



The Role of Rhizobacteria in Climate Change Mitigation: Mechanism, Application, and Future Prospect

Oyawoye O. M¹, Ayantola K. J^{1,2*}, Amubioya I. C², Abdulrozaq Gb², Fasipe D. S², Oyeleye E. A²

¹Department of Microbiology, Faculty of Life Sciences, Federal University Oye Ekiti, Nigeria

²Department of Science Laboratory Technology, Faculty of Life Sciences, Ekiti State, University, Ado Ekiti, Nigeria

*Corresponding Author

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ABSTRACT

Rhizobacteria root-associated microorganisms inhabiting the rhizosphere are increasingly recognized as key biological agents in climate change mitigation due to their multifunctional roles in soil ecosystems and plant health. This review explores the mechanisms through which rhizobacteria contribute to reducing greenhouse gas emissions and enhancing carbon sequestration. These mechanisms include biological nitrogen fixation, phytohormone production, induced systemic resistance, and the modulation of soil organic matter dynamics. Certain plant growth-promoting rhizobacteria (PGPR) enhance plant biomass and root architecture, thereby increasing carbon inputs into the soil and improving soil structure. Additionally, some rhizobacteria influence the emission of nitrous oxide (N₂O) and methane (CH₄) by regulating microbial pathways involved in nitrification, denitrification, and methanotrophy. The application of rhizobacteria in sustainable agriculture is gaining momentum through the development of biofertilizers and biostimulants that reduce reliance on chemical inputs while improving crop resilience to abiotic stresses such as drought, salinity, and temperature extremes. Field-level implementation, however, remains constrained by variability in environmental conditions, microbial survival, and host specificity. Looking forward, advances in genomics, synthetic biology, and microbiome engineering present promising avenues to enhance the efficacy and consistency of rhizobacterial applications. Integrating rhizobacteria into climate-smart agricultural practices could play a significant role in achieving global sustainability targets. Future research should focus on large-scale field validation, formulation technologies, and policy frameworks to support widespread adopt

Keywords: Greenhouse gas, biofertilisers, biostimulants, metagenomics, microbial engineering, carbon sequestration, climate change

CHAPTER ONE

INTRODUCTION

Background of the study

Climate change is broadly understood as the warming of soil and atmospheric temperatures alongside shifts in rainfall patterns, dwindling groundwater reserves, flooding from intense rainfall, and rising sea levels driven by melting ice. Amid the alarm surrounding global warming, two competing explanations are commonly put forward for this phenomenon (Tariq et al., 2023). The first attributes the recent rise in global temperatures to the release of natural greenhouse gases, principally carbon dioxide (CO₂) (Thakur et al., 2024). While CO₂ release can occur naturally, human ("anthropogenic") activity interacts constantly with the carbon cycle, since it is one of the most influential drivers of environmental change. Geological evidence shows that climate has always been in flux and remains a pressing global concern; change itself is not a new phenomenon (Wang et al., 2024). What is new is the scale of anthropogenic sources behind rising CO₂ levels — deforestation, fossil



fuel extraction, land-use change, intensive farming, breakdown of soil biology, erosion, wildfires, and the industrialization that accompanies population growth (Wang et al., 2024). These human activities have pushed CO₂ concentrations up by roughly 35 percent relative to pre-industrial levels, with wide-ranging consequences. As one of the most abundant greenhouse gases, carbon dioxide warms the planet by trapping long-wave radiation and re-directing it back to the Earth's surface (Lesk et al., 2022). The second explanation instead points to variability in solar activity as the driver of recent warming, framing it as falling within the normal range of temperature fluctuation observed over long timescales. This theory links solar influence to the sun's magnetic field and solar wind, which modulate the intensity of cosmic radiation reaching Earth and, in turn, affect low-altitude cloud cover and atmospheric water vapor — both of which help regulate climate (Ahmed et al., 2023). Global warming brings about numerous challenges that threaten both human comfort and the foundations of survival, and represents only one facet of the broader climate crisis. Related consequences include rising sea levels, ocean acidification, shrinking cryosphere features (glaciers, permafrost, and the Greenland ice sheet), altered freshwater and saltwater distribution, shifting habitat ranges, greater disease and pest pressure, degraded coral reefs, disrupted hydrological cycles, and changes to plant and animal life (Bahram et al., 2018). At its core, global warming is surface-level heating caused by greenhouse gas emissions, which raises air temperatures over extended periods; the resulting shifts in temperature and precipitation over time are what constitute climate change (Mostofa et al., 2022). Earth's atmosphere has undergone major shifts throughout history, evidenced by past ice ages, sea-level changes, and records spanning human civilization, though the causes of these earlier shifts are not always fully understood — ocean currents, solar radiation, and volcanic activity are among the natural forces most closely associated with them (Zhao et al., 2021). What sets the present apart is the unusually rapid pace of warming over recent decades. Because climate change is closely tied to agriculture and soil health — governing essential soil functions and processes that directly affect crop productivity, food security, and sustainability — this review provides an overview of climate change, its implications for soil health, and the measures available for managing agriculture under a rapidly shifting climate (Du et al., 2024).

The concept of Plant Growth-Promoting Rhizobacteria (PGPR) dates back to the 1990s as an approach for advancing agricultural science. In recent years, research in this area has matured to the point where these microorganisms are now routinely applied to stimulate plant growth and boost crop output across diverse field conditions (He et al., 2024). PGPR owe their effectiveness to their capacity to influence plant condition through both direct and indirect means. Acting as biological catalysts, these rhizobacteria alter soil chemistry to create conditions more favorable for plant growth. Certain bacterial strains act directly on plant physiology by mimicking the synthesis of key plant hormones or by improving nutrient uptake through greater nitrogen and mineral availability. A single isolate often exhibits several plant-growth-promoting traits at once, working synergistically to support growth, strengthen rooting — as seen in apple cultivation — or expand the population of beneficial soil microbes (Singh et al., 2023).

In line with its core objectives, this review examines the versatile role rhizobacteria play as a foundation for sustainable agriculture and ecological restoration. Central to this inquiry is carbon sequestration, through which these microbes help move atmospheric carbon into stable soil organic matter via root exudates and microbial biomass. In doing so, rhizobacteria offer a vital biological pathway for countering global emissions by strengthening the soil's capacity to function as a long-term carbon sink (Patel et al., 2024).

Beyond carbon storage, this study also considers the mitigation of other significant greenhouse gases. By optimizing the nitrogen cycle, particular rhizobacterial strains can meaningfully cut nitrous oxide emissions from agricultural soils, addressing a notable contributor to global warming. This microbial contribution extends into abiotic stress tolerance as well, where inoculation acts as a protective mechanism that helps crops withstand climate-driven stresses such as prolonged drought, salinity, and temperature extremes (Zeng et al., 2025).

The review further explores how rhizobacteria can reduce dependence on chemical inputs by functioning as highly effective biofertilizers. Substituting synthetic chemicals with microbial inoculants would not only help restore soil biology but also substantially lower the carbon footprint tied to industrial fertilizer manufacturing. Finally, the study examines the underlying synergistic mechanisms responsible for these benefits, including



biochemical pathways such as ACC deaminase activity and exopolysaccharide synthesis that allow these microorganisms to thrive under stress. Taken together, these functions underscore the considerable importance of rhizobacteria in mitigating climate change (Jansson et al., 2020).

Knowledge research Gap

Despite the mounting evidence that rhizobacteria are capable of plant-growth promotion, nutrient acquisition and mobilisation, drought, salinity, heat, flood-tolerance, and soil carbon and greenhouse-gas fluxes, understanding of rhizobacterial functions and specificity remains siloed within individual microbial functions and uses in agriculture (Wang & Xu, 2026; Kumar et al., 2026). Recent reviews find that PGPR-mediated plant-microbial interactions, mobilisation of nutrients, and plant drought-stress tolerance are reasonably well supported by the literature, but highly context-dependent. Most research has been limited to one or more defined mechanisms (e.g., biological nitrogen fixation, phosphate solubilisation, ACC deaminase activity, exopolysaccharide production, carbon sequestration, plant growth promotion, greenhouse-gas regulation, etc.), without synthesis and consideration of combinations. Moreover, relationships between specific rhizobacterial functions at the molecular and cellular level and climate impact metrics at the soil, plant, and ecosystem level are not well integrated. Similarly, reviews of effects of climate change on soil microbial communities reveal that microbial effects on nutrient cycling, plant-soil carbon processes and net greenhouse-gas fluxes are highly ecosystem- and environment-specific and difficult to generalise.

Additionally, substantial uncertainty exists around rhizobacterial performance in the field. Factors such as soil characteristics, crop genotype, native microbiota, temperature, moisture, salinity and other abiotic stresses all affect rhizobacterial survival and colonisation and can have varying effects on gene expression of the introduced organisms. Here, recent literature has reported competition between native microbiota, difficulty establishing rhizobia and context-dependent effects as challenges that need to be addressed to ensure consistent performance in the field (Wang & Xu, 2026). Well-designed field studies are also needed to account for the complex interactions between native microflora, the introduction of rhizobacterial inoculants and other environmental factors that have been shown to influence PGPR activity.

As with microbial traits to promote plant growth, such knowledge can translate into new formulations and techniques for the development of climate-resilient microbial inoculants, including via the use of metagenomics, functional genomics, metabolomics, (synthetic) biology, or synthetic microbial consortia. Nonetheless, these recent advancements still need to be more successfully translated into application strategies and handle reliably formulation, root colonisation, delivery, biosafety, regulatory approval and farmer uptake. Considerable advances are being made, with recent work highlighting improved formulations, encapsulation strategies, biofilm-based approaches and systematically designed synthetic microbial consortia to overcome the challenge of achieving and maintaining microbial persistence and performance in the field. Consequently, knowledge still lags in establishing links between rhizobacterial trait combinations, in planta functioning and climate-mitigation outcomes and reproducible benefits to field-scale agricultural systems.

Justification of the Review

Consequently, the severity of climate change impacts on productivity, soil quality and ecosystem health has heightened the demand for sustainable biological solutions that can address both the reduction of agriculture's environmental footprint and the enhancement of its climate resilience. Rhizobacteria are now being recognised as key players within the soil-plant interface because they affect a wide range of biological functions that influence plant growth, plant nutrient nutrition, soil organic matter dynamics, greenhouse- gas cycles, and plant resilience to biotic and abiotic stress factors. The review is thus warranted due to its focus of integrating all of these functions in the context of climate-change mitigation strategies and climate-resilient cropping systems. The authors will show how rhizobacteria may help to sequester additional carbon via mechanisms such as increased root biomass, rhizodeposition, microbial biomass and soil aggregation, and via alterations in soil nitrogen cycling and the balance of greenhouse gases (e.g., NO, CH).

A further reason for this is the current 'patchwork' of knowledge around the diverse roles of rhizobacteria. Biological nitrogen fixation, phosphate solubilisation, production of phytohormones, ACC deaminase activity,



production of exopolysaccharides, stress tolerance and regulation of greenhouse-gases are often studied as separate functions of the microbial community. Yet all these processes are 'hybrids' in the soil-plant-microbe system. It is therefore necessary to take an integrated approach to understanding how individual rhizobacterial traits combine to affect soil-crop carbon stocks, nutrient-use efficiency, climate change gases and crop yields with climate change. This focus is also of interest because a number of plant-growth promoting functions are not directly part of mitigating climate change, but instead promote climate change adaptation by improving plant tolerance to drought, heat, salinity or inundation.

The reasons for the review are threefold: one, the application in practice of rhizobacteria goes well beyond the roles they play in laboratory conditions; two, research is exploring their use as biofertilisers, biostimulants and in organic, conservation and regenerative agriculture systems; and three, the technology may help to reduce reliance on synthetic fertilisers and other inputs with positive climate and environmental implications. The effectiveness of microbial inoculants can be variable because of interactions with soil, the genotype of a crop, environmental stresses and the survival and colonisation by native organisms. The complex and sometimes contradictory outcomes of rhizobacterial research in the lab, greenhouse and field require a synthesis of knowledge to establish what has been proven, what is likely to be, and what factors are critical to take a technology successfully to the farm.

Lastly, rapid advances in metagenomics, functional genomics, metabolomics, microbial engineering, and synthetic microbial consortia are opening new avenues for the characterization and synergy of rhizobacterial traits that are linked with climate resilience and mitigation. The application of these enabling technologies, coupled with microbial formulation, delivery, in-field validation, and sustainable agriculture best practices, could result in the development of more robust and scalable rhizobacteria-based solutions. In this light, the present review is essential for the comprehensive and nuanced synthesis of rhizobacterial carbon mitigation in the context of climate change, mechanisms by which rhizobacteria increase climate resilience, limitations for field applications, and how emerging biotechnological tools could lead to their reliable use in climate-smart agriculture.

Objectives of the Review

General Objective

The overall aim of this review is to critically examine the mechanisms, applications and emerging biotechnological approaches through which rhizobacteria contribute to climate-change mitigation and climate-resilient agriculture.

Specific Objectives

The review specifically aims to:

1. Examine the major mechanisms through which rhizobacteria contribute to climate-change mitigation, with particular emphasis on soil carbon sequestration and stabilisation, regulation of nitrous oxide and methane emissions, biological nitrogen fixation and improved nutrient cycling.
2. Evaluate the contribution of rhizobacteria to plant tolerance of climate-related abiotic stresses, including drought, heat, salinity and flooding, with emphasis on ACC deaminase activity, osmolyte production, root-system modification, ion homeostasis, antioxidant defence and plant stress-signalling pathways.
3. Assess the role of rhizobacteria in climate-smart and sustainable agricultural systems, including their use as biofertilisers and biostimulants and their integration with organic farming, conservation agriculture, regenerative practices and other approaches aimed at reducing dependence on synthetic agricultural inputs.



4. Critically examine the genomic, metagenomic, metabolomic and synthetic-biology approaches used to identify and enhance rhizobacterial traits associated with climate mitigation and crop resilience, including the development of climate-resilient strains and synthetic microbial consortia.
5. Identify the major constraints limiting the translation of rhizobacteria-based technologies from laboratory and greenhouse studies to reliable field-scale applications, including environmental variability, host specificity, microbial survival and colonisation, formulation, delivery, biosafety and regulatory considerations.
6. Identify research priorities and future strategies for improving the efficacy, consistency, scalability and adoption of rhizobacteria-based climate-smart technologies, with particular emphasis on multi-omics approaches, microbial consortia, targeted inoculants, field validation, formulation technologies and supportive agricultural policies.

METHODOLOGY

Review Design

This study adopted an **integrative narrative literature review approach** to critically synthesise published evidence on the role of rhizobacteria in climate-change mitigation and climate-resilient agriculture. The review was designed to integrate findings from microbiology, soil science, plant physiology, agricultural biotechnology, microbial ecology and climate-smart agriculture in order to establish relationships between rhizobacterial functional traits, soil and plant processes, greenhouse-gas dynamics, carbon sequestration and agricultural resilience. Rather than treating individual plant-growth-promoting traits as isolated functions, the review examined their potential contribution to climate-change mitigation within the broader soil–plant–microbe system.

Literature Search Strategy

Relevant literature for this review was identified through searches of major scientific databases, including **Scopus, Web of Science, PubMed and Google Scholar**, using combinations of keywords such as *rhizobacteria, plant-growth-promoting rhizobacteria (PGPR), climate change, climate-change mitigation, carbon sequestration, soil organic carbon, greenhouse gases, N₂O, CH₄, biological nitrogen fixation, nutrient cycling, drought, heat, salinity, flooding, biofertilisers, biostimulants, metagenomics, microbial engineering and synthetic microbial consortia*. Priority was given to recent peer-reviewed publications, particularly studies published within the last ten years, while older studies were included where they provided foundational evidence for established mechanisms. Retrieved publications were screened for relevance to the objectives of the review, and studies providing mechanistic, experimental or application-based evidence were prioritised for synthesis.

MECHANISMS OF CLIMATE CHANGE MITIGATION BY RHIZOBACTERIA

Carbon Sequestration and Soil Organic Carbon Stabilization

Rhizobacteria contribute to the biological processes that regulate the terrestrial carbon cycle, particularly through their interactions with plant roots and soil organic matter (Wu et al., 2024). In the context of climate mitigation, soil carbon sequestration refers to the accumulation and long-term stabilisation of carbon in soil organic matter and associated soil pools, thereby reducing the proportion of carbon returned rapidly to the atmosphere as CO₂ (Mason et al., 2023). The rhizosphere is a major interface for this process because photosynthetically fixed carbon is transferred belowground through roots and rhizodeposition, where it becomes available to soil microorganisms and can subsequently enter more stable soil-carbon pools (Wang & Kuzyakov, 2023). PGPR can contribute to these processes by enhancing plant nutrient acquisition, root development, biomass production and tolerance to environmental stresses, thereby potentially increasing the amount of plant-derived carbon entering the soil (Mason et al., 2023). Microbial growth, turnover and necromass formation can further contribute to the transformation and stabilisation of organic carbon in soil



(Wu et al., 2024). Moreover, thanks to rhizobacterial metabolic activity, this carbon is not short-lived — it is converted into stable organic fractions capable of persisting in soil for centuries (Avasiloaiei et al., 2023).

The primary pathway by which carbon enters the soil ecosystem is through increased root biomass and the resulting rise in rhizodeposition. Rhizobacteria release various phytohormones — most notably Indole-3-Acetic Acid (IAA) — that trigger structural changes in the host plant's root system, including elongation of the primary root and a substantial increase in lateral roots and root hairs, which greatly expands root surface area. This expanded structure allows the plant to release more carbon-rich exudates — sugars, amino acids, and organic acids — into the rhizosphere. Recent research identifies these exudates as building blocks of soil organic carbon (SOC), since they are rapidly taken up by microorganisms and converted into more complex, less volatile compounds (Zhao et al., 2024).

Carbon is also stabilized physically through the formation of soil macro-aggregates, a process facilitated by rhizobacteria acting as biological binding agents. The physical structure of soil determines how accessible organic carbon is to decomposing organisms; carbon trapped within stable aggregates is shielded from enzymatic breakdown and oxidative loss. Rhizobacteria achieve this by secreting sticky, high-molecular-weight polymers known as exopolysaccharides (EPS), which bind silt, clay, and organic material together into water-resistant aggregates that protect the enclosed organic matter. This activity also helps rhizobacteria reduce soil erosion and improve water retention, reinforcing the soil's role as a carbon sink — particularly important given the growing threat of climate-driven drought and extreme weather (Ndabankulu et al., 2022).

The transition of carbon from a labile to a more recalcitrant, long-term form occurs through the deposition of microbial necromass and the biochemical transformation of organic residues. As rhizobacteria die off, cellular remnants — proteins, lipids, and peptidoglycans — become chemically bound to soil mineral surfaces. Soil scientists have found that this microbially derived carbon tends to be more resistant to breakdown than the original plant material from which it formed, and often persists longer. Rhizobacteria also drive humification, the process by which simple organic compounds are converted into complex, hard-to-degrade humic substances. By promoting high microbial turnover and efficient carbon use, rhizobacterial communities help agricultural land retain carbon over the long term, offering a scalable, nature-based approach to offsetting anthropogenic greenhouse gas emissions (Avasiloaiei et al., 2023).

Reduction of Greenhouse Gas Emissions

Rhizobacteria serve as important biological regulators of nitrous oxide (N₂O) and methane (CH₄) — two potent greenhouse gases with far greater warming potential than carbon dioxide. Agricultural soils are a major source of these emissions, largely due to nitrogen fertilizer application and the anaerobic conditions present in certain cropping systems. Rhizobacteria help counter this by intervening in the biogeochemical cycles that govern gas production and consumption within the soil matrix. By reshaping microbial community structure and optimizing metabolic pathways, these beneficial bacteria reduce the overall release of warming gases from the rhizosphere, offering a nature-based solution for lowering the environmental footprint of global food production (Jonassen et al., 2021).

Improving plant nitrogen use efficiency (NUE) is a central strategy for reducing nitrous oxide emissions. N₂O commonly forms as a by-product of nitrogen cycling in soil, where excess synthetic nitrogen applied by farmers is converted through nitrification and denitrification into N₂O. PGPR such as *Azospirillum* and *Pseudomonas* species help crops acquire nutrients more efficiently by enhancing root architecture and organic nitrogen mineralization. This raises the proportion of applied nitrogen actually captured by the crop, leaving less reactive nitrogen available to denitrifying microorganisms that would otherwise release N₂O into the atmosphere (Shah et al., 2021).

Beyond improving host nutrient uptake, certain rhizobacterial strains have been genetically engineered specifically to counteract nitrous oxide. These nitrous oxide-respiring bacteria (NRB) possess the only known biological catalyst — the enzyme nitrous oxide reductase — capable of converting N₂O into harmless dinitrogen (N₂) gas. Studies show that inoculating soils with these specialized rhizobacteria can substantially

enhance N₂O capture in agricultural settings. By consuming N₂O before it escapes to the surface, these microbes actively help protect the ozone layer and stabilize global temperatures (Jonassen et al., 2021).

Rhizobacteria also play a significant climate role by reducing methane emissions, particularly in wetland crops such as rice. Methanotrophic rhizobacteria, residing in aerobic micro-niches around plant roots, rely on methane as their sole carbon and energy source, oxidizing it into CO₂ — a gas with roughly 28 times lower warming potential than methane. These microbes act as a biological filter, intercepting methane generated in deeper, anaerobic soil layers before it reaches the surface. Certain PGPR further suppress methanogenic archaea through competitive exclusion and the production of distinct metabolites. This combined ability to encourage methane consumption while discouraging its production underpins climate-smart approaches to irrigation and soil management (El Bied et al., 2024).

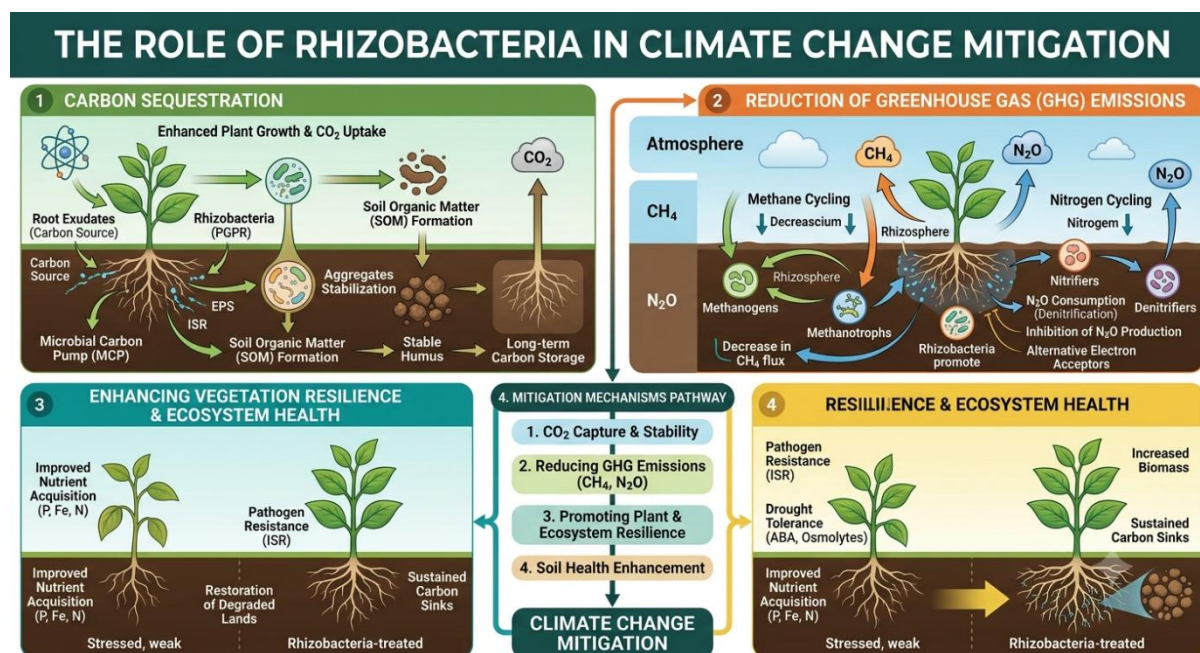


Figure 1: The role of rhizobacteria in climate change mitigation

Biological Nitrogen Fixation and Reduced Synthetic Fertilizer Use

Biological Nitrogen Fixation (BNF) is a transformative microbial process that has emerged as a major alternative to the energy-intensive Haber-Bosch process used in synthetic fertilizer production. Diazotrophic rhizobacteria drive this process by breaking the strong triple bond of atmospheric dinitrogen (N₂) to produce ammonia (NH₃), a nitrogen form readily usable by plants (Olivares et al., 2013). These bacteria fall into two broad categories: symbiotic fixers, such as *Rhizobium* species that form specialized nodules on legume roots, and free-living or associative fixers, such as *Azotobacter* and *Azospirillum*, which inhabit the wider rhizosphere (Aasfar et al., 2021). By supplying nitrogen continuously and locally within the root zone, these rhizobacteria reduce reliance on external chemical inputs and form a cornerstone of sustainable, climate-resilient agriculture (Kebede, 2021).

The ecological and climate costs of synthetic nitrogen fertilizers are increasingly viewed as incompatible with global warming targets. Producing these fertilizers accounts for roughly 2 percent of global energy use and generates nearly 450 million tonnes of CO₂ annually (Sarker et al., 2021). Once applied, synthetic nitrogen is notoriously inefficient — on average, only about 50 percent is taken up by crops, with the remainder lost to nitrate leaching into groundwater or volatilized as nitrous oxide (N₂O), a greenhouse gas with a global warming potential nearly 300 times that of CO₂ (Jonassen et al., 2021). Rhizobacteria not only reduce dependence on these synthetic sources but also improve Nitrogen Use Efficiency (NUE) — the extent to which available nitrogen is converted into plant biomass rather than lost to the atmosphere or waterways (de Andrade et al., 2023).



Incorporating nitrogen-fixing rhizobacteria into modern cropping systems marks a strategic shift toward low-carbon farming and the restoration of long-term soil health. Beyond directly supplying nutrients, these bacteria improve soil fertility by boosting the activity of other beneficial microbes and enhancing soil structure through the synthesis of organic acids and extracellular polymers (Shaaban et al., 2025). Research shows that microbial inoculants can substantially cut the amount of chemical nutrients needed to sustain crop yields, thereby lowering the carbon footprint of staple food production (Zhao et al., 2024). This shift is essential for achieving sustainable intensification — maximizing agricultural output while conserving natural resources and addressing climate stability concerns (Sarker et al., 2021).

Phosphate Solubilization and Improved Nutrient Cycling

Phosphate solubilization is a key microbial process for climate change mitigation, addressing widespread inefficiencies in global phosphorus (P) management. Although phosphorus is essential for plant development, much of the phosphorus in soil remains locked in insoluble mineral or organic forms and unavailable to plants, driving heavy reliance on synthetic phosphate fertilizers. Phosphate-solubilizing bacteria (PSB) bridge this gap by secreting organic acids — such as gluconic and citric acid — along with enzymes like phosphatases that break down these stable compounds (Timofeeva et al., 2022). By converting unavailable phosphorus into bioavailable orthophosphate, these rhizobacteria help plants sustain high photosynthetic rates and carbon sequestration capacity even in nutrient-poor soils, thereby stabilizing the biological carbon sink (Palit et al., 2021).

Synthetic phosphate fertilizers contribute considerably to the carbon footprint of modern agriculture through their environmental impact. Manufacturing these fertilizers is highly energy-intensive, requiring the mining of rock phosphate and chemical processing that releases substantial CO₂ and other pollutants. Overuse of phosphate fertilizers can also cause nutrient runoff and eutrophication of water bodies, which in turn triggers methane and nitrous oxide release from aquatic systems (Rawat et al., 2021). PSB-based biofertilizers help farmers conserve significant amounts of mined phosphorus. This shift reduces industrial emissions tied to fertilizer production while also supporting a circular nutrient economy that recovers the large reserves of legacy phosphorus already present in agricultural soils (Timofeeva et al., 2022).

Improved nutrient cycling through rhizobacteria extends beyond phosphorus to include the mobilization of key micronutrients such as potassium, zinc, and iron. This comprehensive approach to soil fertility strengthens overall plant metabolic capacity, supporting stronger growth with fewer external inputs. By improving nutrient use efficiency (NUE) across the agro-ecosystem, rhizobacteria help ensure nutrients accumulate in the root zone and are absorbed by plants rather than lost to groundwater or the atmosphere. Efficient, localized cycling is essential for maintaining soil health and preventing the degradation of soil organic matter — the largest terrestrial reservoir of sequestered carbon (Rawat et al., 2021).

Finally, the relationship between phosphate solubilization and stress resilience forms another pillar of climate-smart agriculture. Plants with adequate phosphorus develop deeper, more extensive root systems, which are essential for withstanding climate-related stresses such as drought and heatwaves. Stronger root systems also improve soil structure and carbon deposition, creating a positive feedback loop between climate mitigation and nutrient availability. Incorporating phosphate-solubilizing rhizobacteria into sustainable farming systems can therefore make food production more resilient to environmental change while reducing the greenhouse gas intensity of agriculture (Palit et al., 2021).

RHIZOBACTERIA-MEDIATED ENHANCEMENT OF PLANT STRESS TOLERANCE UNDER CLIMATE CHANGE

Drought and Heat Stress Tolerance

Drought and heat stress tolerance mediated by rhizobacteria is a multifaceted biological process that allows plants to maintain physiological stability under extreme temperatures and water scarcity. PGPR draw on a combination of enzymatic regulation and metabolic signaling to counter the negative effects of abiotic stress.



Through this symbiotic rhizosphere relationship, the microbes function as stress modulators, ensuring that essential developmental processes such as root elongation and photosynthesis continue even when environmental conditions exceed normal thresholds (Shahid et al., 2023).

One of the primary mechanisms for alleviating drought and heat stress is the production of the enzyme 1-aminocyclopropane-1-carboxylate (ACC) deaminase. Under stress, plants often produce elevated levels of stress ethylene, which can suppress root growth and accelerate leaf senescence. *Bacillus* and *Pseudomonas* strains that produce ACC deaminase break down ACC — the direct precursor to ethylene — into ammonia and alpha-ketobutyrate (Shahid et al., 2023). This lowers endogenous ethylene levels, blocking the hormonal signals that would otherwise trigger developmental arrest, and allows plants to maintain a healthy root system and remain green through extended dry periods (Mukhtar et al., 2020; Yuan et al., 2023).

In addition to hormonal regulation, rhizobacteria promote drought tolerance by inducing osmotic adjustment and modifying root architecture. These microbes prompt plants to accumulate compatible solutes — most commonly proline and soluble sugars — which help maintain cell turgor and protect protein structure against dehydration damage (Jasso-Arreola et al., 2025). The release of microbial exopolysaccharides (EPS) further forms a protective biofilm around roots, improving the soil's water-retention capacity and shielding plants from excessive heat (Mukhtar et al., 2020). Rhizobacteria also encourage greater root branching and lateral root development, allowing plants to access moisture in deeper soil layers and reducing the impact of surface-level drought (Shahid et al., 2023).

ACC Deaminase Activity and Stress Ethylene Regulation

Drought- and heat-stress tolerance mediated by rhizobacteria is a complex biological mechanism that helps plants maintain physiological stability under severe temperature extremes and water scarcity. PGPR draw on coordinated enzymatic activity and metabolic signaling to counter the effects of abiotic stress, functioning within the rhizosphere as stress modulators that keep critical developmental processes — including root elongation and photosynthesis — running even when environmental conditions fall outside optimal ranges (Shahid et al., 2023).

A major mechanism for reducing drought and heat stress is the synthesis of 1-aminocyclopropane-1-carboxylate (ACC) deaminase. Under adverse conditions, plants typically produce excess stress ethylene, which can suppress root growth and cause premature leaf senescence. ACC deaminase-producing rhizobacteria, including *Bacillus* and *Pseudomonas* strains, break down ACC — the immediate precursor of ethylene — into ammonia and alpha-ketobutyrate (Shahid et al., 2023). This reduction in endogenous ethylene prevents the hormonal signaling that would otherwise trigger developmental arrest, enabling the plant to sustain a healthy root system and stay green through long dry spells (Mukhtar et al., 2020; Yuan et al., 2023).

A direct outcome of lower ethylene levels is the preservation and expansion of a robust root system, essential for surviving drought and heat. Whereas stress ethylene typically stunts primary root growth and blocks root hair formation, ACC deaminase-producing PGPR support longer, more branched root systems (Yuan et al., 2023). This improved architecture allows plants to reach deeper into the soil profile for residual moisture and provides greater physical resilience against environmental stress. Studies show that crops inoculated with these specialized rhizobacteria display notably better root-to-shoot ratios and higher survival rates during extended heat waves compared with non-inoculated plants (Mukhtar et al., 2020; Shahid et al., 2023).

Furthermore, rhizobacterial regulation of stress ethylene has a substantial effect on a plant's broader biochemical and antioxidant status. Lower hormonal stress reduces the buildup of reactive oxygen species (ROS) and limits membrane lipid peroxidation. By preventing the physiological damage associated with ethylene-driven oxidative stress, ACC deaminase-producing rhizobacteria allow the plant to channel metabolic energy toward growth and reproduction rather than emergency survival responses (Jasso-Arreola et al., 2025). This biological support not only eases the immediate impacts of a warming climate but also helps maintain long-term yield stability in regions increasingly affected by environmental variability (Shahid et al., 2023).



Osmolyte Production and Root Architecture Modification

Rhizobacteria-driven osmolyte production is a critical physiological adaptation that helps plants maintain cellular turgor and metabolic function under severe water deficit and heat stress. When plants face drought, rhizobacteria such as *Bacillus subtilis* and *Serratia* sp. stimulate the accumulation of compatible solutes, including proline, glycine betaine, and soluble sugars (Bouremani et al., 2023; Fadiji et al., 2022). These osmolytes raise the osmotic potential inside plant cells, creating a favorable gradient for drawing water from drying soil. Beyond hydration, they act as chemical chaperones that stabilize proteins and cell membranes, preventing the denaturation and membrane rigidity typically caused by extreme heat and water stress (Fadiji et al., 2022).

Alongside these biochemical adjustments, rhizobacteria substantially reshape the plant's root system architecture (RSA) to enhance water foraging. Through production of phytohormones such as Indole-3-Acetic Acid (IAA), PGPR promote lateral and adventitious root growth, greatly increasing the total absorptive surface area (Chieb and Gachomo, 2023; Ojuederie et al., 2019). This structural flexibility allows plants to reach deeper and more distant soil zones for residual moisture unavailable to non-inoculated plants (Bouremani et al., 2023). By adjusting the root-to-shoot ratio, rhizobacteria help plants prioritize resource acquisition over vegetative expansion — a critical trade-off for survival under shifting climate conditions (Ahmad et al., 2022).

The rhizosphere's physical environment is further enhanced through microbial secretion of exopolysaccharides (EPS), which serve as both a biological adhesive and a moisture reservoir. EPS forms protective biofilms around root surfaces, improving water retention and sustaining a hydrated micro-environment even as surrounding soil dries (Fadiji et al., 2022; Ojuederie et al., 2019). These biofilms also stabilize soil structure, preventing pore collapse and maintaining access to water and air at the root-microbe interface (Fadiji et al., 2022). Together, these physical, morphological, and biochemical strategies give rhizobacteria a comprehensive defense system that helps stabilize crop productivity amid increasingly unpredictable global precipitation patterns (Buragohain et al., 2024; Shahid et al., 2023).

Salinity and Flood Stress

Salinity and flood stress rank among the most serious threats to agricultural productivity under climate change, with particularly severe effects on coastal and low-lying regions. Soil salinization induces a form of "physiological drought" by lowering soil water potential and causing ion toxicity, while flooding creates anaerobic conditions that suffocate root tissue. Rhizobacteria offer a sophisticated biological response to both stressors by regulating the plant's internal chemical balance and preserving root function. Through specialized metabolite production and modulation of host gene expression, these microbes allow plants to keep growing in conditions that would otherwise prove lethal (Arora et al., 2020).

One of the main ways rhizobacteria counter salinity is by regulating ion homeostasis — particularly the balance between sodium (Na^+) and potassium (K^+). Under high-salt conditions, plants often absorb toxic levels of Na^+ , which impairs enzyme activity and photosynthesis. Salt-tolerant rhizobacteria, such as those from the *Bacillus* and *Pseudomonas* genera, help maintain a favorable K^+/Na^+ ratio by upregulating high-affinity potassium transporters and the SOS (Salt Overly Sensitive) signaling pathway. These bacteria also secrete substantial amounts of exopolysaccharides (EPS) that physically bind Na^+ in the soil, limiting its entry into root systems and reducing the plant's overall osmotic burden (Afridi et al., 2019; Kumar et al., 2020).

Under waterlogged or flooded conditions, oxygen deprivation (hypoxia) rapidly boosts production of 1-aminocyclopropane-1-carboxylate (ACC), the ethylene precursor. This surge in "stress ethylene" causes chlorophyll breakdown and root tissue death. Rhizobacteria possessing ACC deaminase play a critical role here, breaking ACC down into ammonia and alpha-ketobutyrate and preventing the hormonal surge that leads to plant collapse. This enzymatic action functions as a biological safety valve, helping plants maintain root integrity until floodwaters recede — essential for crop stability in flood-prone regions (Arora et al., 2020; Kumar et al., 2020).

Beyond hormonal and ion regulation, rhizobacteria strengthen a plant's antioxidant defenses to counter oxidative stress. Both salinity and flooding drive overproduction of Reactive Oxygen Species (ROS), which damage cell membranes and DNA. Beneficial rhizobacterial strains prime plants by boosting activity of key antioxidant enzymes such as Superoxide Dismutase (SOD), Catalase (CAT), and Peroxidase (POD), which neutralize free radicals and protect the photosynthetic machinery. This allows plants to direct metabolic energy toward recovery and growth rather than simply managing cellular damage, making this multifaceted biological support a cornerstone of climate-smart agriculture and food security under shifting environmental conditions (Afridi et al., 2019; Bhat et al., 2020).

Ion Homeostasis and Hormone Modulation

Rhizobacteria play a decisive role in maintaining plant ion homeostasis, as salinity and flooding present a dual pressure intensified by ongoing climate trends. In saline soils, excessive sodium (Na^+) accumulation causes metabolic toxicity while limiting access to essential potassium (K^+). Salt-tolerant rhizobacteria, such as *Bacillus* and *Pseudomonas* species, help offset this by adjusting expression of high-affinity potassium transporters and SOS (Salt Overly Sensitive) pathway genes in the host plant to maintain a favorable K^+/Na^+ ratio (Ali et al., 2022). These microbes also generate exopolysaccharides (EPS) that physically bind Na^+ within the soil matrix, limiting its uptake into the plant's vascular system and easing osmotic stress (Ke et al., 2021).

Beyond ion regulation, rhizobacteria play a crucial role in managing plant hormones — particularly ethylene and abscisic acid (ABA) — to help plants cope with the hypoxia and salinity associated with flooding. Waterlogged plants typically produce a burst of stress ethylene, often leading to root decay and chlorosis. Rhizobacteria equipped with ACC deaminase break down the ethylene precursor, preventing hormonal overload and preserving root integrity (Ali et al., 2022). At the same time, these microbes influence ABA signaling to support stomatal function, helping plants conserve water in saline environments while maintaining gas exchange — ultimately stabilizing plant physiology amid unpredictable climate shifts (Ke et al., 2021; Santoyo et al., 2021).

Improved Water and Nutrient Uptake

Rhizobacteria substantially improve plant water relations and nutrient uptake under the stress of salinity and flooding. PGPR use a range of biochemical mechanisms to increase the availability of essential minerals — phosphorus, potassium, and nitrogen — that often become fixed or inaccessible in waterlogged or saline soils (Bhat et al., 2023; Vejan et al., 2016). By secreting organic acids and siderophores, these microbes improve the solubility of mineral phosphates and capture iron, helping plants avoid nutritional decline in hostile conditions (Gupta and Pandey, 2019; Thepbandit and Athinuwat, 2024). Additionally, solute-rich microbial biomass, including proline and trehalose, can be absorbed by plant roots, directly boosting internal osmotic concentration and supporting greater water uptake in saline soils (Kumar et al., 2022).

Beyond these biochemical effects, rhizobacteria drive structural changes in root systems that are vital for surviving climate-induced hydrological extremes. Microbial induction of phytohormones, especially Indole-3-Acetic Acid (IAA), stimulates root hair growth and lateral branching, expanding the total absorptive surface (Backer et al., 2018; Shilev, 2020). This enhanced root structure is particularly valuable during floods, where it supports hydraulic conductance, and during high salinity, where it sustains nutrient uptake despite a toxic ion gradient (Dodd and Alfocia, 2012; Gupta and Pandey, 2019). By stabilizing the root-to-shoot ratio and improving water use efficiency, rhizobacteria help keep plants physiologically active and productive, reducing the yield losses typically caused by unpredictable climatic conditions (Bhat et al., 2023; Shilev, 2020).

Induced Systemic Tolerance and Antioxidant Defense

Induced Systemic Tolerance (IST) refers to a state of physiological readiness that rhizobacteria trigger in plants, enabling them to withstand multiple environmental stressors simultaneously. Unlike Induced Systemic Resistance (ISR), which primarily targets biological pathogens, IST is directed at building resistance to abiotic climate conditions such as drought, temperature extremes, and heavy metal toxicity (Ahmad et al., 2022; Bouremani et al., 2023). When beneficial microbes such as *Pseudomonas* or *Bacillus* colonize the root zone,



they trigger systemic signals — via phytohormones and secondary metabolites — that travel to distant plant tissues. This signaling primes the plant's defense genes ahead of time, so that when actual environmental stress arrives, the response is faster and more effective, closing the gap between microbial activity and overall plant survival (Ahmad et al., 2022; Yu et al., 2022).

A key element of IST is the substantial boost it gives to a plant's antioxidant defense system against oxidative damage caused by climate-induced Reactive Oxygen Species (ROS). Under high heat or salinity, excess ROS such as hydrogen peroxide (H₂O₂) can cause lipid peroxidation and cell death; however, plants treated with rhizobacteria show marked increases in major antioxidant enzymes, including Superoxide Dismutase (SOD), Catalase (CAT), and Ascorbate Peroxidase (APX). These enzymes are central to neutralizing free radicals and protecting the photosynthetic machinery from oxidative harm (Hidri et al., 2022; Sobahan et al., 2025). By promoting cellular redox balance, rhizobacteria help plants preserve membrane integrity and chlorophyll content even under drastic climate shifts (Sobahan et al., 2025).

The activation of these defense pathways also involves a coordinated metabolic shift that balances growth with stress endurance. Rhizobacteria-induced production of non-enzymatic antioxidants, such as glutathione and ascorbic acid, provides additional protection against protein denaturation (Bouremani et al., 2023; Hidri et al., 2022). Transcriptomic studies have shown that microbial inoculation activates specific stress-responsive genes and chaperone proteins, including late embryogenesis abundant (LEA) proteins, which help stabilize cell structures under severe dehydration (Ahmad et al., 2022). This combination of enzymatic scavenging, metabolic flexibility, and systemic signaling positions rhizobacteria as invaluable partners for stabilizing agricultural production amid an increasingly unpredictable global climate (Ahmad et al., 2022; Hidri et al., 2022).

Activation of Plant Defense and Stress Response Pathways

Rhizobacteria function as biological elicitors that activate complex plant defense and stress response pathways through a process known as priming. Rather than causing an immediate reaction, microbial priming prepares the plant's immune system to respond more rapidly and forcefully to a future stressor, such as heat or drought (Yu et al., 2022). This process begins when plant roots detect microbial-associated molecular patterns (MAMPs) — such as bacterial flagellin and cell wall components — triggering a cascade of systemic signals throughout the host (Pieterse et al., 2014; Yu et al., 2022). These signals extend to the shoots, ensuring the entire plant — not just the colonized root tissue — enters a state of heightened physiological readiness (Pieterse et al., 2014; Su et al., 2024).

Regulation of the Induced Systemic Resistance (ISR) and Systemic Acquired Resistance (SAR) pathways is central to this microbial activation. While SAR is generally triggered by pathogens and relies on salicylic acid (SA), rhizobacteria-mediated ISR depends primarily on jasmonic acid (JA) and ethylene (ET) signaling (Pieterse et al., 2014; Yu et al., 2022). These pathways govern the expression of numerous defense-related genes, including those coding for pathogenesis-related (PR) proteins, as well as secondary metabolites such as phenylpropanoids and flavonoids (Pieterse et al., 2014). By fine-tuning the balance between these hormonal pathways, rhizobacteria help plants prioritize survival and defense during climate-induced stress events without significantly compromising vegetative growth (Yu et al., 2022).

At the molecular level, rhizobacteria activate specific stress-responsive transcription factors and chaperone proteins that safeguard cellular integrity. Inoculation with beneficial microbes has been shown to boost expression of genes such as DREB (Dehydration-Responsive Element Binding), along with Heat Shock Protein (HSP) and Late Embryogenesis Abundant (LEA) protein genes (dos Reis et al., 2012; Yu et al., 2022). These proteins act as molecular chaperones that prevent denaturation of essential cellular proteins and help stabilize membranes under extreme thermal and osmotic conditions (dos Reis et al., 2012). Volatile organic compounds (VOCs) released by microbes can further amplify these responses, acting as airborne signals that activate antioxidant genes across the plant canopy (Chandrasekaran et al., 2022).

Activation of these pathways also produces significant physiological and structural reinforcement in plants. Rhizobacteria-induced signaling promotes callose and lignin deposition in cell walls, creating a physical



barrier that reduces water loss and increases resistance to environmental stress (Yu et al., 2022). Calcium-dependent protein kinase (CDPK) and mitogen-activated protein kinase (MAPK) cascades are also activated, coordinating responses that optimize stomatal behavior and photosynthetic efficiency (Su et al., 2024). This combination of biochemical and structural protection is essential for keeping plants alive amid the unpredictability of a changing climate (Pieterse et al., 2014; Yu et al., 2022).

Finally, root exudate-driven recruitment of beneficial microbes establishes a self-reinforcing cycle of resilience. Stress conditions alter the composition of sugars and organic acids released by roots, attracting PGPR capable of alleviating stress (Yu et al., 2022). These recruited microbes, in turn, produce metabolites that reshape the rhizosphere microbiome, increasing the presence of beneficial taxa while suppressing pathogenic species (Pieterse et al., 2014). This interactive relationship offers both immediate protection and long-term adaptive flexibility for the plant-soil system, forming a robust biological foundation for climate-resilient agriculture (Pieterse et al., 2014; Yu et al., 2022).

CHAPTER FOUR

ROLE OF RHIZOBACTERIA IN CLIMATE-SMART AGRICULTURE

Rhizobacteria as Biofertilizers And Biostimulants

Plant-growth-promoting rhizobacteria (PGPR) are central to climate-smart agriculture as highly effective biofertilizers that increase the bioavailability of mineral nutrients. Residing in the plant rhizosphere, these microorganisms use direct fixation pathways, including biological nitrogen fixation (BNF), which converts atmospheric nitrogen (N_2) into ammonia (NH_3) via nitrogenase enzyme complexes (Aloo et al., 2022; Chandran et al., 2021). Many strains within the *Bacillus* and *Pseudomonas* genera also solubilize phosphate, secreting organic acids and phosphatase enzymes that convert insoluble soil phosphorus into monobasic ($H_2PO_4^-$) or dibasic (HPO_4^{2-}) forms readily absorbed by plants.

As biostimulants, rhizobacteria regulate plant physiological functions by producing and releasing a range of phytohormones, including auxins, cytokinins, and gibberellins. Indole-3-acetic acid (IAA), a key microbial signaling molecule, promotes root branching and growth, expanding root surface area for water and nutrient absorption (Sun et al., 2024). This microbial stimulation not only improves overall plant vigor but also boosts metabolic efficiency, allowing crops to allocate resources more effectively toward growth and defense against environmental stressors (Backer et al., 2018). Unlike conventional chemical biostimulants, these live microbial agents form a dynamic, ongoing relationship with the host plant throughout its growth stages (Sun et al., 2024).

PGPR-based biostimulants also markedly improve crop quality and nutritional density, which is increasingly important for global food security under shifting climate conditions. These microorganisms stimulate the production of defensive biomolecules, antioxidants, and phytochemicals such as phenols and flavonoids, enhancing both the nutritional value and visual appeal of harvested crops (Sun et al., 2024). In climate-sensitive crops such as coffee, inoculation with rhizobacterial consortia has been shown to boost leaf count, root density, and overall yield through improved nutrient uptake and stress tolerance (Basu et al., 2021). By stabilizing the plant's internal biochemical environment, rhizobacteria help sustain yields even as synthetic input use declines.

PGPR also support sustainable agricultural intensification by offering a safe alternative to potentially harmful chemical fertilizers. As renewable nutrient sources, these bioformulations are less prone to environmental leaching and volatilization than their synthetic counterparts, helping maintain soil health and biological activity (Basu et al., 2021; Farooq Khan et al., 2022). Incorporating these microorganisms into agricultural systems allows producers to lower the carbon footprint associated with fertilizer production and loss (Sun et al., 2024). Functioning as both biofertilizer and biostimulant, rhizobacteria represent a sound strategy for maintaining agricultural productivity in a warming world.



Integration into Sustainable and Regenerative Farming Systems

Sustainable and regenerative farming practices such as no-till agriculture and cover cropping create favorable ecological conditions for rhizobacterial populations to flourish. By reducing soil disturbance and maintaining high organic matter levels, these techniques support strong microbial biofilms and greater soil aggregate stability (Ahmed et al., 2024). Supplementing degraded soils with rhizobacterial inoculants can accelerate soil restoration, as a healthy microbiome acts as a biological binding agent, holding soil particles together and improving both carbon sequestration and resistance to physical erosion.

The synergy between conservation management and microbial activity produces a self-sustaining ecosystem better able to withstand the extreme weather events characteristic of a changing climate. In no-till systems, for example, rhizobacteria help accumulate legacy phosphorus and recalcitrant organic carbon that crops can draw on across multiple growing seasons (Katherasala, 2025). This reduces the energy and fuel costs typically associated with plowing and chemical application under conventional methods. Regenerative practices emphasize the concept of "living soil," treating rhizobacteria as active participants in nutrient cycling rather than passive recipients of chemical inputs.

Incorporating PGPR into crop rotation and intercropping systems also increases microbial and soil diversity, naturally suppressing soil-borne diseases. A more diverse microbial community competes more effectively with pathogens, reducing reliance on synthetic pesticides that can harm beneficial insects and pollinators (Sagar et al., 2021). This holistic approach can transform agricultural landscapes from sources of environmental stress into productive carbon sinks. By aligning microbial processes with regenerative principles, farmers can support long-term soil health while contributing to atmospheric carbon mitigation.

These microbial-based systems also advance the One Health concept, which recognizes the interconnection between soil, plant, and human health. Rhizobacteria help move key micronutrients through the soil matrix into edible plant tissue, offering a potential avenue for addressing malnutrition in climate-vulnerable regions (Ahmed et al., 2024). This regenerative cycle keeps soil productive for future generations while delivering immediate climate adaptation benefits. Ultimately, effectively integrating PGPR into farming systems is essential for the shift toward a circular, resilient bio-economy.

Contribution to Yield Stability Under Changing Climate

A central challenge in modern agriculture is maintaining stable crop yields amid increasingly frequent extreme weather, including erratic rainfall and temperature swings (Yahya et al., 2023). Rhizobacteria help stabilize yields by buffering plants against these environmental shocks, regulating physiological processes so that nutrient uptake and water-use efficiency remain steady during abiotic stress (Ali et al., 2022). This makes rhizobacterial integration a form of biological insurance for the food supply chain in regions facing environmental disruption, by boosting overall crop resilience (Kelbessa et al., 2023).

Yield regulation is largely driven by microbial influence on plant hormones and root system development. Increased root hair density and deeper primary root penetration, both promoted by rhizobacteria, allow crops to access moisture and nutrients from deeper soil layers during dry periods (Tan et al., 2022). This structural benefit is reinforced by ACC deaminase activity, which suppresses ethylene and delays premature senescence, allowing plants to sustain photosynthesis over longer periods (Kelbessa et al., 2023). Together, these physical and chemical adaptations support stable harvests even under a deteriorating climate (Chandran et al., 2021).

Ultimately, achieving long-term yield stability requires shifting toward complex, multi-microbe interactions capable of withstanding diverse environmental stresses, rather than relying on individual strains (Yahya et al., 2023). Single-strain inoculants can perform inconsistently depending on soil temperature or pH, whereas diverse rhizobacterial communities offer functional redundancy — ensuring that useful processes continue even under a given stressor (Tan et al., 2022). As climate change progresses, climate-smart agriculture must increasingly focus on these resilient microbial communities to make yield stability a lasting feature of regenerative farming systems, not just a one-season success (Chandran et al., 2021).



Synergies With Organic Farming and Conservation Agriculture

Integrating rhizobacteria into organic farming systems produces a strong biological synergy that offsets the absence of synthetic inputs. In organic systems, where nitrogen and phosphorus availability often limits productivity, rhizobacterial inoculants act as biocatalysts, enhancing nutrient release through the mineralization of organic compounds (Agbodjato & Babalola, 2024). These microbes convert complex organic materials into plant-accessible forms, supplying nutrients in step with crop development needs. This relationship narrows the yield gap commonly associated with the transition to organic farming, without compromising soil ecology (Backer et al., 2018).

Rhizobacteria are also foundational to the success of conservation agriculture, particularly no-till and cover-cropping systems. Because conservation agriculture relies on minimal soil disturbance and continuous soil cover, it provides a stable habitat for microbial communities to thrive (Fasusi et al., 2021). Rhizobacteria support this system by producing exopolysaccharides and glomalin-like proteins that bind soil particles into stable micro-aggregates. This biological binding improves soil structure and water infiltration while limiting the oxidation of soil carbon, reinforcing the climate benefits of conservation practices (Chandran et al., 2021).

This synergy also extends to pest and disease management through Induced Systemic Resistance (ISR). In organic and regenerative systems that avoid chemical pesticides, rhizobacteria serve as a primary line of defense by strengthening the plant's innate immune system (Yang et al., 2024). This microbial priming allows plants to respond more quickly and effectively to pathogen attack without the environmental costs of conventional fungicides. By fostering a diverse and active rhizosphere, farmers can create suppressive soil conditions where beneficial microorganisms naturally outcompete soil-borne pathogens, resulting in a more resilient, self-sustaining agro-ecosystem (Fasusi et al., 2023).

Finally, combining rhizobacterial inoculation with organic amendments such as compost or biochar produces a priming effect that improves long-term soil health. These organic materials provide bacteria with carbon and physical support, improving their survival and colonization in the field (Verma et al., 2024). As agriculture shifts toward more holistic, climate-smart management, pairing microbial biotechnology with established conservation strategies offers a scalable path to sustainable food production — one that maximizes the soil's biological potential to address both food security and climate change together.

Biotechnological and Genomic Approaches

Advances in genomic technology are increasingly driving the shift toward climate-resilient agriculture, offering a deeper understanding of complex rhizosphere interactions. Metagenomics has become essential for identifying the functional traits of microbial communities that support soil health and crop yields across diverse environments (Nwachukwu & Babalola, 2022). Next-generation sequencing allows researchers to move beyond traditional cultivation-based methods, identifying biologically important genes and bioactive molecules directly from environmental samples (Nwachukwu and Babalola, 2022). This meta-omic approach — spanning transcriptomics, proteomics, and metabolomics — provides a comprehensive picture of how rhizobacteria respond to climate stressors such as heat and drought (Agbodjato et al., 2026).

Beyond identification, synthetic biology offers the means to develop more efficient, climate-resistant rhizobacterial strains. Recent innovations such as CRISPR/Cas9 gene editing and nanoparticle-based gene delivery are being investigated to enhance microbial traits like nitrogen fixation and ACC deaminase production (Agbodjato et al., 2026). These biotechnological approaches aim to produce customized microorganisms capable of maintaining high productivity even under severe environmental stress. For instance, engineered strains can be designed to synthesize specific signaling molecules that prime plant defenses more effectively than their wild-type counterparts (Backer et al., 2018).

A key frontier in this field is the development of synthetic microbial consortia (SynComs). Rather than relying on a single super-strain, SynComs harness a diverse group of microbes to maintain stable performance across variable soils, exploiting functional redundancy and synergistic interactions (Agbodjato et al., 2026). Compared with single isolates, these consortia offer more consistent benefits, including improved nutrient



uptake and greater soil structural stability through exopolysaccharide production (Agbodjato et al., 2026; Chandran et al., 2021). This move toward multi-species inoculants represents the next stage in climate-smart biostimulant development (Backer et al., 2018). Commercializing these biotechnological advances further requires rigorous field testing and improved formulation methods — isolates and synthetic consortia must be evaluated under both controlled stress conditions and diverse field settings to confirm real-world benefits for crop resilience (Backer et al., 2018). AI-based phenotyping and environmental genomic selection can help accelerate the breeding of plants and their associated microbes (Agbodjato et al., 2026), ensuring these microbial solutions are both scientifically sound and practically viable for sustainable agriculture worldwide.

Metagenomics and Functional Genomics of Rhizobacteria

Metagenomics has transformed rhizosphere research by providing a culture-independent window into the vast diversity of soil microbial communities. Unlike conventional techniques, which are limited to a small fraction of culturable bacteria, metagenomic sequencing captures the full genetic material extracted from soil samples. This approach enables researchers to map the structural composition of rhizobacterial communities and understand how they respond to climate-related stressors such as drought and salinity (Nwachukwu & Babalola, 2022). Mapping the taxonomic diversity of the rhizosphere in this way clarifies how different microorganisms interacting with plant roots coexist symbiotically (Olowe et al., 2023).

Beyond identifying which organisms are present, functional genomics investigates what they actually do by examining the genes responsible for climate-mitigating traits. Techniques such as shotgun metagenomics allow researchers to detect plant growth promotion (PGP) genes and disease-resistance genes within rhizosphere microbiomes (Enagbonma et al., 2023). Functional profiling shows that healthy rhizospheres consistently contain a much higher abundance of these beneficial genes compared with diseased or bulk soils, pointing to a largely untapped genetic reservoir capable of enhancing plant resilience (Dlamini et al., 2023). This genetic resolution is essential for identifying the most effective candidate strains for developing biofertilizers suited to changing agro-ecosystems.

Combining these omics tools provides a framework for predicting how microbial functions will adapt to future climate conditions. By comparing genomic data with environmental variables, researchers can build models linking soil health and microbial activity to different fertilization regimes (Fadiji et al., 2021). This predictive capability is key to advancing precision agriculture, where microbial interventions can be tailored to the specific genomic profile of local soils. Ultimately, metagenomics and functional genomics provide the scientific foundation for broader biological solutions to global food security.

Engineering Climate-Resilient Rhizobacterial Strains

Engineering climate-resilient rhizobacterial strains marks a shift from simply selecting naturally occurring isolates toward deliberately optimizing specific microbial traits. As climate change increases the frequency of multi-stress environments, conventional wild-type strains often perform inconsistently across different soils and temperatures. Genetic engineering can enhance robustness by, for example, boosting ACC deaminase production to counteract stress ethylene or increasing exopolysaccharide (EPS) biosynthesis to retain moisture. Tailoring these genetic pathways allows scientists to develop "designer microbes" with the specific traits needed to survive future climate extremes.

Advanced molecular tools, particularly CRISPR/Cas9 and other site-specific mutagenesis systems, are being applied to optimize rhizobacterial function. Unlike random mutagenesis, these precision techniques allow researchers to insert beneficial genes or remove metabolic pathways that consume energy without benefiting plant health. For example, boosting siderophore production can improve iron uptake in alkaline soils, while enhancing nitrogen-fixation genes can extend biofertilization benefits to non-leguminous crops. This genomic control helps microbial inoculants remain metabolically active and functional even under thermal or osmotic shock.

Beyond single-gene modifications, the field is moving toward developing synthetic chassis bacteria — organisms with reduced genomes designed for high-level expression of beneficial traits. These synthetic strains



provide stable platforms for supporting climate-mitigation functions such as phosphate solubilization and greenhouse gas reduction. By optimizing the metabolic flux of these organisms, researchers can ensure that bacteria focus more energy on plant-growth-promoting activities rather than general survival. This engineering approach not only improves microbial efficacy but also helps engineered strains compete more effectively against native soil populations.

Finally, introducing engineered rhizobacteria into the field requires pairing them with sophisticated delivery systems to ensure long-term viability. Encapsulation technologies and nanomaterial-based carriers protect engineered cells from rapid environmental degradation while enabling controlled release. As regulations around genetically modified organisms (GMOs) continue to evolve, there is growing emphasis on biocontainment strategies to prevent unintended transfer of engineered genetic material into the broader ecosystem. Together, these genomic and delivery innovations position engineered rhizobacteria as a scalable, highly efficient approach to stabilizing agricultural output in a warming world.

Synthetic Microbial Consortia for Climate Mitigation

The development of synthetic microbial consortia (SynComs) represents a paradigm shift in agricultural biotechnology, moving away from single-strain approaches toward multi-functional, multi-microbe communities. While individual rhizobacterial isolates often struggle to survive in competitive soil environments or lack the metabolic range to respond to varied stressors, SynComs are designed to provide functional redundancy and synergistic interaction. These engineered communities are built by combining compatible strains that occupy different environmental niches or provide complementary functions — such as simultaneous nitrogen fixation, phosphorus solubilization, and pathogen suppression — helping ensure the inoculant performs reliably across diverse soils and weather conditions.

A key advantage of synthetic consortia is their ability to enhance soil organic matter stability and carbon sequestration through coordinated metabolic activity. Within a SynCom, different members may specialize in producing various exopolysaccharides (EPS) and glomalin-like proteins, which are essential for forming and stabilizing soil macro-aggregates. This coordinated biological network allows consortia to sequester carbon more effectively than individual strains while limiting microbial carbon oxidation. This structural strength helps reduce greenhouse gas emissions and improves soil water-holding capacity, offering crops an added layer of protection during extended droughts.

SynComs are also being developed to optimize nutrient cycling while reducing agriculture's carbon footprint. By combining strains with varying affinities for nitrogen and phosphorus, these consortia can sustain plant nutrient uptake even when soil nutrient levels are low or unpredictable. Metabolic cooperation within a SynCom allows efficient decomposition of organic residues, providing a steady nutrient supply without heavy reliance on synthetic fertilizers. This reduced chemical dependency directly lowers nitrous oxide (N₂O) emissions associated with nitrogen leaching and denitrification, aligning with climate-smart agricultural principles.

Successfully deploying SynComs depends on a deep understanding of microbial social behaviors, including quorum sensing and cross-feeding. Researchers use advanced mathematical modeling and omics data to predict how different consortium members will interact once introduced into a native soil microbiome. A major commercialization challenge is ensuring the synthetic community can outcompete indigenous populations while maintaining internal stability. As precision agriculture advances, increasingly customized SynComs — tailored to specific crops and regional climate profiles — are likely to become standard practice for achieving long-term yield stability and environmental resilience.

Decoding the complex signaling pathways through which rhizobacteria adapt to climate change requires combining multiple omics approaches, including genomics, transcriptomics, proteomics, and metabolomics. While genome sequencing reveals the potential for beneficial traits, transcriptomics and proteomics show which genes and proteins are actually expressed in response to specific environmental triggers, such as elevated CO₂ or high temperature (Fadiji et al., 2022). These "molecular snapshots" allow researchers to observe real-time metabolic changes during plant-microbe interactions, confirming that identified microbial



candidates possess the functional capacity needed to succeed in the field (Agbodjato & Babalola, 2024). This integrated approach helps identify the key regulatory hubs governing carbon and nitrogen efficiency, offering a clearer picture of how microbial activity translates into ecosystem-level climate resilience.

Use of Omics Tools to Unravel Mitigation Pathways

Metabolomics serves as the functional link in this framework, decoding the chemical signals rhizobacteria use to communicate with host plants and the surrounding soil community. By profiling root exudates and microbial metabolites, scientists can identify specific signaling molecules — such as specialized volatile organic compounds (VOCs) and osmolytes — that increase under climate stress (Ajilogba & Babalola, 2019). These metabolites not only aid nutrient mobilization but also act as chemical triggers that activate the plant's internal stress-response systems (Olowe et al., 2023). Understanding the metabolic signatures associated with successful rhizobacterial colonization supports the design of targeted biostimulants capable of activating specific mitigation pathways, such as enhanced soil carbon stabilization or reduced nitrous oxide production.

The future of climate-smart agriculture depends on integrating this high-throughput data into predictive systems biology models. Using bioinformatics to compare multi-omics data with field environmental variables, scientists can model how different microbial communities will behave under future climate scenarios (Enagbonma et al., 2023). This predictive capability is central to moving agricultural management from a reactive to a proactive, evidence-based approach, enabling timely, localized microbial interventions. Ultimately, omics tools are reshaping how rhizobacteria are understood — not as isolated biological agents, but as integral components of a complex, climate-resilient agro-ecosystem.

CONCLUSION

Plant Growth-Promoting Rhizobacteria (PGPR) may serve as a powerful natural remedy to the climate change. These microscopic partners live in the rhizosphere the narrow zone of soil around plant roots- and are a vital waystation between vegetation and the environment. Rhizobacteria not only promote the growth of the plants by increasing their ability to sequester carbon, reduce the use of chemical fertilizers (a major source of greenhouse gases like nitrous oxide), and make the plants more resilient to adverse weather conditions but also proactively stabilize the ecosystem. They are not a silver bullet to replace the process of decarbonization in the industry, but they are needed to create climate-resilient agriculture and to restore damaged carbon sinks.

RECOMMENDATIONS

To move from theory to large-scale impact, the following strategies are recommended:

- **Create Location Bio-Inoculants:** No longer one-size-fits-all. To achieve a greater survival and efficacy rate, tailor rhizobacteria to particular soil types, native microbial communities and local weather conditions.
- **Combine with Regenerative Practices:** Combine the use of rhizobacteria with no-till agriculture, cover cropping and organic additives. The soils remain unaltered and in their natural form because of these practices, which are conducive to the growth of PGPR.
- **Invest in "Omics" Research:** metagenomics and proteomics can be used to learn more about the behavior of rhizobacteria in extreme drought or salinity to select the most resilient "climate-ready" strains.
- **Policy and Incentives:** Governments ought to subsidize or give carbon credits to those farmers who switch to microbial-based bio-fertilizers as opposed to synthetic nitrogen fertilizers.
- **Public Awareness:** Educate stakeholders as to the long-term benefits of soil health. Rhizobacteria are unlike the immediate "green-up" of chemicals, and therefore have cumulative, sustainable benefits that safeguard the land to the future generation.

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