comprise numerous bacterial genera such as *Bacillus*, *Pseudomonas*, *Enterobacter*, *Azospirillum*, and *Rhizobium*, which play critical roles in nutrient transformation, phytohormone synthesis, and biocontrol activity (Gupta and Mishra, 2023) [25]. Weed-derived bacterial endophytes frequently exhibit enhanced abiotic stress tolerance, enabling them to sustain root colonisation, nutrient transformation, and phytohormone production even under adverse conditions such as drought or heat (White *et al.*, 2019) [59]. The rhizosphere of non-cultivated plants often selects for microbial taxa with high functional redundancy in nutrient cycling and stress mitigation, rendering these communities valuable sources of potential bio-inoculants for nearby crops (Saeed *et al.*, 2021) [45]. Invasive and wild weed species are known to harbor unique microbial assemblages capable of cross-colonizing crop rhizospheres via soil or root-mediated interactions, hence boosting nutrient uptake, stress tolerance, and overall plant performance (Dubey *et al.*, 2022) [18]. Weeds growing in marginal soils and arid environments also promote the selection of microbial taxa with specialized traits such as heat-shock protein synthesis, exopolysaccharide secretion, and osmolyte accumulation, all of which contribute to improved microbial and plant resilience (Sarathambal *et al.*, 2014) [50].

The ecological interactions between weeds, their associated microbes, and neighbouring crop plants are multifaceted ranging from competition for nutrients to beneficial associations that indirectly enhance soil fertility and crop resilience. Weeds typically grow in marginal soils exposed to extreme conditions of heat, drought, and nutrient deficiency, which drive their microbiota to develop robust adaptive mechanisms including the synthesis of osmolytes, antioxidant enzymes, and heat-shock proteins. Recent studies indicate that certain bacterial strains can strengthen rice tolerance to heat by boosting antioxidant defence systems, stabilising cellular membranes, and modulating the expression of key stress-related genes (Kang *et al.*, 2021; Kumari *et al.*, 2022) [32, 35]. These protective mechanisms align with growing evidence that weeds serve as reservoirs of microorganisms naturally adapted to harsh and fluctuating environments. Owing to these inherent stress-tolerant traits, bacteria isolated from weeds represent

valuable candidates for formulating bioinoculants capable of functioning under variable field conditions (Khan *et al.*, 2020; Li *et al.*, 2021; Gupta and Mishra, 2023) [33, 37, 25]. Overall, the adaptive strength and multifunctional capacities of weed-associated microbial communities highlight their potential as overlooked sources of beneficial, stress-alleviating bacteria for advancing sustainable and heat-resilient rice production.

Weed-Associated Bacteria (WAB) as Novel Plant Growth Promoters and Stress Mitigators

Weed-derived bacteria harbour an extensive repertoire of physiological, biochemical and ecological traits that promote plant growth through multiple direct and indirect mechanisms. Investigations on the rhizosphere and endosphere of widely distributed weeds such as *Cyperus rotundus*, *Echinochloa crus-galli* and *Amaranthus* spp. have revealed the presence of diverse microbial isolates capable of performing key plant growth-promoting (PGP) functions. These include atmospheric nitrogen fixation, solubilisation of otherwise unavailable pools of phosphorus and potassium, and siderophore-mediated iron acquisition—all of which substantially enhance nutrient availability and uptake in the rhizosphere, thereby strengthening plant nutritional status (Kumar *et al.*, 2022) [34].

Beyond nutrient mobilisation, many weed-derived bacterial strains synthesise osmoprotectants, antioxidants and exopolysaccharides (EPS). These metabolites not only improve bacterial survival under environmental stresses such as drought and high temperature but also confer improved resilience to host plants by enhancing water retention, stabilising cellular structures and reducing oxidative damage (Khan *et al.*, 2020) [33]. Importantly, recent studies have highlighted that weed rhizospheres and endospheres act as rich reservoirs of bacteria expressing multiple PGP attributes simultaneously. Such isolates frequently produce phytohormones—including indole-3-acetic acid (IAA) and gibberellins—and possess ACC-deaminase activity, which collectively modulate root system architecture, stimulate shoot development and mitigate ethylene-induced growth inhibition, especially under stress conditions (de Andrade *et al.*, 2023; Leontidou *et al.*, 2020) [16, 36].

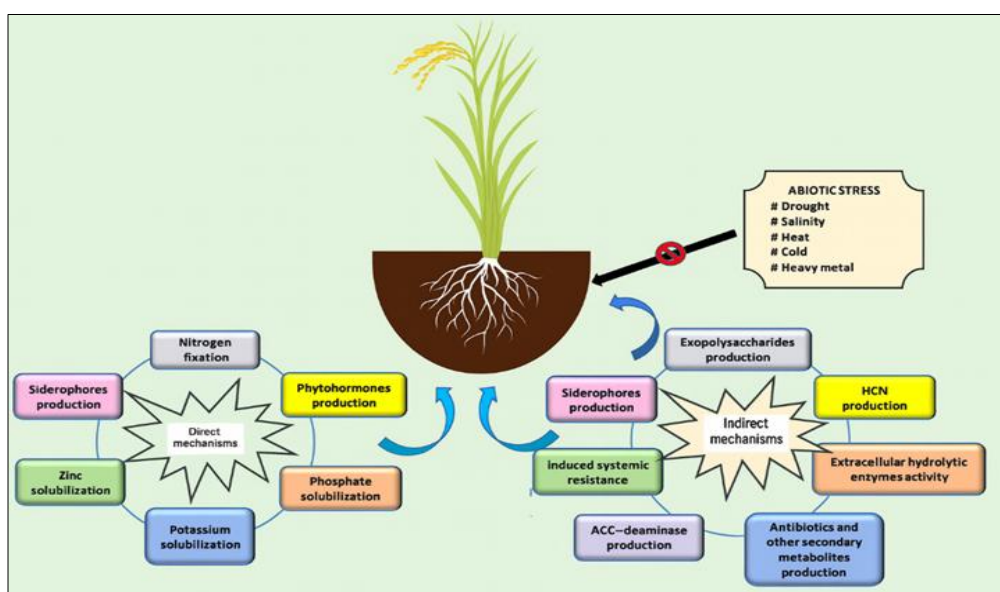


Fig 1. Direct and indirect mechanisms of weed associated bacteria in rice under stress

In addition to their growth-promoting functions, WABs also contribute to plant protection. Several isolates synthesise hydrogen cyanide, extracellular lytic enzymes and antifungal volatile compounds that suppress soil-borne pathogens. The formation of EPS-rich biofilms and secretion of osmolytes further enhances microbial persistence and supports root colonisation, thereby strengthening plant tolerance to abiotic stresses including drought and heat (Jeyanthi *et al.*, 2019; Carezzano *et al.*, 2023) ^[30, 10]. The phyllosphere of rice and associated wild grasses also hosts methylotrophic bacteria with complementary PGP functions. These organisms can contribute phytohormones and, in some cases, biologically fixed nitrogen, resulting in improved crop vigour, yield and stress resilience in field conditions (Sanjenbam *et al.*, 2022; Danso Ofori *et al.*, 2024) ^[19, 15]. Bacteria associated with weeds frequently emit diverse volatile organic compounds (VOCs) that play a crucial role in promoting plant growth without requiring direct root

contact. These small, easily diffusible molecules including acetoin, 2,3-butanediol, sulfur-containing volatiles and various alcohols can travel through the soil matrix and influence plant physiology from a distance. Studies show that such VOCs enhance chlorophyll accumulation, improve photosynthetic efficiency and activate growth-related hormonal signalling pathways that stimulate root elongation and lateral root formation (Bitas *et al.*, 2013) ^[9]. These findings suggest that VOC-producing microbes from weeds represent an underexplored biological resource for enhancing plant performance and abiotic stress resilience. Taken together, the convergence of nutrient mobilisation, phytohormonal regulation, stress alleviation and biocontrol traits observed in WAB underscores their potential as powerful bioinoculant candidates. Their multifunctional PGP capabilities position them as ideal components for designing microbial consortia tailored for nutrient-efficient, climate-resilient and sustainable rice and cereal production systems (Bakki *et al.*, 2024) ^[6].

Table 1: Plant growth promoting associations of weed-derived bacteria

Host Weed	Associated Bacterium	Isolation Source / Niche	Primary Documented Function or Effect	References
<i>Cyperus rotundus</i> (Purple nutsedge)	<i>Bacillus aryabhatai</i>	Rhizosphere	Strengthens root growth and drought resilience via ACC deaminase and auxin (IAA), enhancing osmotic balance	Panwar <i>et al.</i> , 2016 ^[41]
<i>Echinochloa crus-galli</i> (Barnyard grass)	<i>Bacillus cereus</i> strain SA1	Roots	Promotes plant growth and heat tolerance through hormonal (IAA, GA), antioxidant (SOD, APX), and stress-regulation mechanisms.	Khan <i>et al.</i> 2020 ^[33]
<i>Suaeda</i> spp. (Sea-blite)	<i>Zhihengliuella halotolerans</i> and <i>Brachybacterium</i> sp.	Roots	Highly salt-tolerant diazotrophs capable of growing in nitrogen-free medium with 6% NaCl, offering potential for saline agriculture.	Alishahi <i>et al.</i> 2020 ^[2]
<i>Parthenium hysterophorus</i> (Congress grass)	<i>Bacillus paramycoides</i> strain Ph-04	Etiolated seedlings	Boosts heat tolerance through early seedling growth, membrane stability, and antioxidant protection.	Dubey <i>et al.</i> 2022 ^[18]
<i>Arthrocnemum macrostachyum</i> (Saltwort)	<i>Kushneria endophytica</i> and <i>Kushneria phyllosphaerae</i>	Internal tissues	Salt-tolerant, PGP bacteria that promote growth in saline conditions.	Navarro-Torre <i>et al.</i> 2018 ^[39]
<i>Echinochloa crus-galli</i> (Barnyard grass)	<i>Cronobacter dublinensis</i> strain BC-14	Seed	Improves root growth and drought tolerance by boosting chlorophyll, proline and antioxidant enzymes (SOD, CAT, POD) and reducing MDA.	Cheng <i>et al.</i> 2024 ^[12]

Comparative Advantages of WABs Over Crop-Associated PGPR

Weed-derived bacteria possess a range of ecological and functional advantages over conventional crop-derived PGPR because they naturally thrive in habitats that are continually exposed to multiple abiotic pressures, such as extreme heat, sporadic drought episodes and persistent soil degradation. These demanding environmental conditions act as strong selective forces, enabling the microbes associated with weeds to develop exceptionally resilient physiological traits that promote their survival and functionality under stress (Sukumar *et al.*, 2016) ^[54]. In contrast to cultivated crops, which typically grow in fertilized, nutrient-enriched and carefully managed agricultural soils, weeds often establish themselves in marginal, nutrient-deficient or frequently disturbed habitats. Moreover, many endophytic bacteria isolated from weeds display remarkably strong colonization efficiency. This is largely because they originate from hosts that possess highly competitive and vigorous root systems, which naturally select for microbes with advanced root adhesion capabilities, improved biofilm-forming potential and the ability to rapidly and firmly establish themselves within the rhizosphere once introduced into rice plants (Singh *et al.*,

2022) ^[52]. These colonization traits also contribute to their durability and persistence under fluctuating temperature regimes, irregular moisture availability and other environmental uncertainties—conditions under which many crop-associated inoculants often fail to survive or maintain their activity (Sukumar *et al.*, 2016) ^[54]. Owing to these inherent advantages, WAB isolates frequently outperform traditional PGPR strains in enhancing rice growth, maintaining physiological stability and improving tolerance to high temperatures. Consequently, these underexplored microbes represent a valuable biological resource for designing resilient agricultural systems in the face of intensifying climate change (Bhat *et al.*, 2023) ^[8].

Heat Stress Alleviation Through Weed-Derived Microbial Resources

Weed-derived bacteria employ a suite of biochemical, physiological and molecular strategies that collectively enhance plant tolerance to heat, drought and other abiotic stresses. Exposure to high temperature disrupts cellular homeostasis in rice by accelerating reactive oxygen species (ROS) generation, triggering membrane lipid peroxidation, impairing protein assembly and destabilising chloroplast and

mitochondrial structures—as reflected by elevated malondialdehyde (MDA) levels (Zhang *et al.*, 2020; Hasanuzzaman *et al.*, 2013) [61, 26]. Heat further disturbs

plant water balance, causing dehydration stress that compromises membrane integrity, enzyme functioning and metabolic activity (Ihsan *et al.*, 2019; Wahid *et al.*, 2007) [27, 58].

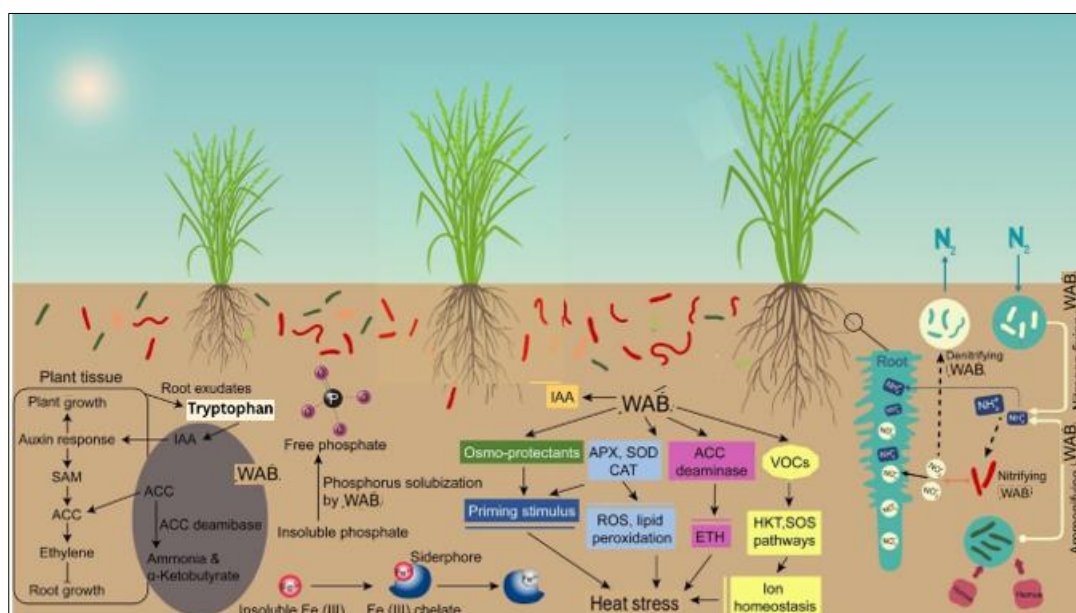


Fig 2. Beneficial traits of weed associated bacteria in plant growth and heat stress mitigation

To counteract these injuries, weed-derived bacteria activate multiple defence pathways. Many isolates from the rhizosphere and phyllosphere of heat-resilient weeds such as *Echinochloa crus-galli*, *Cyperus rotundus* and *Eclipta prostrata* accumulate compatible solutes including proline, trehalose and glycine betaine, which stabilise proteins and membranes and help prevent cellular dehydration (Khan *et al.*, 2020) [33]. These microbes also stimulate the host plant's antioxidant machinery by elevating the activities of superoxide dismutase (SOD), ascorbate peroxidase (APX), catalase (CAT) and peroxidase (POD), thereby maintaining redox homeostasis during heat-induced oxidative stress (Al-Turki *et al.*, 2023) [3]. Microbial volatile compounds have been shown to influence ionic balance in plants, possibly by modulating sodium transport regulators such as high-affinity potassium transporter (HKT) and components of the salt overly sensitive (SOS) signaling pathway (Kanchiswamy *et al.*, 2015) [31]. The metabolic relationship between auxin and ethylene is closely connected, since S-adenosyl-methionine (SAM) functions as the common precursor for indole-3-acetic acid (IAA) and 1-aminocyclopropane-1-carboxylic acid (ACC), while ACC deaminase-producing bacteria degrade ACC, subsequently reducing ethylene formation and facilitating auxin-driven enhancement of root development (Glick *et al.*, 2014) [23]. Additionally, they improve water uptake and sustain cellular hydration through the production of osmoprotective metabolites and by enhancing root system functionality (Chieb *et al.*, 2023) [13]. WAB also contribute to thermotolerance by improving micronutrient availability. Siderophore-producing strains chelate Fe^{3+} in the rhizosphere and deliver it to plant tissues, stabilising photosynthetic electron transport, maintaining iron-dependent enzymatic functions and reducing ROS formation under high temperatures (Saha *et al.*, 2016; Dimkpa *et al.*, 2019) [46, 17]. At the physiological level, microbial inoculants fine-tune stomatal behaviour by modulating abscisic acid and cytokinin pathways, together with ROS-NO signalling—the interactive network between

reactive oxygen species and nitric oxide that governs plant stress responses. This integrated signalling optimises stomatal aperture, reduces excessive transpiration and maintains sufficient evaporative cooling to prevent heat-induced cellular injury (Vurukonda *et al.*, 2016) [57].

In addition to maintaining water balance and redox stability, weed-associated microbes strengthen plant structural integrity. They promote lignin deposition, callose accumulation and adjustments in membrane fatty acid composition, reinforcing cell walls and stabilising membranes against thermal disruption (Wahid *et al.*, 2007; Hasanuzzaman *et al.*, 2013) [58, 26]. These bacteria also interact with salicylic acid (SA), jasmonic acid (JA) and abscisic acid (ABA) pathways, shaping heat-responsive transcriptional networks and enhancing stress memory formation, antioxidant activation and cellular recovery (Reddy *et al.*, 2010; Gamir *et al.*, 2021) [44, 22]. Furthermore, they modulate phytohormone levels such as auxins, cytokinins and gibberellins, which support root development, sustain source-sink balance and maintain biomass production despite thermal injury (Compant *et al.*, 2010; Khan *et al.*, 2020) [44, 33].

Alongside biochemical and hormonal adjustments, weed-derived bacteria markedly improve root system architecture—enhancing lateral root formation, root hair proliferation and total root length—thereby boosting water acquisition during heat episodes (Vacheron *et al.*, 2013) [56]. They also stimulate the synthesis of osmoprotectants like proline and glycine betaine and induce protective proteins including heat shock proteins (HSPs), HSFA2 and HSFB1 transcription factors, and MAPK signalling pathways that regulate protein folding, detoxification and cellular resilience (Saijo *et al.*, 2020; Li *et al.*, 2021) [47, 37]. Collectively, the physiological and molecular adjustments triggered by WAB underscore their value as a naturally adapted microbial reservoir with high potential for improving heat resilience in rice production systems.

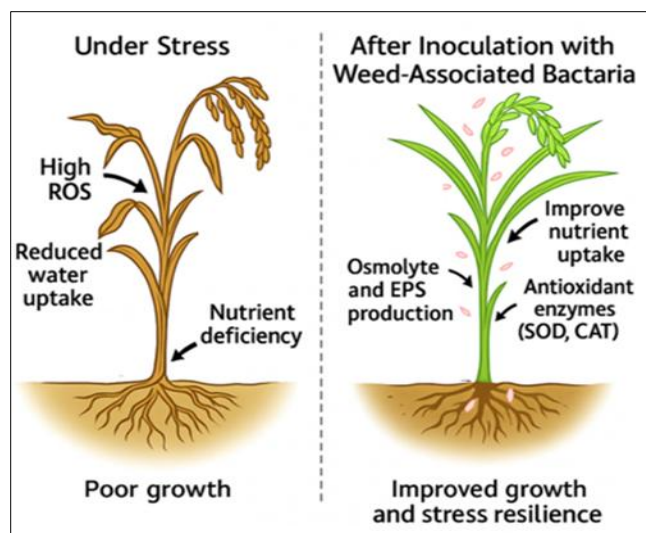


Fig 3: Comparative response of rice plants under stress and after inoculation with weed-associated bacteria.

Abiotic Stress Tolerance Mechanisms Driven by Weed-Associated Microbes

Weed-associated PGPR significantly strengthen drought tolerance in rice by promoting deeper and more fibrous root systems, thereby improving water acquisition and maintaining cellular hydration during dry periods. These microbes trigger the accumulation of compatible solutes such as proline and trehalose, which help protect proteins and membranes from dehydration-induced damage (Sandhya *et al.*, 2010) ^[48].

Weed-associated halotolerant bacteria also support rice under saline conditions by regulating ionic balance, maintaining a favourable Na^+/K^+ ratio, and mitigating sodium toxicity (Egamberdieva *et al.*, 2019) ^[19]. These strains synthesize osmolytes and exopolysaccharides (EPS) that reinforce osmotic stability and prevent cellular dehydration when plants face high salinity (Numan *et al.*, 2018) ^[40]. Also, many isolates produce phytohormones such as IAA and cytokinins, which enhance lateral root formation, nutrient uptake and overall growth in salt-affected soils (Egamberdieva *et al.*, 2019) ^[19].

During flooding or waterlogging, weed-derived PGPR help rice tolerate low-oxygen environments by reducing excess ethylene (ETH) through ACC deaminase activity, preventing premature senescence and root decay (Arif *et al.*, 2020) ^[4]. Some isolates stimulate the development of aerenchyma and activate anaerobic metabolic pathways, enabling roots to maintain respiration and nutrient absorption even under hypoxic conditions (Xiong *et al.*, 2017) ^[60]. Their capacity to boost antioxidant defences further protects rice roots from oxidative bursts associated with reoxygenation after flooding (Arif *et al.*, 2020) ^[4].

Cold-tolerant weed-associated PGPR contribute to chilling resilience by stabilizing cell membranes, preserving membrane fluidity, and reducing cold-induced leakage of cellular contents (Subramanian *et al.*, 2016) ^[53]. Moreover, several isolates induce the expression of cold-responsive genes, particularly the CBF/DREB pathway, enhancing the plant's physiological readiness for chilling and improving recovery after exposure to low temperatures (Subramanian *et al.*, 2016) ^[53]. Microbial inoculation has been shown to significantly improve plant cold tolerance by enhancing physiological stability and activating stress-responsive metabolic pathways (Zhang *et al.*, 2020) ^[61].

Weed-associated metal-tolerant bacteria also protect rice grown in contaminated soils by immobilizing toxic heavy metals through biosorption, intracellular sequestration or active efflux, thereby limiting their entry into root tissues (Rajkumar *et al.*, 2010) ^[43]. These strains often produce siderophores that chelate metal ions, decreasing their bioavailability and reducing toxic effects on plants (Ma *et al.*, 2016). Moreover, EPS secretion and biofilm formation create protective barriers in the rhizosphere, immobilizing metals and maintaining a physiologically favourable environment around rice roots (Rajkumar *et al.*, 2010) ^[43].

Collectively, these integrated responses ranging from osmoprotection and antioxidant defense to hormone regulation and EPS formation allow WAB to function as effective bio-buffers for rice and other crops facing climate-induced stresses. Their dual adaptability, developed through long-term association with resilient weed hosts, positions them as valuable microbial resources for bioformulations aimed at improving plant thermotolerance and drought resilience in sustainable cropping systems.

Role of WAB in Sustainable Agriculture and Circular Bioeconomy

Weed-derived bacteria are increasingly recognized as valuable biological tools for shaping sustainable and resource-efficient agricultural systems. These microbes possess a diverse array of functional traits—including nutrient mobilization, organic matter mineralization, biocontrol activity, and strong abiotic stress tolerance that collectively align with the principles of a circular bioeconomy, which promotes the conversion of agricultural waste into useful inputs and encourages the ecological reuse of microbial resources. Harnessing the microbial communities that naturally inhabit resilient weed species provides an opportunity to reduce the heavy dependence on synthetic fertilizers and pesticides, thereby lowering both environmental impact and production costs. Moreover, their application can significantly enhance soil fertility, improve nutrient-use efficiency, and restore beneficial soil microbial diversity, ultimately contributing to healthier and more productive cropping systems (Gupta and Mishra, 2023) ^[25].

Their enzymatic potential particularly cellulase, lignin peroxidase, and laccase activities facilitates the breakdown of lignocellulosic residues, transforming them into nutrient-rich composts suitable for organic farming (Kumar *et al.*, 2022) ^[34]. Weed-derived bacteria are increasingly recognized as contributors to sustainable agriculture and circular bioeconomy by enhancing nutrient recycling, waste valorization, and ecological resilience. Their ability to transform agricultural residues into bio-enriched composts and biofertilizers supports resource-efficient farming while maintaining soil fertility and microbial diversity (Suman *et al.*, 2022) ^[55]. In addition, biofertilizer formulations developed from *Bacillus*, *Pseudomonas* and other weed-associated genera improve nutrient use efficiency, carbon sequestration, and soil structure, thereby lowering dependence on chemical inputs (Kumar *et al.*, 2022) ^[34]. By incorporating these isolates, microbial consortia support plant nutrition and soil health, directly supporting the ideas of a circular bioeconomy (Fatima *et al.*, 2025) ^[21].

Microbial inoculants offer strong potential for integration into climate-smart rice systems because they enhance the crop's ability to withstand rising temperatures and moisture stress. These microbes also facilitate biological nitrogen

fixation and phosphorus mobilization, helping reduce dependence on synthetic fertilizers while maintaining productivity (Silva *et al.*, 2023) ^[51]. In addition, many PGPR strains enhance antioxidant enzyme activity, osmolyte accumulation, and membrane stability, thereby strengthening plant tolerance to heat and drought (Chakraborti *et al.*, 2022) ^[11]. Field evaluations further demonstrate that bacterial inoculants can improve water-use efficiency and yield stability when used alongside climate-adapted varieties and improved agronomic practices (Bhat *et al.*, 2023) ^[8]. Together, these findings highlight the value of microbial bioinoculants as an integral component of climate-smart rice cultivation.

From a sustainability perspective, weed-associated microbes can be integrated into multi-functional consortia that enhance crop resilience under climate-induced stresses. These consortia can be customized to specific agro-ecosystems to improve nutrient use efficiency, maintain soil biodiversity, and promote long-term ecological balance (Khan *et al.*, 2020) ^[33]. Thus, harnessing the functional diversity of weed-microbe associations aligns with the global shift toward regenerative agriculture and circular bioeconomy, where biodiversity and sustainability serve as complementary pillars for future food security.

Potential Applications and Future Prospects of Weed-Associated Microbes in Rice Cultivation

WAB represent an untapped microbial resource with significant potential for sustainable rice production. Their ability to enhance nutrient availability, regulate phytohormones, and confer abiotic stress tolerance can be strategically utilized in biofertilizer and biostimulant development. The use of such microbes can reduce the dependence on synthetic fertilizers and enhance soil health through restoration of microbial diversity and organic-matter turnover (Gupta and Mishra, 2023) ^[25].

Integrating weed-derived beneficial microbes into rice ecosystems offers the dual advantages of improved crop productivity and eco-friendly weed management. These microbes may influence weed-crop interactions by modifying rhizosphere microbiomes and nutrient fluxes, potentially reducing weed competitiveness while supporting rice growth (Kumar *et al.*, 2022) ^[34]. High-throughput genomic and metabolomic studies have begun revealing the immense biotechnological potential of these microbes.

Future research should focus on genome-based screening and functional validation of weed-associated isolates for traits linked to thermotolerance, drought adaptation, and nutrient use efficiency. Metagenomic and metabolomic approaches will be crucial for understanding their ecological roles and compatibility with rice genotypes under different climatic regimes. Moreover, developing stable formulations and field-level trials under variable agro-climatic zones will facilitate their commercial deployment as “next-generation bioinoculants.” In this context, exploring the weed microbiome offers an innovative pathway for achieving climate-resilient rice cultivation within a circular bioeconomy framework (Khan *et al.*, 2020) ^[33].

Conclusion

Weed-associated microbes form a valuable but underexplored microbial resource capable of enhancing plant growth and resilience in sustainable agriculture. Their ability to solubilize nutrients, produce growth-promoting phytohormones, and boost antioxidant defenses strengthens root development, water balance, and stress tolerance particularly under heat, drought, and salinity. Integrating these weed-derived microbial isolates into biofertilizer formulations and bio-enriched composts can simultaneously recycle organic residues and reduce dependence on synthetic inputs, aligning with the principles of circular bioeconomy. Such consortia-based inoculants could play a transformative role in restoring soil microbial diversity, improving nutrient-use efficiency, and enhancing ecosystem resilience under changing climatic conditions. Future research should emphasize large-scale validation of elite isolates under field environments, optimization of carrier materials for shelf-stable bioformulations, and multi-omics-based elucidation of the underlying molecular pathways responsible for stress alleviation and nutrient mobilization. By strategically exploiting the biodiversity of weed-associated microbiomes, agriculture can transition toward a climate-resilient, low-input production paradigm that ensures both environmental sustainability and food security.

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References

1. Afzal I, Shinwari ZK, Sikandar S, Shahzad S. Plant beneficial endophytic bacteria: mechanisms, diversity, host range and genetic determinants. *Microbiol Res.* 2019;221:36-49.
2. Alishahi F, Alikhani HA, Khoshkholgh-Sima NA, Etesami H. Mining the roots of various species of the halophyte *Suaeda* for halotolerant nitrogen-fixing endophytic bacteria with the potential for promoting plant growth. *Int Microbiol.* 2020;23(3):415-427.
3. Al-Turki A, Murali A, Omar M, Rehan S, Sayyed RZ. Recent advances in PGPR-mediated resilience toward interactive effects of drought and salt stress in plants. *Front Microbiol.* 2023;14:1214845.
4. Arif Y, Singh P, Siddiqui H, Bajguz A, Hayat S. Responses of plants and beneficial microbes to flooding stress. *Physiol Plant.* 2020;168:1-15.
5. Backer R, Rokem JS, Ilangumaran G, Lamont J, Praslickova D, Ricci E, *et al.* Plant growth-promoting rhizobacteria: mechanisms and applications. *Front Plant Sci.* 2018;9:1473.
6. Bakki M, Mammeri M, Djenadi B, *et al.* Phosphate-solubilizing *Pseudomonas* and *Bacillus* combined as biofertilizers and biopesticides for tomato. *Front Microbiol.* 2024;15:1289466.
7. Bhardwaj D, Ansari MW, Sahoo RK, Tuteja N. Biofertilizers function as key players in sustainable agriculture by improving soil fertility, plant tolerance and crop productivity. *Microb Cell Fact.* 2014;13:66.
8. Bhat MA, Rasool R, Mir RA. Plant-associated microbes enhance resilience and productivity of rice under climate stress. *Rhizosphere.* 2023;25:100647.

9. Bitas V, Kim HS, Bennett JW, Kang S. Sniffing on microbes: diverse roles of microbial volatile organic compounds in plant health. *Mol Plant Microbe Interact.* 2013;26:835-843.
10. Carezzano ME, Di Martino C, Castagnola NB, *et al.* Exopolysaccharides synthesized by rhizospheric bacteria: structure, function and biotechnological applications. *BioTech.* 2023;3:86.
11. Chakraborti D, Verma M, Bhattacharyya P. PGPR-mediated mitigation of heat and drought stress in rice. *Environ Exp Bot.* 2022;198:104851.
12. Cheng S, Wang Q, Yang D, He Q, Deng J, Zhou Y, *et al.* A seed endophytic bacterium *Cronobacter dublinensis* BC-14 enhances the growth and drought tolerance of *Echinochloa crus-galli*. *Microorganisms.* 2024;12(12):2544.
13. Chieb M, Gachomo EW. The role of plant growth-promoting rhizobacteria in plant drought stress responses. *BMC Plant Biol.* 2023;23:407.
14. Compant S, Clément C, Sessitsch A. Plant growth-promoting bacteria in the rhizo- and endosphere of plants: their role in plant stress responses. *Soil Biol Biochem.* 2010;42:669-78.
15. Danso Ofori A, Radutoiu S, Saito A, *et al.* Roles of phyllosphere microbes in rice health and productivity. *Plants.* 2024;13:3268.
16. de Andrade LA, Santos CHB, Frezarin ET, Sales LR, Rigobelo EC. Plant growth-promoting rhizobacteria for sustainable agricultural production. *Microorganisms.* 2023;11:1088.
17. Dimkpa C, Zia A, Bindraban PS. Micronutrients and their diverse functions in plant stress tolerance. *Plant Soil.* 2019;434:1-20.
18. Dubey A, Sharma M, Singh G, Gupta R, Kumar V, Chauhan A, Meena KK. Invasive weed-associated bacteria confer enhanced abiotic stress resilience to non-host crops. *Agric Ecosyst Environ.* 2022;339:108203.
19. Egamberdieva D, Wirth S, Behrendt U, Abd-Allah EF, Berg G. Salt-tolerant PGPR enhance plant performance under salinity. *Front Microbiol.* 2019;10:2791.
20. Food and Agriculture Organization (FAO). Rice Market Monitor. Rome: FAO; 2021.
21. Fatima H, Khan M, Ali S, Shah S. Microbial biotechnology for soil health and plant nutrition: advancing circular bioeconomy in agroecosystems. *Agric.* 2025;15:307.
22. Gamir J, Pastor V, Flors V. Signalling in plant immune response under heat stress. *J Exp Bot.* 2021;72:1550-64.
23. Glick BR. Bacteria with ACC deaminase can promote plant growth and help to feed the world. *Microbiol Res.* 2014;169(1):30-39.
24. Grover M, Ali SZ, Sandhya V, Rasul A, Venkateswarlu B. Plant growth-promoting microbes and climate resilience in crops. *Agriculture.* 2022;12(4):485.
25. Gupta R, Mishra A. Ecological significance of weed microbiomes in sustainable agriculture: potentials and perspectives. *Rhizosphere.* 2023;26:100664.
26. Hasanuzzaman M, Nahar K, Alam MM, Roychowdhury R, Fujita M. Physiological, biochemical and molecular mechanisms of heat stress tolerance in plants. *Int J Mol Sci.* 2013;14:9643-9668.
27. Ihsan MZ, El-Nakhlawy FS, Ismail SM, Fahad S. Influence of heat stress on growth, chlorophyll content and yield traits of diverse rice genotypes. *Pak J Bot.* 2019;51:203-213.
28. IPCC. Climate Change 2021: The Physical Science Basis. Cambridge: Cambridge University Press; 2021.
29. Jagadish SVK, Bahuguna RN, Djanaguiraman M, Gamuyao R, Prasad PVV, Craufurd PQ. Impairment of pollen function under high temperature in rice. *Plant Cell Environ.* 2016;39(4):790-806.
30. Jeyanthi V, Anand P, Ravikesavan R, Naveen G. Plant growth-promoting rhizobacteria (PGPR): Prospective and mechanisms - a review. *Int J Microbiol Res.* 2019;10:98-110.
31. Kanchiswamy CN, Malnoy M, Maffei ME. Biological diversity of microbial volatiles and their roles in plant abiotic stress tolerance. *Front Plant Sci.* 2015;6:774.
32. Kang SM, Radhakrishnan R, You YH, Joo GJ, Lee IJ. Thermotolerant *Bacillus* strains improve rice growth under heat stress. *Plant Physiol Biochem.* 2021;162:10-20.
33. Khan MA, Asaf S, Khan AL, Jan R, Kang SM, Kim KM, Lee IJ. Thermotolerance effect of plant growth-promoting *Bacillus cereus* SA1 on soybean during heat stress. *BMC Microbiol.* 2020;20:175.
34. Kumar A, Verma R, Sharma P. Phosphate-solubilizing and nitrogen-fixing bacteria associated with paddy-field weeds and their PGP potential. *Arch Microbiol.* 2022;204(5):287-298.
35. Kumari S, Singh P, Tripathi R. Bacterial endophytes for heat stress mitigation in rice seedlings. *Plant Stress.* 2022;3:100060.
36. Leontidou K, Genitsaris S, Papadopoulou A, Kamou N, Matsi T, Madesis P, Vokou D, Mellidou I. Plant growth-promoting rhizobacteria isolated from halophytes and drought-tolerant plants: genomic characterization and exploration of phyto-beneficial traits. *Sci Rep.* 2020;10:14857.
37. Li Y, Wang M, Xu J, Li J, Shen Q. Metagenomic insights into functional gene diversity in the rhizosphere of weeds from rice agro-ecosystems. *Soil Biol Biochem.* 2021;157:108243.
38. Ma Y, Oliveira RS, Freitas H, Zhang C. Metal-resistant bacteria promote plant growth in contaminated soils. *J Hazard Mater.* 2016;301:451-460.
39. Navarro-Torre S, Barcia-Piedras JM, Pérez MM, García G, Rodríguez-Llorente ID, Caviedes MA. Two new endophytic species of *Kushneria* isolated from the halophyte *Arthrocnemum macrostachyum*. *Int J Syst Evol Microbiol.* 2018;68(7):2204-2213.
40. Numan M, Bashir S, Khan Y, Mumtaz R, Shinwari ZK, Khan AL, Khan A, Al-Harrasi A. Plant growth-promoting bacteria: mechanisms and applications in sustainable agriculture. *Front Microbiol.* 2018;9:2143.
41. Panwar M, Tewari R, Nayyar H. Drought-tolerant *Bacillus aryabhattai* from *Cyperus rotundus* improves plant stress resilience. *Ecol Eng.* 2016;91:431-436.
42. Qaisrani MM, Zaheer A, Abbas T, Nadeem SM, Kiran S. Weed rhizosphere-associated bacteria: potential bioresource for enhancing crop productivity under stress conditions. *Appl Soil Ecol.* 2019;136:10-18.
43. Rajkumar M, Ae N, Prasad MNV, Freitas H. PGPR-assisted phytoremediation of metal-contaminated soils. *Biotechnol Adv.* 2010;28:190-199.

44. Reddy PS, Jageswar G, Rasineni GK. ABA and SA interplay in plant abiotic stress tolerance. *Plant Cell Rep.* 2010;29:853-866.
45. Saeed Q, Wang X, Haider FU, Kučerik J, Mumtaz MZ, Holatko J, Naseem M, Kintl A, Ejaz M, Naveed M. Rhizosphere bacteria in plant growth promotion, biocontrol and remediation of contaminated sites: a comprehensive review. *Int J Mol Sci.* 2021;22(19):10529.
46. Saha M, Sarkar S, Barik AJ. Siderophore-mediated iron acquisition in stress tolerance. *J Plant Nutr.* 2016;39:1250-1260.
47. Saijo Y, Loo EP, Yasuda M. Plant immune priming under environmental stress. *Nat Plants.* 2020;6:650-60.
48. Sandhya V, Ali SZ, Grover M, Reddy G, Venkateswarlu B. Drought-tolerant bacteria enhance maize growth. *Appl Soil Ecol.* 2010;46:54-60.
49. Sanjenbam P, Das B, Devi N, *et al.* Impact of phyllosphere *Methylobacterium* on host rice landraces. *Microbiol Spectr.* 2022;10:e00810-22.
50. Sarathambal C, Ramesh K, Selvarajan R, Manoharan K, Balakrishnan S. A review on weeds as source of novel plant-growth-promoting microorganisms. *Biocatal Agric Biotechnol.* 2014;3(4):408-416.
51. Silva TF, Vieira JM, Baldani VLD. Biological nitrogen fixation and PGPR: contributions to sustainable rice production. *Appl Soil Ecol.* 2023;185:104735.
52. Singh RP, Pandey DM, Jha PN, Ma Y. ACC deaminase-producing rhizobacterium *Enterobacter cloacae* ZNP-4 enhances abiotic stress tolerance in wheat. *PLoS One.* 2022;17(5):e0267127.
53. Subramanian P, Kim K, Krishnamoorthy R, Mageswari A, Sundaram S. Cold-tolerant PGPR improve plant performance under chilling. *Sci Rep.* 2016;6:19773.
54. Sukumar P, Legué V, Vayssières A. Plant-microbe interactions under abiotic stress: ecological pressures and microbial adaptation. *Front Plant Sci.* 2016;7:1123.
55. Suman J, Kumar R, Bhattacharyya P, Sharma R. Microbiome as a key player in sustainable agriculture and circular bioeconomy: role in nutrient cycling and organic residue valorization. *Front Soil Sci.* 2022;2:821589.
56. Vacheron J, Renoud S, Ballini E. PGPR-mediated root system modulation. *Front Plant Sci.* 2013;4:356-3570.
57. Vurukonda SSKP, Vardharajula S, Shrivastava M, Ali SZ. PGPR for drought stress mitigation in crops. *Microbiol Res.* 2016;184:13-24.
58. Wahid A, Gelani S, Ashraf M, Foolad MR. Heat tolerance in plants: an overview. *Environ Exp Bot.* 2007;61:199-223.
59. White JF, Kingsley DH, Sattely ES, Tsolowaki K, Schardl CL. Endophytic microbes and their potential applications in crop systems. *Pest Manag Sci.* 2019;75(12):3245-3255.
60. Xiong H, Li J, Liu P, *et al.* Rice anaerobic germination and adaptive pathways. *Plant Physiol.* 2017;175:1653-66.
61. Zhang X, Li J, Liu T, *et al.* Microbial inoculation enhances cold tolerance in plants. *Appl Soil Ecol.* 2020;148:103480.
62. Zhao C, Liu B, Piao S, Wang X, Lobell DB, Huang Y, *et al.* Temperature increase reduces global yields of major crops in four independent estimates. *Proc Natl Acad Sci USA.* 2017;114:9326-9331.