

PLANT GROWTH-PROMOTING BACTERIA FOR ENHANCING GROWTH, NUTRIENT USE AND RESILIENCE IN TEA (*CAMELLIA SINENSIS*)

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ABSTRACT

Tea (*Camellia sinensis* (L.) O. Kuntze) is an economically important perennial crop whose productivity and long-term performance depend strongly on successful plant establishment and efficient nutrient acquisition, particularly during the nursery stage. Tea is predominantly cultivated in acidic soils where phosphorus and potassium availability are restricted and where intensive use of chemical fertilizers can contribute to soil acidification, nutrient losses and deterioration of soil health. Plant growth-promoting microorganisms associated with the tea rhizosphere, phyllosphere and endosphere offer an important biological resource for improving plant growth, nutrient availability and stress tolerance. This review summarizes the current understanding of tea-associated beneficial microorganisms, with particular emphasis on biological nitrogen fixation, phosphate, potassium, zinc and silicate solubilisation, indole-3-acetic acid and siderophore production, ACC deaminase activity, biofilm and exopolysaccharide formation, and tolerance to acidic, saline and osmotic stresses. The review further examines the role of compatible microbial consortia in enhancing root development, seedling establishment, nutrient acquisition, and plant defence, together with their potential to reduce chemical fertilizer requirements. Particular attention is given to the complementary functions of nitrogen-fixing bacteria, phosphate-solubilizing bacteria, and potassium-releasing bacteria as candidate components of a tea-adapted microbial consortium. Existing studies indicate that consortium-based inoculation can improve tea growth and nutrient-use efficiency and may facilitate partial replacement of chemical fertilizers. However, relatively few studies have developed microbial consortia specifically for tea nursery establishment using functionally complementary and mutually compatible indigenous microorganisms. Important gaps also remain concerning strain compatibility, acid tolerance, formulation stability, shelf life, fertiliser dose optimization and field-scale validation. Developing stable, tea-adapted microbial consortia therefore represents a promising strategy for improving seedling establishment, nutrient-use efficiency and the sustainability of tea production.

KEYWORDS: *Camellia sinensis*; plant growth-promoting microorganisms; microbial consortium; nutrient-use efficiency; tea seedling establishment.

INTRODUCTION

Tea (*Camellia sinensis* (L.) O. Kuntze) is among the most economically and culturally important plantation crops of the world. Commercial tea is propagated vegetatively and remains in production for several decades, so the vigour of the root system during the earliest nursery stages largely determines later field establishment and plantation performance (Manivel et al., 2021; Iqbal et al., 2015). Seedling losses and poor early growth in the nursery cannot be corrected later, which makes this stage a critical point for intervention. Tea is cultivated almost exclusively on acidic soils that are frequently deficient in available phosphorus, potassium and micronutrients. Nursery seedlings commonly experience nutrient stress before visible deficiency symptoms appear (Balamurugan et al., 2013). Heavy reliance on chemical fertilizers to offset this stress raises production costs. Long-term intensive fertilisation has also been linked to soil acidification, decline in microbial biomass and functional diversity, and nutrient run-off (Kong et al., 2008; Ampofo et al., 2009). Sustainable alternatives that improve nutrient availability and seedling vigour while reducing fertiliser dependence are therefore urgently needed.

Plant growth-promoting rhizobacteria (PGPR) are now recognised as key components of biofertiliser and biostimulant technology (Sattiraju et al., 2017; Tripathi et al., 2026). They promote plant growth directly through biological nitrogen fixation, solubilisation of phosphorus, potassium, zinc and silicate, and production of indole-3-acetic acid, siderophores and ACC deaminase. They also act indirectly by suppressing pathogens and inducing systemic resistance (Hazarika et

al., 2021; Gore et al., 2025). In tea, bacterial isolates with these traits have been extensively characterised (Borah et al., 2019; Kabir et al., 2023). Plant growth-promoting fungi, endophytes and phyllosphere microorganisms are also known to occur in tea and to contribute to plant health. Combining compatible PGPR strains with complementary functions into consortia offers more consistent benefits than single-strain inoculants (Gehlot et al., 2021; Folorunso et al., 2026). In tea, rhizobacterial consortia and soil series-specific PGPR formulations have improved growth and allowed partial replacement of chemical fertilizers (Dutta and Thakur, 2017; Tennakoon et al., 2019; Deshappriya et al., 2019; Sorongpong et al., 2025).

Despite this progress, a critical gap remains. Most tea studies have evaluated single strains, or consortia assembled from isolates originally selected for other purposes. Very few consortia have been designed specifically for nursery-stage establishment, where nutrient demand and root development are most limiting (Dutta and Thakur, 2017; Sorongpong et al., 2025). Evidence on strain compatibility, acid tolerance, formulation stability and shelf life, and on optimum fertiliser dose in combination with inoculants, is scattered across crops and regions (Malusá et al., 2012; Goswami et al., 2017; Ding et al., 2021).

Although diverse microorganisms are associated with the rhizosphere, phyllosphere and endosphere of tea, increasing attention has been directed towards plant growth-promoting rhizobacteria because of their potential to directly influence root development, nutrient acquisition and overall plant performance. However, the available literature on PGPR in tea remains fragmented, with individual studies predominantly addressing specific bacterial strains or isolated plant growth-promoting traits rather than integrating their functional mechanisms with measurable improvements in tea growth. In particular, the contribution of PGPR to the early establishment and development of tea seedlings, including root proliferation, biomass production and nutrient acquisition, has received comparatively limited systematic consideration, despite the importance of the nursery stage for subsequent field establishment and productivity of this perennial crop. Moreover, the relationship between individual PGPR functions including biological nitrogen fixation, phosphorus and potassium mobilization, micronutrient solubilization, phytohormone production, siderophore synthesis, ACC deaminase activity, and exopolysaccharide and biofilm formation and their physiological consequences in tea remain insufficiently synthesized. Information is also limited regarding the selection of functionally efficient tea-associated PGPR, their adaptation to the acidic soil conditions characteristic of tea-growing regions, and the consistency of their effects across nursery and field environments. Therefore, a critical synthesis is required to connect the functional attributes of PGPR with their actual contributions to tea growth and nutrient-use efficiency. Accordingly, this review focuses specifically on PGPR associated with *Camellia sinensis*, with emphasis on their diversity, plant growth-promoting mechanisms, effects on seedling establishment and plant growth, contributions to nutrient availability and uptake, and potential to improve plant resilience under relevant environmental constraints. The review further evaluates current approaches for PGPR selection, inoculation and application in tea, identifies limitations in existing experimental evidence, and highlights key research priorities needed for the development of effective and reproducible PGPR-based strategies for sustainable tea production.

Tea

The tea plant (Theaceae), is believed to have evolved in the region encompassing the eastern Himalayas, south-western China and northern Myanmar. Because the species has been cultivated and moved by humans for thousands of years, its precise centre of origin is difficult to reconstruct (Meegahakumbura et al., 2016). Molecular studies indicate three genetically distinct lineages, namely China-type tea and two independently domesticated Assam-type lineages (Meegahakumbura et al., 2018). Cultivation has since spread to more than fifty countries with warm, humid climates and well-drained, acidic soils (Wambulwa et al., 2021). Tea is a labour-intensive plantation crop of major economic and social importance, supporting rural livelihoods, export earnings and regional development, particularly in Tamil Nadu (Premkumar et al., 2025). Global production in 2025 is estimated at about 7.3 million tonnes (FAO, 2026), and the global tea market is projected to reach USD 73.78 billion by 2030 (FAO, 2026; International Tea Committee, 2025). The Indian industry directly employs about 1.16 million workers in the organised sector, nearly 58% of them women (Tea Board of India, 2025). India is the world's second-largest tea producer. Commercial cultivation began in Assam in the 1820s, and tea now covers about 6.19 lakh hectares, mainly in Assam, West Bengal, Tamil Nadu, Kerala and Karnataka (Gupta et al., 2025). Assam accounts for nearly half of national output, and Darjeeling holds a Geographical Indication tag for its orthodox tea (Kumbasaroglu et al., 2026). South India, led by the Nilgiris, contributes about 15–17% of national production from high-elevation plantations, and the sector is regulated and promoted by the Tea Board of India under the Tea Act of 1953 (Mahapatra et al., 2020). The industry faces competition from other producers, fluctuating prices and labour-related problems, while moving increasingly towards organic and sustainable practices (Nair et al., 2023).

Plant Growth-Promoting Microorganisms

Plant growth-promoting microorganisms (PGPM) constitute a functionally defined group of rhizospheric or phyllospheric bacteria and fungi that colonise the vicinity of plant tissues and confer measurable growth benefits on the host, either by improving nutrient availability, modulating hormonal balance, or protecting the plant against biotic and abiotic stress (Sattiraju et al., 2017). The term is most commonly applied to plant growth-promoting rhizobacteria, a designation originally coined for free-living soil bacteria capable of aggressively colonising plant root systems and enhancing plant growth (Neuhoff et al., 2024). PGPM are now regarded as key components of biofertiliser and biostimulant technology, offering a more environmentally sustainable alternative to synthetic fertilizers and agrochemicals across a wide range of cropping systems (Tripathi et al., 2026).

Direct mechanisms

PGPM promote plant growth directly by improving the availability of essential nutrients and by synthesising plant growth regulators that act on host physiology without the involvement of a third organism. Plant growth-promoting microorganisms, including those associated with tea, promote plant growth directly through several mechanisms. These include fixing atmospheric nitrogen and releasing ammonia, and converting insoluble or bound forms of phosphorus, potassium, zinc and silicon in the soil into plant-available forms. They also synthesise the phytohormones indole-3-acetic acid (IAA) and gibberellic acid (GA3), and secrete siderophores that chelate iron when it is scarce. In addition, many produce the enzyme 1-aminocyclopropane-1-carboxylate (ACC) deaminase, which breaks down the ethylene precursor ACC and so reduces stress-induced ethylene in the host plant (Hazarika et al., 2021; Jia et al., 2023).

Indirect mechanisms

The indirect benefits come from keeping pathogens and other harmful microbes in check, which lets the host plant grow closer to its full potential without diverting resources to fight disease. These mechanisms include the production of antibiotics, hydrolytic enzymes such as chitinases, proteases, and cellulases that degrade fungal cell walls, hydrogen cyanide, and induction of systemic resistance (ISR) through activation of host jasmonic acid and salicylic acid signalling pathways (Gore et al., 2025). Rhizosphere isolates of *Bacillus* and *Streptomyces* from tea can inhibit important pathogens, including *Fusarium oxysporum*, *Exobasidium vexans* and *Colletotrichum gloeosporioides*. They do this in three ways: producing antimicrobial compounds, occupying root surfaces by forming biofilms ahead of the pathogens, and raising the plant's defence enzymes linked to systemic resistance, namely peroxidase, polyphenol oxidase and phenylalanine ammonia-lyase (Wu et al., 2024; Hazarika et al., 2022). Figure 1 illustrates how the tea microbiome promotes plant growth.

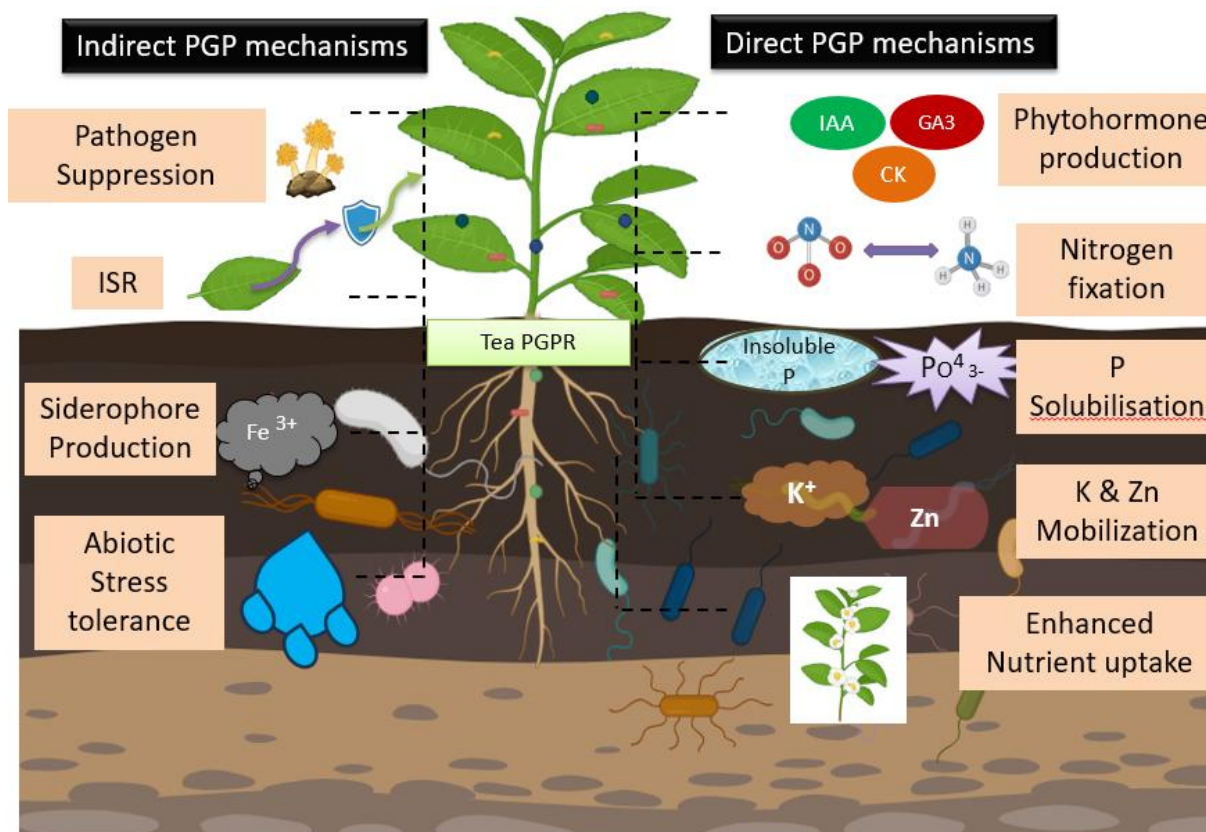


Figure 1: Schematic representation of direct and indirect plant growth-promoting (PGP) mechanisms mediated by Tea Plant Growth-Promoting Rhizobacteria (PGPR)

PGPR: Plant Growth-Promoting Rhizobacteria; ISR: Induced Systemic Resistance; IAA: Indole-3-acetic acid; GA3: Gibberellic acid; CK: Cytokinin; P: Phosphorus (PO_4^{3-}); K: Potassium (K^+); Zn: Zinc; Fe^{3+} : Iron/Ferric ion. Direct mechanisms promote growth via nutrient bioavailability and hormonal stimulation, whereas indirect mechanisms protect the host plant against phytopathogens and environmental stresses

PGPM in tea cultivation

A substantial and growing body of tea-specific literature has characterised PGPM across rhizosphere isolates and phyllosphere colonisers, with the majority of reported taxa drawn from the genera *Bacillus*, *Pseudomonas*, *Streptomyces*, *Burkholderia*, *Herbaspirillum*, and *Methylobacterium* (Kabir et al., 2023; Hazarika et al., 2021; Borah et al., 2019). These isolates have been demonstrated to promote tea growth through mechanisms including biological nitrogen fixation, phosphate and potassium solubilisation, biosynthesis of IAA and ACC deaminase, and biocontrol of major tea fungal pathogens; furthermore, their formulation into rhizobacterial consortia capable of substituting for a portion of chemical fertiliser input in tea has already been validated at both pot and field scale (Sorongpong et al., 2025).

Plant Growth-Promoting Traits of Beneficial Microorganisms

Nitrogen fixation

Diazotrophic bacteria carry the nitrogenase enzyme complex, which converts atmospheric dinitrogen (N₂) into ammonia. This works best where oxygen is scarce, as it typically is close to the roots, and the ammonia released adds directly to the nitrogen available to the host plant. Among tea-associated rhizobacteria, genera such as *Bacillus*, *Pseudomonas*, and *Alcaligenes* have been widely reported to exhibit ammonia production and nitrogenase activity, with rhizosphere-derived isolates displaying robust expression of nitrogen-related traits consistent with the root-soil interface favouring active nitrogen transformation (Puri et al., 2018). Whole-genome analysis of plant-associated isolates such as *Erwinia aphidicola* shows that they carry the nitrogen-regulatory genes *ntrB* and *ntrC* but lack the *nif* gene cluster that encodes nitrogenase. This indicates that growth on nitrogen-free media does not prove an isolate is a true nitrogen fixer, so genomic confirmation remains important in these studies.

Phosphate solubilisation

Phosphate-solubilising bacteria and fungi convert fixed, plant-unavailable forms of soil phosphorus into soluble orthophosphate through the secretion of organic acids that chelate phosphate-bound cations, and through the production of phosphatase and phytase enzymes that hydrolyse organic phosphorus compounds (Onlamun et al., 2023). Among tea-associated microorganisms, *Bacillus altitudinis* and *Bacillus safensis* have shown particularly strong phosphate-solubilising activity, while fungal strains of *Penicillium sclerotiorum* have demonstrated comparably consistent solubilisation capacity, with the extent of solubilisation varying between strains of the same genus depending on the specific organic acids and enzymes produced (Kabir et al., 2023; Nath et al., 2015).

Potassium solubilisation

Potassium-solubilising microorganisms release the macronutrient potassium from mineral-bound forms through the secretion of organic acids such as citric and oxalic acid, which chelate and progressively convert mineral-bound potassium into soluble ionic forms, a process that has been shown to proceed gradually and consistently over the incubation period rather than instantaneously (Pandey and Saharan, 2025). Additional exopolysaccharide secretion by these organisms is thought to retain organic acids in close proximity to mineral surfaces, sustaining a locally acidic microenvironment that accelerates dissolution, while specific enzymes such as silicase further target silicate bonds within aluminosilicate minerals to co-release potassium and silica (Manimaran et al., 2025).

Zinc solubilisation

Zinc solubilisation by beneficial microorganisms proceeds mainly through the secretion of organic acids, including gluconic, citric, and oxalic acid, which lower the local pH and thereby favour dissolution of insoluble zinc salts, supplemented in some organisms by the production of zincophore-type chelating agents that bind zinc directly and release it in a soluble, chelated form (Jaivel et al., 2017; Mostafazade et al., 2024).

Silicate solubilisation

Silicate-solubilising bacteria (SSB) convert insoluble aluminosilicate minerals into orthosilicic acid, the soluble form of silicon that can be readily absorbed by plant roots, primarily through the secretion of organic acids and the enzyme silicase (Cruz et al., 2022). Silicon nutrition assumes particular importance for perennial crops grown under mineral and abiotic stress, since it is incorporated into cell walls and physiological signalling pathways that confer tolerance to drought, heat, and pathogen attack, and inoculation with combined silicate-solubilising and plant-growth-promoting bacteria has been shown to enhance heat-stress tolerance and Si-transporter gene expression in crop seedlings (Chaganti et al., 2023). Genera such as *Bacillus*, *Enterobacter*, and *Pseudomonas* have most frequently been identified among silicate-solubilising isolates recovered from agricultural soils, several of which simultaneously possess other plant-growth-promoting traits such as ACC deaminase and IAA production (Barbaccia et al., 2022).

Indole-3-acetic acid production

Indole-3-acetic acid (IAA) is the main auxin made by microbes living in association with plants. It is usually produced through the tryptophan-dependent indole-3-pyruvic acid pathway, and in the host, it controls cell elongation, root initiation and lateral root branching (Jia et al., 2023; Gravel et al., 2007). Among bacterial isolates from tea, *Ochrobactrum* sp. and *Stenotrophomonas* sp. have been reported to be especially strong IAA producers (Hazarika et al., 2021; Sandri et al., 2024).

ACC deaminase activity

1-Aminocyclopropane-1-carboxylate deaminase-producing bacteria hydrolyse ACC, the immediate biosynthetic precursor of the stress hormone ethylene, into α -ketobutyrate and ammonia, thereby lowering the ethylene burst that would otherwise be triggered in the host plant under drought, salinity or nutrient stress and that would inhibit root elongation and accelerate senescence if left unchecked (Gamalero and Glick, 2015). By intercepting this pathway before ACC oxidase can convert it to ethylene, ACC deaminase-producing bacteria allow improved root system architecture, reduced oxidative damage, and sustained photosynthetic activity under stress, while simultaneously facilitating their own colonisation by dampening the ethylene-mediated host immune response that would otherwise restrict microbial establishment (Indiragandhi et al., 2008). Several salt-tolerant tea rhizosphere isolates, including *Herbaspirillum aquaticum* and *Burkholderia pyrrocinia*, have demonstrated ACC deaminase activity together with measurable improvement of tea plant growth under saline conditions (Wang et al., 2022).

Siderophore production

Plant-associated bacteria respond to iron limitation by releasing siderophores, which are compact, high-affinity iron chelators synthesised through either the NRPS or the NIS pathway. By solubilising ferric iron, these compounds make it available to the host plant. (Carroll and Moore, 2018; Garg et al., 2021). Among tea-associated PGPR, *Bacillus altitudinis*, *Priestia megaterium*, *Microbacterium testaceum* and *Neobacillus niacini* have been identified as siderophore

producers, with quantitative screening identifying *Bacillus* sp. and *Brevundimonas* sp. isolates as particularly strong producers (Kabir et al., 2023; Hazarika et al., 2021).

Hydrolytic enzyme production

Many plant growth-promoting microorganisms secrete extracellular hydrolytic enzymes such as cellulase, protease, amylase and chitinase that serve a dual function, facilitating active colonisation of internal plant tissue through partial degradation of plant and fungal cell-wall components while simultaneously contributing to biocontrol by lysing the cell walls of co-occurring fungal pathogens (Hazarika et al., 2022). In tea, chitinase-producing endophytic actinobacteria have been shown to suppress spore germination of the major tea pathogens *Exobasidium vexans* and *Fusarium oxysporum*, while also contributing to organic nitrogen mineralisation and release of simple sugars that improve nutrient availability to the host (Kabir et al., 2023; Wu et al., 2024).

Biofilm formation

Bacteria form biofilms when their cells become enclosed in an extracellular polymeric matrix that they produce themselves and that anchors them to root or leaf surfaces. This trait is important because it helps the bacteria colonise the rhizosphere, survive there for longer, and withstand environmental changes and competition from other microbes. Screening of rhizobacterial isolates for biofilm formation using crystal-violet and optical-density assays has demonstrated that strong biofilm formers, generally *Bacillus* and *Pseudomonas* species, also tend to be efficient auxin producers and provide superior growth promotion under field conditions (Rafique et al., 2024). In tea specifically, *Streptomyces* strains selected for biofilm-forming ability, confirmed through confocal laser scanning microscopy and crystal-violet staining, significantly enhanced shoot and root biomass, shoot and root length, and leaf number when tested under nursery conditions, directly demonstrating the relevance of biofilm formation to nursery-stage tea seedling establishment (Hazarika et al., 2022).

Exopolysaccharide production

Exopolysaccharides (EPS) are high-molecular-weight extracellular polymers secreted by bacteria in response to abiotic stresses, including desiccation, salinity, temperature extremes and heavy-metal exposure. They constitute the principal structural component of the biofilm matrix formed on plant root surfaces (Carezzano et al., 2023). Through their capacity to bind and retain water within the biofilm matrix, EPS-producing rhizobacteria generate a hydrated microenvironment in the immediate rhizosphere that mitigates desiccation stress, enhances root–soil contact, and confers protection to both the bacterial population and the host root system against osmotic and drought-induced stress a mechanism that has been consistently associated with improved drought tolerance in inoculated crop seedlings (Bhagat et al., 2021). Furthermore, EPS biosynthesis has been reported to be upregulated in the presence of silica nanoparticles, resulting in a corresponding enhancement of the water-holding capacity of the biofilm matrix and a measurable improvement in plant biomass accumulation under drought-stressed conditions (Bhagat et al., 2021).

Salt tolerance

Salt-tolerant Plant Growth Promoting Bacteria (PGPB) mitigate sodium-induced osmotic and ionic stress in host plants through several complementary mechanisms. These include regulating ion transport via the high-affinity potassium transporter (HKT) and Salt Overly Sensitive (SOS) pathways, which favours K⁺ over Na⁺ uptake, promoting the accumulation of compatible solutes, and producing ACC deaminase, which limits the stress-induced rise in ethylene (Egamberdieva et al., 2019; Gao et al., 2022).

Acid tolerance

Tea is grown almost exclusively on strongly acidic soils, generally with a pH between 3.8 and 5.5. Both the native and the inoculated microbial populations in these soils must therefore tolerate acidity if they are to survive, colonise roots and remain functionally active. Acidophilic and acid-tolerant bacteria maintain a near-neutral cytoplasmic pH despite a steep external proton gradient through a combination of active proton-efflux systems, reversal of the transmembrane electrical potential, and adjustments to membrane composition, alongside passive DNA- and protein-repair mechanisms (Goswami et al., 2017). Tea garden soils from Assam were found to harbour 70 acid-tolerant bacterial isolates from five genera (*Bacillus*, *Lysinibacillus*, *Brevundimonas*, *Alcaligenes* and *Enterobacter*). Under acidic assay conditions resembling those of tea soils, 47 isolates continued to produce IAA and siderophores and to solubilise phosphate, zinc and potassium, which supports acid tolerance as an essential trait for selecting PGPB for tea (Ding et al., 2021).

Proline accumulation under stress

Proline is among the most widely studied compatible osmolytes accumulated by both plants and their associated bacteria under drought, salinity and other osmotic stresses, functioning to lower cellular osmotic potential, stabilise membranes and proteins, and scavenge reactive oxygen species without disrupting normal cellular metabolism (Egamberdieva et al., 2019). Inoculation with proline-accumulating and proline-inducing PGPR has been repeatedly shown to elevate host tissue proline content under stress relative to uninoculated controls; for instance, inoculation of canola with the halotolerant strain *Enterobacter cloacae* HSNJ4 significantly increased proline content while decreasing malondialdehyde, a marker of oxidative membrane damage, under saline conditions (Li et al., 2025). Endophytic bacteria isolated from tea have similarly been implicated in facilitating osmotic adjustment in the host through the regulation of compatible solutes including proline, glycine betaine, trehalose and soluble sugars under saline and drought conditions, linking these traits directly to the broader abiotic-stress-alleviation functions (Omomowo and Babalola, 2019).

Trehalose accumulation under stress

Trehalose, a non-reducing disaccharide of glucose, functions as a compatible solute in both plants and their associated bacteria, conferring desiccation and salinity tolerance by stabilising membranes and macromolecular structures under osmotic stress, in a manner analogous to but biochemically distinct from proline (Al-Turki et al., 2023). Trehalose acts not only as a passive osmoprotectant but also as a signalling metabolite that primes stress-responsive gene expression in

the host, and even very small amounts translocated from inoculated roots can activate downstream tolerance pathways. Evidence for this regulatory role comes from legume-rhizobia symbioses, in which nodules formed by strains overexpressing trehalose-6-phosphate synthase showed strong upregulation of genes involved in stress tolerance and carbon-nitrogen metabolism. This suggests that bacterial trehalose has a regulatory function rather than a purely osmotic one (Suárez et al., 2008). Similar results were obtained in maize inoculated with an *Azospirillum brasilense* strain engineered for increased trehalose biosynthesis, which showed improved drought tolerance and significantly greater biomass than plants inoculated with the wild-type strain (Rodríguez-Salazar et al., 2009). In addition to its role within the host, trehalose accumulation is important for the bacterium itself, enhancing the desiccation tolerance and post-inoculation survival of PGPR strains during commercial formulation and extended storage, a property with direct relevance to the shelf-life and field viability of bacterial inoculants (Al-Turki et al., 2023).

Glycine betaine accumulation under stress

Glycine betaine (GB) is a zwitterionic, highly water-soluble quaternary ammonium compound that accumulates in the cytoplasm and organelles of stressed plants and bacteria, where it maintains osmotic balance, protects the photosynthetic apparatus, and stabilises the quaternary structure of proteins and membrane complexes without interfering with normal cellular biochemistry (Al-Turki et al., 2023). In plants, glycine betaine is produced by a two-step oxidation of choline, catalysed first by choline monooxygenase and then by betaine aldehyde dehydrogenase. Its build-up under stress is closely linked to how the genes encoding these biosynthetic enzymes are regulated. PGPR inoculation has been repeatedly shown to enhance endogenous GB accumulation in host tissue under both drought and salinity stress: maize and rice plants treated with *Bacillus subtilis* and *Pseudomonas* spp. accumulated significantly higher GB content than uninoculated controls under drought conditions, correlating with reduced water loss and improved stress tolerance (Sandhya et al., 2010). Under salinity stress, inoculation of maize with the halotolerant strain *Enterobacter cloacae* PM23 similarly elevated glycine betaine and proline content alongside other compatible solutes, while simultaneously enhancing antioxidant enzyme activity and reducing oxidative stress markers, illustrating the coordinated deployment of multiple osmolytes as part of a broader PGPR-induced stress-tolerance response (Kumar et al., 2021). Collectively, these findings identify glycine betaine, along with proline and trehalose, as a major compatible solute through which PGPR-mediated osmotic adjustment helps alleviate stress in the host. They also strengthen the case for including osmolyte-modulating strains in microbial consortia designed to mitigate stress in perennial crops such as tea.

Development of Microbial Consortia

Concept of microbial consortium

A microbial consortium is broadly defined as a rationally assembled combination of two or more compatible microbial strains, formulated to act synergistically and thereby deliver a broader or more consistent spectrum of plant growth-promoting or biocontrol benefits than could be achieved by any single strain applied in isolation (Gehlot et al., 2021). Inoculation with a single strain often gives only partial or unstable results under field conditions, and the outcome depends heavily on the environment. Well-designed synthetic communities (SynComs), by comparison, have repeatedly achieved stronger and more consistent functional performance. For instance, a four-strain consortium reconstructed from disease-suppressive soils successfully controlled bacterial wilt in tomato, despite none of its four constituent strains conferring any protective effect when tested individually; similarly, a multi-strain maize SynCom enhanced root development more reliably than any of its individual component isolates (Folorunso et al., 2026).

Selection of compatible bacterial isolates

Compatibility screening constitutes a critical and non-negotiable first step in consortium development, as candidate strains must be verified as mutually non-antagonistic prior to combination most commonly through in vitro cross-streak or dual-culture assays on agar media, in which the absence of a zone of growth inhibition between paired isolates is taken as evidence of compatibility (Tsalgatidou et al., 2023). Beyond simple non-antagonism, functional compatibility wherein strains occupy complementary rather than directly overlapping ecological or trait niches is increasingly emphasised as a design principle, since strains competing for an identical resource or niche are less likely to persist together stably than those that are functionally complementary (Jia et al., 2026). A four-strain rhizobacterial consortium selected for tea nursery application, for instance, was formulated on the basis of complementary plant-growth-promoting traits together with confirmed mutual compatibility, its efficacy subsequently validated through nursery trials conducted on two tea cultivars (Dutta and Thakur, 2017).

Consortium formulation

Once compatible strains have been identified, they must be formulated into a stable inoculant product capable of maintaining an adequate viable cell density from the point of manufacture through storage, transport, and eventual field or nursery application, generally targeting a delivery density in the order of 10^7 to 10^8 colony-forming units per millilitre or gram of formulation (cfu/g) (Bashan et al., 2014). The two broad formulation strategies, carrier-based (solid) and liquid formulations, involve fundamentally different approaches to protecting and sustaining the viability of the constituent strains, and are discussed separately below, while emerging approaches such as alginate encapsulation and biofilm-based inoculant technology aim to combine the advantages of both while offering additional protection against desiccation and environmental stress during storage and application (Malusá et al., 2012).

Carrier-based formulations

Carrier-based (solid) biofertiliser formulations use finely powdered or granular organic or inorganic carrier materials, most commonly lignite, peat, charcoal, vermicompost or talc, as a physical matrix in which the microbial inoculant is mixed, packaged and distributed, offering the advantages of low production cost, ease of handling, and simple field or nursery application by direct mixing with soil or potting medium (Tabassam et al., 2015). However, carrier-based formulations characteristically show a progressive decline in viable microbial population from the time of manufacture,

and are prone to significant contamination and quality deterioration after three to four months of storage, particularly under ambient, non-refrigerated conditions typical of on-farm storage, which represents a persistent limitation of this otherwise economical formulation approach (Paiva et al., 2021).

Liquid formulations

Liquid biofertiliser formulations suspend the microbial inoculant in a nutrient broth or oil-in-water emulsion base amended with cell-protectant compounds such as trehalose, glycerol or polyvinylpyrrolidone, together with a suspending agent, dispersant and surfactant, and have gained increasing favour over carrier-based products because of their superior storage stability, more uniform cell distribution, and greater ease of application through standard spraying or drenching equipment (Kanishka et al., 2025). Liquid formulations supplemented with suitable cell protectants can maintain viable microbial populations for six to twelve months or more, which is considerably longer than the usual effective shelf life of three to four months for carrier-based products. However, they generally demand more advanced manufacturing infrastructure and are therefore more expensive to produce (Shravani et al., 2019; Gopi et al., 2019).

Shelf-life of microbial inoculants

The shelf life of a microbial inoculant, defined as the period over which it retains a viable cell count adequate for effective field or nursery performance, remains one of the most significant constraints on the commercial and on-farm adoption of biofertiliser technology, since poor shelf-life stewardship translates directly into unreliable performance and consequent poor uptake by growers (Gopi et al., 2019). Cell protectants such as trehalose have been shown to be particularly effective in extending shelf life; for instance, incorporation of ten millimolar trehalose into a liquid *Azospirillum brasilense* formulation sustained peak growth and multifunctional plant-growth-promoting traits for eight months, considerably longer than unamended formulations (Santhosh et al., 2015). Storage temperature is an equally important determinant of shelf life, with refrigerated storage consistently outperforming ambient room-temperature storage in maintaining viable cell counts and minimising contamination across both carrier-based and liquid formulations of *Rhizobium* and phosphate-solubilising bacteria (Kumari et al., 2022).

Influence of Microbial Consortia in Tea

Studies on microbial consortia in tea

The bulk of the literature on beneficial microbes of tea deals with isolating and characterising individual endophytes or rhizobacteria and testing them one strain at a time. Fewer studies, though an increasing number, have assessed multi-strain consortia in tea specifically. A four-isolate rhizobacterial consortium selected from indigenous Darjeeling tea-estate isolates significantly increased the growth of tea plants of two commercial cultivars, TV-1 and Teenali-17, under nursery conditions relative to uninoculated controls, directly demonstrating consortium-level benefit at the nursery stage the most relevant to the present study (Dutta and Thakur, 2017). More recently, a bacterial consortium comprising *Lysinibacillus fusiformis*, five strains of *Serratia marcescens* and two *Bacillus* sp., selected on the basis of complementary phosphate and zinc solubilisation together with ACC deaminase, IAA and siderophore production, was evaluated in both pot and field trials on two tea clones and shown to enhance growth, biomass and antioxidant activity while substantially reducing reliance on chemical fertiliser (Sorongpong et al., 2025). A separate multi-carrier trial evaluating triple-bacteria biofertiliser combinations formulated with seven different carriers on the Pazar-20 tea clone similarly demonstrated measurable improvement in seedling growth parameters, chlorophyll content and leaf yield relative to unfertilised controls (Ertürk et al., 2021).

Effect on root development

Root-development responses to microbial consortium inoculation in tea have been shown to be genotype-specific, reflecting differential recruitment of, or response to, particular bacterial taxa by different tea clones. In field trials of a rhizobacterial consortium comprising *Lysinibacillus fusiformis* and *Serratia marcescens* strains, one tea clone (S3A3) showed root-development benefits associated with enrichment of Acidobacteria and Gemmatataceae in the surrounding soil, while a second clone (TS491) instead showed predominantly shoot-growth benefits linked to Bacillota and *Bacillus* enrichment, indicating that consortium performance cannot be assumed to be uniform across tea genotypes and should ideally be validated on the specific cultivar of interest (Sorongpong et al., 2025). Consortium-mediated improvements in root architecture have also been linked mechanistically to ACC deaminase-driven suppression of stress ethylene, which otherwise inhibits root elongation, together with auxin-mediated stimulation of lateral root initiation (Gamalero and Glick, 2015; Wang et al., 2022).

Effect on seedling establishment

At the nursery stage specifically, inoculation with biofilm-forming, plant-growth-promoting actinobacteria significantly enhanced shoot and root biomass, shoot and root length, and leaf number in tea seedlings under controlled nursery conditions, and the same actinobacterial isolates additionally improved seed germination and root architecture when tested as a seed-biopriming agent in tomato, indicating a mechanism of action that is not narrowly tea-specific (Hazarika et al., 2022). Consistent with this, indigenous tea rhizobacterial consortium application under nursery conditions produced significantly greater growth than uninoculated controls across two commercial tea cultivars, directly supporting the general premise of the present investigation, that a purpose-designed multi-strain microbial consortium can improve tea seedling establishment in the nursery (Dutta and Thakur, 2017).

Effect on tea quality and yield

Beyond vegetative growth parameters, microbial consortium inoculation of tea has been shown to influence biochemical quality indicators associated with both plant defence and consumer-relevant tea quality. Field-scale application of a rhizobacterial consortium in tea significantly increased total phenolic content together with catalase, glutathione and superoxide dismutase activity relative to chemically fertilised and untreated controls, reflecting enhanced antioxidant capacity and stress resilience of the treated plants (Shang et al., 2023). Soil metagenomic analysis following consortium

application further revealed enrichment of functional genes associated with siderophore biosynthesis, nitrogen metabolism and indole-alkaloid biosynthesis, providing a mechanistic link between consortium-driven changes in soil microbial community function and downstream improvements in plant physiology and quality-related metabolite accumulation (Sorongpong et al., 2025). A consolidated overview of evaluated tea-associated rhizobacteria, detailing their specific functional traits, inoculation carriers, and recorded impacts on tea growth and fertilizer substitution, is summarized in Table 1.

Target PGPR Taxa	Isolation Source / Soil Habitat	In Vitro PGP Traits Evaluated	Evaluation System / Host Genotype	Inoculation Regime / Formulation	Key Plant & Soil Responses	Fertilizer Substitution / Stress Mitigation Potential	References
<i>Azospirillum</i> sp. combined with <i>Rhodococcus</i> sp., <i>Microbacterium</i> sp., or <i>Pseudomonas</i> sp.	Rhizosphere of mature tea plantations across contrasting soil series	Biological N ₂ fixation, phosphate solubilization, organic acid secretion	Mature tea bushes; 5 multi-location field estates representing 3 distinct soil series	Soil-series-specific liquid dual-inoculants applied as soil drenches	Significant increase in root activity; maintained green leaf yield comparable to 100% standard fertilization	Enabled a 33% reduction in chemical N and a 50% reduction in chemical P without yield penalty	Deshapriya et al. (2019); Tennakoon et al. (2019)
<i>Lysinibacillus fusiformis</i> + <i>Serratia marcescens</i> (5 strains) + <i>Bacillus</i> sp. (2 strains)	Indigenous rhizosphere soil of commercial tea estates	Mineral P-solubilization, Zn-solubilization, ACC deaminase activity, IAA synthesis, siderophore production	Nursery seedlings and field-established tea bushes (Clones TS491 and S3A3)	Multi-strain bacterial consortium; liquid culture suspension and carrier-based inoculants	Genotype-dependent root proliferation (enrichment of Acidobacteria in S3A3) and shoot biomass accumulation (Bacillota enrichment in TS491); enhanced catalase, SOD, and total phenolics	Substantial reduction in synthetic NPK input; enriched rhizosphere functional genes for siderophore and indole alkaloid biosynthesis	Sorongpong et al. (2025); Shang et al. (2023)
Four-isolate rhizobacterial consortium (<i>Bacillus</i> and allied rhizosphere genera)	Rhizosphere soil of Darjeeling tea gardens	Qualitative/quantitative phosphate solubilization, IAA excretion, ammonia production	Nursery-stage vegetative stem cuttings; commercial tea cultivars TV-1 and Teenali-17	Multi-strain liquid broth applied during nursery potting and rooting stage	Significant increases in rooting percentage, root elongation, shoot height, and total dry matter yield under nursery conditions	Accelerated nursery cutting establishment; reduced cutting mortality during vegetative propagation	Dutta and Thakur (2017)

<i>Herbaspirillum aquaticum</i> strain ZXN111	Tea rhizosphere soil from purple tea germplasm	ACC deaminase activity, IAA production, biological nitrogen fixation	Purple tea seedlings (C. sinensis var. assamica cv. 'Zijuan') under non-saline and saline conditions	Bacterial cell suspension drench (10^8 cfu/ml) applied to nursery potting substrate	Increased total chlorophyll and carotenoids; accelerated shoot and lateral root elongation; enhanced net photosynthetic rate	Alleviated salt-induced oxidative stress; suppressed stress ethylene burst via ACC deaminase	Wang et al. (2022)
<i>Bacillus altitudinis</i> P4-7, <i>Bacillus safensis</i> P5-4, and allied phosphate solubilizers	Acidic tea plantation soils (pH 4.0–5.2)	Mineral phosphate solubilisation, phosphatase secretion, low-pH organic acid production	Clonal tea seedlings and potted plants (Cultivars 'Longjing 43' and 'Huangjinya')	Single-strain and combined liquid bioinoculants applied to the root zone	Elevated available nitrogen, available phosphorus, available potassium, and bioavailable selenium (Se) in acidic rhizosphere soil	Mobilized fixed Al-P and Fe-P complexes; elevated downstream theanine, tea polyphenol, and caffeine contents	Zhang et al. (2025); Kabir et al. (2023)
<i>Streptomyces costaricanus</i> strain A-m1 and allied actinobacteria	Tea rhizosphere and root-zone soil	Hydrolytic enzyme excretion (cellulase, protease, chitinase), siderophore production	Established nursery seedlings and micro-plot plantation soils	Spore-suspension drench and enriched vermicompost-based carrier matrix	Significant upregulation of soil urease, protease, and catalase activities; augmented alkali-hydrolysable nitrogen	Suppressed soil-borne fungal pathogens; accelerated native organic matter turnover in low-pH soils	Han et al. (2025); Hazarika et al. (2022)
Triple-strain bacterial biofertilizer combinations	Rhizosphere soil of high-altitude tea plantations	Biological nitrogen fixation, mineral P and K solubilization, auxin production	Clonal nursery tea seedlings (C. sinensis cv. 'Pazar-20')	Multi-carrier formulations evaluated across 7 organic/inorganic carrier substrates	Enhanced seedling vigour index, total leaf chlorophyll content, lateral root branching, and scion survival rate	Identified optimal carrier matrices for maintaining high viable cell shelf life ($>10^8$ cfu/g) during storage	Ertürk et al. (2021)
Acid-tolerant rhizobacteria (<i>Bacillus</i> , <i>Lysinibacillus</i> , <i>Brevundimonas</i> , <i>Alcaligenes</i> , <i>Enterobacter</i>)	Strongly acidic tea garden soils (Assam, pH 3.8–4.8)	Growth and metabolic activity sustained at pH 4.0; rock P and silicate solubilisation, zinc mobilisation	Screening in low-pH liquid broth and nursery cutting rooting substrates	Liquid inoculant tailored for low-pH rhizospheric survival	Sustained root colonizing efficiency without loss of viable population density in strongly acidic soil	Overcame inoculant failure caused by native rhizosphere acidity; mobilised structural nutrients under low-pH regimes	Ding et al. (2021); Goswami et al. (2017)

Biofertilizers and Sustainable Tea Cultivation

Integrated nutrient management in tea

Integrated nutrient management in tea seeks to combine judicious use of chemical fertiliser with organic amendments and microbial biofertilizers so as to sustain yield and quality while minimising the well-documented negative consequences of long-term intensive chemical fertilisation on tea soil health. Region-specific PGPR-based biofertiliser formulations, tailored to the dominant soil series of a given tea-growing tract, have similarly been advocated as a means of partially substituting chemical fertiliser while maintaining tea yield, based on field evaluation across multiple soil series in Sri Lanka's mid-country tea belt (Tennakoon et al., 2019).

Reduction of chemical fertilizers

Field-scale evidence increasingly supports the capacity of Plant Growth Promoting Bacteria -based biofertilizers to substantially reduce, rather than merely supplement, chemical fertiliser input in tea without compromising yield. Field trials in Sri Lanka demonstrated that inoculation of mature tea with indigenous PGPR formulations enabled a significant reduction in fertiliser application while maintaining tea yield at levels comparable to full chemical fertilisation, with inoculants performing best when matched to the specific soil series from which they were originally isolated (Tennakoon et al., 2019). Comparable fertiliser-substitution benefits have been reported for a rhizobacterial consortium developed specifically for tea, which sustained plant growth and productivity indicators while reducing reliance on synthetic NPK inputs (Sorongpong et al., 2025).

Modulation of Soil Nutrient Dynamics and Plant Nutrient Uptake by Beneficial Microbial Consortia

Tea plants are predominantly cultivated in strongly acidic soils (pH 4.5–5.5) where the availability and plant uptake of essential macronutrients nitrogen (N), phosphorus (P), and potassium (K) are severely constrained by nutrient fixation, leaching, and low cation exchange capacity, necessitating high inputs of chemical fertilizers that simultaneously degrade soil microbial diversity and long-term soil health. Bacterial inoculation represents a powerful biological strategy to overcome these edaphic limitations by enhancing soil nutrient availability and improving plant nutrient acquisition efficiency through multiple direct and indirect mechanisms.

Diazotrophic endophytes and rhizobacteria from genera such as *Bacillus*, *Pseudomonas*, *Burkholderia* and *Herbaspirillum* improve nitrogen availability by biological nitrogen fixation, reducing atmospheric dinitrogen to plant-assimilable ammonium and thereby adding directly to the soil nitrogen pool. Ammonia-producing endophytes contribute further by mineralising organic nitrogen into bioavailable inorganic forms. By contrast, prolonged application of chemical nitrogen fertilizers in tea plantations has been reported to disturb soil nitrogen cycling. It stimulates nitrification by ammonia-oxidising bacteria and enhances denitrification, which causes nitrogen loss as N₂O and raises environmental risks. These effects highlight the ecological advantage of bacterial inoculants as a sustainable nitrogen source (Dincă et al., 2022; Zhang et al., 2025). Phosphorus availability in the acidic soils of tea plantations is severely restricted because phosphate is strongly fixed by iron and aluminium oxides. Phosphate-solubilising bacteria (PSB) among tea endophytes, including *Bacillus altitudinis* P4-7 and *Bacillus safensis* P5-4, release this bound phosphorus through organic acid secretion and enzymatic hydrolysis, converting insoluble phosphate into plant-available orthophosphate. In the tea cultivars Longjing and Huangjinya, inoculation with three exogenous PSB strains significantly raised available nitrogen, phosphorus, potassium and selenium in rhizosphere soil. Phosphorus and selenium availability improved consistently in both cultivars, showing that PSB inoculants enrich several soil nutrient pools at once and not phosphorus alone (Zhang et al., 2025; Wang et al., 2026).

Furthermore, the co-application of biochar with PGPR and phosphorus- and potassium-bearing minerals has emerged as a highly promising integrated strategy for improving soil P and K availability in tea plantations, with synergistic effects driven by improved soil microbial diversity, enzyme activity, and nutrient retention capacity (Islam, 2026, 2025).

Application of *Streptomyces costaricanus* strain A-m1 as a bioinoculant in tea garden soil significantly increased urease, protease, and catalase activities alongside alkali-hydrolysable nitrogen content and total microbial populations, confirming that bacterial inoculants improve soil enzyme-mediated nutrient cycling in tea plantations (Han et al., 2025). Collectively, these findings establish that bacterial inoculation enhances the availability and plant uptake of N, P, K, and micronutrients through coordinated biological and biochemical mechanisms, offering a scientifically validated foundation for reducing chemical fertilizer dependency in tea cultivation systems.

Response of Tea Seedlings to Graded Fertilizer Levels in Combination with Microbial Bioinoculant

The integration of bacterial bioinoculants with graded levels of chemical fertilizers represents one of the most economically and environmentally significant advances in sustainable tea cultivation, offering the potential to substantially reduce fertiliser input costs while maintaining or improving yield and quality. The conceptual basis for graded fertiliser bioinoculant integration rests on the principle that biologically fixed or solubilised nutrients can partially substitute for chemically supplied nutrients, enabling a dose-reduction approach that preserves plant productivity at lower economic and environmental cost.

The most direct evidence for this approach in tea comes from a field study involving dual PGPR inoculants formulated with soil series-specific strains *Azospirillum* sp. combined with *Rhodococcus* sp., *Microbacterium* sp., or *Pseudomonas* sp. depending on soil series which demonstrated that application of nitrogen-fixing and phosphate-solubilising dual inoculants permitted a 33% reduction in the recommended nitrogen dose and a 50% reduction in the recommended phosphorus dose without compromising tea yield across five field locations representing three soil series (Deshappriya et al., 2019), with indigenous strains consistently outperforming introduced strains, underscoring the critical importance of habitat-matched inoculant selection for tea systems (Prabina et al., 2024). In broader crop systems, PGPR inoculants have been demonstrated to reduce chemical fertiliser requirements by up to 25% while maintaining yield, lowering production costs, and increasing profitability, with reports of net income increases of up to 79% and significant benefit-to-cost ratio improvements in PGPR-supplemented low-fertiliser treatments compared to full-dose chemical fertiliser

controls (Shuvo et al., 2026). The co-application of bioinoculants at 75% of the recommended fertiliser dose has been shown in multiple crops to match or exceed the growth performance of 100% chemical fertiliser treatments, establishing the feasibility of at least a 25% fertiliser dose reduction across diverse agricultural systems (Hammami et al., 2024).

Fertilizer Use Reduction and Cost Optimization through Microbial Consortium Application

In tea-specific systems, the economic implications of fertiliser dose reduction are considerable. Chemical fertilizers constitute one of the largest recurrent costs in tea plantation management, and tea-growing soils characterised by low pH, high phosphate fixation, and elevated aluminium and iron concentrations require disproportionately high fertiliser applications to achieve comparable plant-available nutrient concentrations relative to neutral pH soils. Under such conditions, bacterial inoculants capable of acidifying the rhizosphere, chelating phosphate-bound cations, and producing siderophores offer a biologically targeted solution to nutrient immobilisation that chemical fertilizers cannot address mechanistically. Co-inoculation strategies employing functionally complementary strains combining nitrogen fixers, phosphate solubilisers, and potassium solubilisers have demonstrated additive or synergistic effects on plant nutrient uptake that cannot be achieved by single-strain inoculants alone, reinforcing the value of multi-strain consortia over single-inoculant approaches in complex tea cultivation systems (Biswas et al., 2024). The integration of bioinoculants with organo-mineral fertilizers (OMFs) also represents an emerging strategy for improving fertiliser use efficiency in tea under acidic highland soil conditions, with graded OMF applications at 100, 150, and 200 kg N ha⁻¹ demonstrating differential effects on N, P, and K uptake across different tea clones (Natumanya et al., 2026).

Addressing commercial scalability, key barriers to large-scale adoption of fertiliser-integrated bioinoculant programmes in tea include inoculant shelf-life and field survival, the requirement for soil-series-specific strain selection, compatibility of inoculant strains with existing agrochemical regimes, and the absence of standardised dose-response data specific to Indian and Sri Lankan tea-growing conditions. Future research should prioritise multi-location, multi-season field trials under graded fertiliser regimes with well-characterised tea-specific endophytic consortia to generate the dose-response datasets required for evidence-based fertiliser replacement recommendations in commercial tea cultivation.

Environmental benefits

Reduced reliance on chemical fertiliser in tea cultivation carries direct environmental benefits, since intensive long-term application of nitrogenous and other chemical fertilizers in tea plantations has been repeatedly linked to soil acidification, decline in microbial biomass and functional diversity, and nutrient run-off into adjacent water bodies (Kong et al., 2008; Ampofo et al., 2009). Because biofertiliser-based approaches work with, rather than against, the native tea soil microbiome, they additionally support beneficial ecosystem functions such as nutrient cycling, soil aggregate stabilisation through microbial exopolysaccharide production, and suppression of soil-borne pathogens, all of which contribute to the longer-term ecological sustainability of tea plantations beyond the immediate yield benefit (Gehlot et al., 2021).

LIMITATIONS

The current evidence base on PGPR-mediated growth promotion in tea is constrained by substantial variation in experimental design and by the predominance of short-term, controlled studies. Reported effects have been generated using diverse bacterial strains, tea genotypes, growth substrates, inoculum concentrations, nutrient regimes and experimental durations, making quantitative comparison among studies difficult. Consequently, the magnitude and reproducibility of PGPR effects across different tea-growing conditions remain uncertain. Traits such as phosphate solubilisation, potassium mobilisation, indole-3-acetic acid production, siderophore synthesis, nitrogen fixation and ACC deaminase activity provide useful indicators of microbial potential, but their detection under culture conditions does not establish their expression, contribution or importance in the tea rhizosphere. Microbial activity in planta is influenced by root-derived substrates, soil chemistry, nutrient availability, microbial competition and environmental fluctuations. Therefore, the presence of a particular functional trait cannot by itself be considered sufficient evidence of agronomic effectiveness.

The assessment of plant responses is also inconsistent among studies. Growth promotion is commonly inferred from individual parameters such as shoot length, root length or biomass, whereas simultaneous assessment of root architecture, nutrient acquisition, nutrient-use efficiency and physiological responses is less frequent. This limits the ability to distinguish direct effects of PGPR from secondary consequences of improved nutrient availability or general increases in plant biomass. In particular, evidence demonstrating that PGPR improve the efficiency with which tea plants acquire and utilise nutrients remains less extensive than evidence demonstrating simple growth enhancement. Another limitation concerns the ecological context in which PGPR are evaluated. Tea is cultivated as a long-lived perennial crop under geographically and edaphically diverse conditions, yet many investigations have been conducted under simplified environments that do not adequately represent established tea soils. The influence of indigenous microbial communities, soil physicochemical properties, cultivar-specific characteristics and seasonal environmental variation on inoculant performance is consequently insufficiently resolved. Similarly, bacterial persistence and root colonisation following inoculation are not consistently monitored, leaving uncertainty regarding whether observed plant responses result from sustained microbial activity or transient interactions. Finally, the transition from experimental efficacy to practical application remains inadequately addressed. Information on inoculation timing, application frequency, effective bacterial population density and compatibility with routine nursery and fertilizer management is inconsistent. Long-term evidence demonstrating that PGPR-mediated improvements observed during early plant growth persist under subsequent production conditions is particularly limited. These limitations collectively constrain the reliability with which currently reported PGPR effects can be generalised across tea production systems.

Research Gap and Future thrust

Future research should prioritise the transition from descriptive characterisation of PGPR towards mechanistic and agronomically validated understanding of their effects in tea. A major priority is the development of standardised, sequential screening strategies that progress from microbial identification and functional characterisation to root colonisation, plant physiological response, nutrient acquisition and agronomic performance.

Such approaches would allow microbial traits to be judged by their demonstrated effect on plant performance and not simply by their presence. Future work should also aim at quantitative validation of PGPR-mediated nutrient acquisition. Stronger evidence for gains in nutrient-use efficiency would come from experiments that measure soil nutrient availability, microbial functional activity, plant nutrient concentration, nutrient uptake and biomass production together. Where feasible, isotopic tracing and molecular techniques could help separate the direct microbial contribution to nutrient acquisition from effects arising indirectly through changes in soil or plant physiology.

Host-microbe specificity is another important direction for future research. Comparing tea cultivars, growth stages and root environments would show whether PGPR efficacy transfers broadly or depends on particular host-microbe pairings. These experiments should also include root colonisation dynamics and microbial persistence, so that effective plant responses can be linked to sustained bacterial populations.

Future studies should increasingly employ realistic tea production environments. Nursery experiments using representative substrates and management practices should be followed by transplantation and field evaluation, preferably across contrasting soil types and climatic conditions. Longitudinal experiments extending beyond the initial establishment phase would be particularly valuable for determining the persistence of PGPR-mediated effects in this perennial crop. An additional priority is the integration of PGPR with existing nutrient-management practices. Rather than evaluating microbial inoculation independently of fertilization, factorial experiments should examine bacterial inoculation across defined nutrient regimes and determine its effects on nutrient recovery, plant nutrient status, biomass production and soil fertility. This would establish whether PGPR function primarily as complementary biological inputs or whether their benefits depend strongly on external nutrient availability.

Advances in microbial genomics, metabolomics and spatially resolved approaches could further strengthen mechanistic understanding by identifying bacterial determinants of root association and plant response and by characterizing changes in the rhizosphere following inoculation. However, these technologies should be coupled with well-designed physiological and agronomic experiments so that molecular observations can be connected to measurable plant outcomes.

Finally, successful translation of PGPR research into tea production will require attention to inoculant quality and application technology. Future work should establish reproducible standards for viable cell density, formulation stability, storage, application dose and delivery method, followed by independent validation under nursery and field conditions. Multi-season and multi-location testing will be essential for distinguishing robust PGPR effects from responses that are strongly dependent on particular environmental conditions.

CONCLUSION

Plant growth-promoting rhizobacteria represent an important biological resource for improving the growth and nutritional performance of tea. The available evidence demonstrates that tea-associated PGPR possess diverse functional attributes capable of influencing nutrient availability, root development, plant growth and physiological responses. Nevertheless, the strength of the evidence varies considerably among microbial functions and experimental systems, and the presence of a growth-promoting trait does not necessarily translate into consistent benefits under plant-associated or field conditions. The current literature therefore supports the potential of PGPR in tea but does not yet justify broad generalisation of their effectiveness across cultivars, soils and production environments. Greater emphasis on mechanistic validation, quantitative assessment of nutrient acquisition, root colonisation, host-microbe interactions and long-term plant responses is required to strengthen this evidence base. Demonstrating the agronomic significance of PGPR will depend above all on connecting microbial functions to measurable gains in tea seedling establishment, nutrient-use efficiency and later plant performance. Overall, progress in PGPR research on tea will come less from identifying further bacterial isolates than from establishing reproducible links between microbial function, plant response and production outcome. Combining microbiological, molecular, physiological and agronomic approaches with rigorous validation from nursery to field can supply the evidence needed to turn PGPR from promising biological resources into dependable components of sustainable tea production.

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