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Review Article

Microbial Biotechnology for Climate-Smart Agriculture: Mechanisms, Evidence and Prospects

Aishwarya Sharma[1*], J H Kahodariya[2], Naval Kishore Meena[3], Vishal Prajapati[4]

[1]Research Scholar, Department of Research and Development Cell,
Swami Vivekanand Subharti University, Meerut

[2]Deputy Project Director- ATMA, Botad, Department of Agriculture,
Farmers Welfare and Co-Operation, Govt. Of Gujarat

[3]Ph.D. Scholar, Department of Horticulture (Fruit Science), RCA, MPUAT, Udaipur-313001, Rajasthan

[4]M.Sc. Scholar, Department of Agronomy,
Dr. Rajendra Prasad Central Agricultural University, Pusa, Bihar- 848126

*Corresponding Author E-mail: aish04.biotech@gmail.com

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ABSTRACT

Microbial biotechnology offers promising solutions for advancing climate-smart agriculture by improving crop productivity, nutrient efficiency, soil health, and resilience to environmental stresses. Beneficial microorganisms, including plant growth-promoting bacteria, mycorrhizal fungi, and microbial consortia, enhance nutrient cycling, phytohormone production, biological nitrogen fixation, and stress tolerance. Microbial technologies can also contribute to carbon sequestration, greenhouse-gas mitigation, and sustainable resource utilization. This review examines the mechanisms underlying microbial interactions with plants and soils, evaluates current experimental and field-based evidence, and highlights applications in sustainable crop production. Key challenges involving formulation, field consistency, scalability, biosafety, and regulatory frameworks are discussed. Future prospects emphasize integrated microbial approaches, precision agriculture, and biotechnology-driven climate resilience.

Keywords: *Climate-smart Agriculture; Plant growth-promoting Rhizobacteria; Arbuscular mycorrhizal fungi; Greenhouse gas mitigation; Synthetic microbial communities.*

INTRODUCTION

Agriculture occupies the uncomfortable position of being simultaneously a victim, a driver and a potential solution to climate change. Rising mean temperatures, more erratic rainfall, expanding soil salinity and shifting pest and pathogen ranges are already depressing yields in many production regions, while the sector itself remains a major source of methane (CH_4) and nitrous oxide (N_2O).

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It was against this background that Lipper et al. (2014) articulated climate-smart agriculture (CSA) as an integrating approach built on three pillars: sustainably increasing productivity and incomes, adapting and building resilience to climate change, and reducing or removing greenhouse gas emissions where possible; the same framing underpins the operational guidance of the Food and Agriculture Organization of the United Nations (n.d.). The framework has since been refined, with Segnon et al. (2018) reviewing its institutional dimensions and Hammond et al. (2020) proposing improved metrics for assessing trade-offs among the three pillars. The Intergovernmental Panel on Climate Change (2022) subsequently estimated that improved cropland, rice, livestock and nutrient management together offer roughly 4.1 $GtCO_2$-equivalent per year of economic mitigation potential between 2020 and 2050, making agriculture one of the largest actionable mitigation reservoirs outside the energy sector.

What is often overlooked in policy discussions of CSA is that almost every biogeochemical process the framework seeks to influence is, at its core, microbially mediated. Nitrogen fixation, nitrification, denitrification, methanogenesis, methane oxidation, phosphate mobilisation, organic matter decomposition and the stabilisation of soil carbon are all catalysed by bacteria, archaea and fungi. Soil microbial communities therefore constitute the operational layer through which CSA outcomes are actually realised, a point developed by Ho, Kim and Das (2019) and elaborated more recently by Nguchu et al. (2025), who describe microbial communities as the invisible architects of soil health and climate resilience.

Microbial biotechnology is the deliberate harnessing of these organisms and their functional genes for agronomic benefit. Its portfolio now extends well beyond the classical rhizobial inoculant to include mycorrhizal products, microbial biostimulants, biological control agents, biological nitrification inhibitors, rumen-targeted feed additives and rationally assembled synthetic microbial communities. Field evidence indicates that this portfolio can be agronomically consequential: Datta et al. (2020) reported that cereal-based CSA systems in India restructured topsoil bacterial communities while raising soil organic carbon by up to 111% and available nitrogen, phosphorus and potassium by 38%, 70% and 59% respectively relative to conventional tillage. Ren et al. (2022) similarly showed that long-term integrated soil-crop management restructures the soil microbial community in ways that reduce greenhouse gas emissions and raise yield simultaneously.

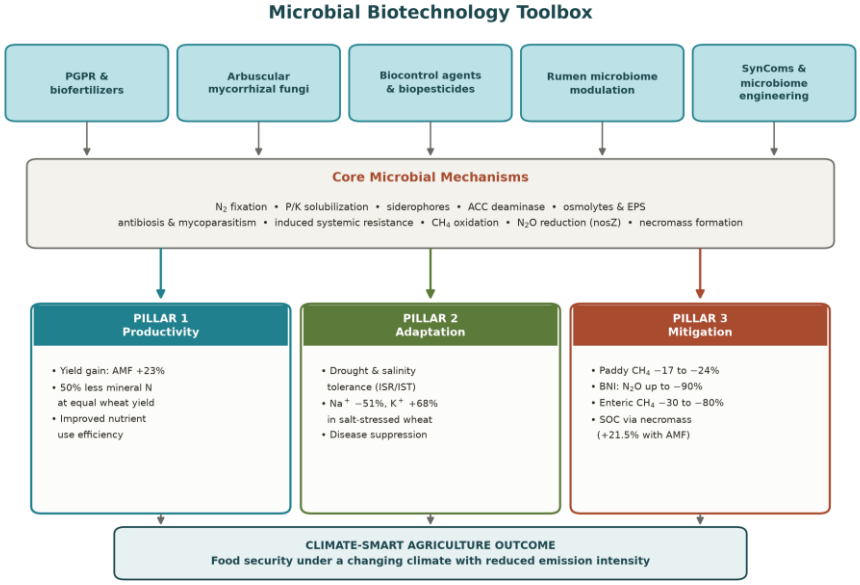

Figure1. Conceptual framework linking microbial biotechnology to the three pillars of climate-smart agriculture. Microbial tools act through a shared set of core mechanisms to deliver productivity, adaptation and mitigation outcomes. Representative quantitative effects are drawn from the studies cited in the text

2. Microbial Biofertilizers and Nutrient-Use Efficiency

Plant growth-promoting rhizobacteria (PGPR) improve crop performance through several complementary mechanisms. Timofeeva, Galyamova and Sedykh (2023) group these into biological nitrogen fixation, solubilisation of poorly available phosphorus and potassium, siderophore-mediated iron acquisition, and the production of 1-aminocyclopropane-1-carboxylate (ACC) deaminase, which lowers stress ethylene in host tissues; Martínez-Romero et al. (2023) provide a complementary taxonomic overview of the bacteria involved. Because these functions target the same nutrients supplied by mineral fertilizers, whose manufacture and field losses are themselves emission-intensive, PGPR act simultaneously on the productivity and mitigation pillars of CSA.

The strongest recent field evidence concerns nitrogen. Aasfar et al. (2024) showed that inoculation of wheat with nitrogen-fixing bacteria under contrasting nitrogen and phosphorus regimes reduced chemical nitrogen fertilizer requirements by up to 50% without penalty to grain yield. For phosphorus, Chouyia, Pepe and Ventorino (2022) reviewed phosphate-solubilising *Streptomyces*, which mobilise fixed soil phosphorus through organic acid exudation and phosphatase activity, and Diksha et al. (2021) documented the broader biofertilizer portfolio spanning *Rhizobium*, *Azotobacter*, *Azospirillum* and potassium-solubilising strains. Aloo et al. (2022) and Alzate Zuluaga et al. (2024) both argue that the decisive constraint is no longer mechanistic understanding but formulation, delivery and rhizosphere establishment.

3. Arbuscular Mycorrhizal Symbioses

Arbuscular mycorrhizal fungi (AMF) form the most quantitatively well-characterised microbial intervention in the CSA literature because a substantial meta-analytical base now exists. Wu et al. (2022), analysing 546 observation pairs across 13 crops, found that AMF inoculation increased yields by an average of 23.0% under rainfed conditions, with shoot and root biomass rising by 24.2% and 29.6% respectively. Effect sizes were larger for non-grain than for grain crops, indicating that benefit is contingent on crop functional type rather than universal.

The adaptation value of AMF is equally well supported. Tang et al. (2024) demonstrated in a global meta-analysis that AMF attenuate the negative impact of drought on soil functions, and Chandrasekaran (2022) quantified AMF-mediated improvements in biomass, root morphology and nutrient uptake specifically under water deficit. Shah et al. (2022) emphasised the dual contribution of AMF to drought tolerance and nitrogen-use efficiency. Crop- and system-specific syntheses refine this picture: Oladele, Gould and Varga (2024) examined potato systems, Java, Paguntalan and Abacan (2023) analysed rice, and Othman, Alananbeh and Tahat (2024) reported that root colonisation reached 61.1% under conventional culture versus 52.3% in hydroponics.

Critically for mitigation, Conti et al. (2025) synthesised 62 trials across 19 studies and found that AMF increased soil organic carbon by an average of 21.5% in agricultural ecosystems, linking mycorrhizal management directly to soil carbon sequestration objectives rather than to productivity alone.

4. Microbially Mediated Abiotic Stress Tolerance

Adaptation is the CSA pillar where microbial biotechnology arguably offers the most immediate practical value, because inoculants can be deployed within a single season and do not require the multi-year timelines of crop breeding. Vurukonda et al. (2016) established the mechanistic canon for drought: bacterial exopolysaccharide production improves soil aggregation and water retention around roots, ACC deaminase suppresses stress ethylene, and osmolyte accumulation sustains cell turgor. Ahluwalia, Singh and Bhatia (2021) and Bano et al. (2022) extended this synthesis to combined drought and salt stress.

Quantitative evidence is available for salinity. Singh and Jha (2016) showed that the halotolerant strain *Bacillus licheniformis* HSW-16 induced systemic tolerance in salt-

stressed wheat, producing growth increases of 6 to 38% while reducing shoot sodium content by 51% and raising potassium and calcium by 68% and 32% respectively. The causal centrality of ACC deaminase has since been confirmed genetically: Kahmen et al. (2024) demonstrated that deleting the ACC deaminase gene from bacterial symbionts converted host plants from water savers into water wasters. Glick et al. (2019) showed that ACC deaminase and trehalose production by *Pseudomonas sp. UW4* act synergistically to protect tomato against salt stress, while Glick and Gamalero (2022) and Kumar et al. (2024) reviewed the wider integration of these traits with host drought-response genes. Freitas, Dias and Ma (2020) provide a comparative treatment across species. The principal mechanisms are summarised in Figure 2.

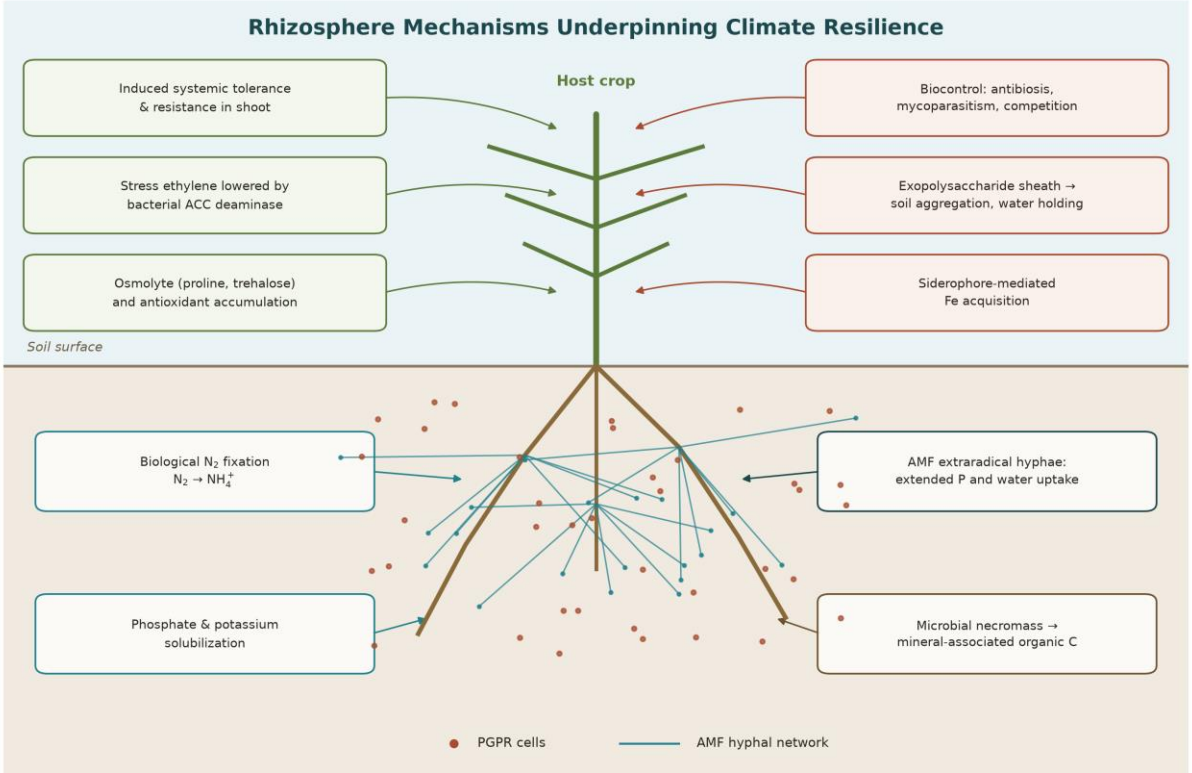

Figure2. Rhizosphere mechanisms through which plant growth-promoting rhizobacteria and arbuscular mycorrhizal fungi confer climate resilience. Above-ground responses (left and right upper panels) are induced systemically, whereas below-ground processes operate directly in the rhizosphere and contribute to nutrient acquisition and soil carbon stabilisation

5. Microbial Mitigation of Greenhouse Gas Emissions

5.1 Methane in flooded rice systems

Methane flux from paddy soils reflects the net balance between methanogenic archaea in the anoxic bulk soil and methanotrophic bacteria in the oxic rhizosphere and floodwater interface. Zheng, Cai and Jia (2024) reviewed the role of methanotrophic communities in atmospheric methane oxidation in paddy soils, and Chen et al. (2024) characterised metabolic coupling between aerobic methanotrophs and denitrifiers, a cross-feeding relationship with the attractive property of addressing CH_4 and N_2O simultaneously.

Management levers that operate through these communities are quantitatively meaningful. Zhou et al. (2024) synthesised paddy methane controls across Monsoon Asia, reporting reductions of 27.66% from water management, 23.78% from off-season straw return and 21.79% from conversion of straw to biochar; Ma et al. (2024) reached comparable conclusions for Chinese rice systems. Direct microbial intervention is also effective: Senoo et al. (2022) found that inoculating rice seed

with the diazotroph *Azoarcus* reduced soil CH_4 emissions by 23.5% under non-fertilized and 17.2% under nitrogen-fertilized conditions, and Pham et al. (2021) recorded an 80% reduction in CH_4 with maintained yield under continuous sub-irrigation, attributable to suppressed methanogenic and methanotrophic abundance.

5.2 Nitrous oxide and biological nitrification inhibition

Nitrous oxide has roughly 273 times the hundred-year warming potential of carbon dioxide and originates largely from microbial nitrification and denitrification of applied nitrogen. Subbarao et al. (2013) proposed biological nitrification inhibition (BNI) as a paradigm shift: certain plants release root exudates that suppress ammonia-oxidising organisms, retaining nitrogen as ammonium and curtailing both nitrate leaching and N_2O formation. Wang, Fahad and Saud (2022) reported that BNI mechanisms can reduce N_2O emissions by up to 90%, with the compound brachialactone from *Brachiaria humidicola* accounting for 60 to 90% of total inhibition capacity. Villegas et al. (2020) phenotyped a core germplasm collection of *Megathyrsus maximus* and found nitrification reduced by 30 to 70% across accessions, confirming that BNI is a heritable, breedable trait. Simon et al. (2020) provided a useful field comparison, showing that *Brachiaria humidicola* pastures emitted 20% less N_2O from cattle urine patches than alternative grasses while the synthetic inhibitor dicyandiamide achieved 40 to 50% reductions.

A complementary strategy targets the terminal step of denitrification. Spor et al. (2015) demonstrated that the diversity of nosZ-carrying N_2O reducers governs the N_2O to N_2 end-product ratio across cropping systems, while Jones et al. (2022) showed that root-associated communities in annual crops are selected towards nosZ clade I over clade II. Managing for abundant and functionally complete N_2O reducers therefore represents a genuine, if still largely experimental, mitigation lever. Figure 3 maps these intervention points onto the underlying biogeochemical cycles.

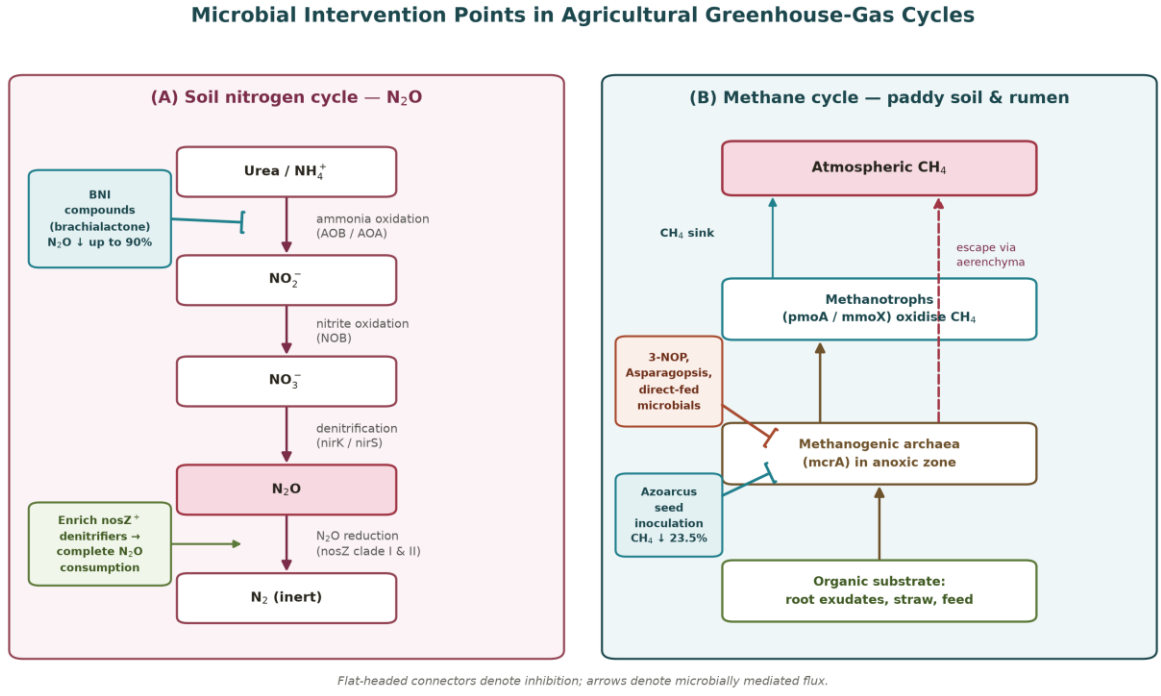

Figure3. Microbial intervention points in the agricultural nitrogen and methane cycles. Panel A shows nitrification and denitrification steps together with biological nitrification inhibition and nosZ enrichment strategies. Panel B shows the balance between methanogenesis and methane oxidation in paddy soil and the rumen, with the principal inhibitory interventions indicated

5.3 Enteric methane and rumen microbiome modulation

Livestock production carries the strongest quantitative evidence base of any topic in this review. Box, Black and Davison (2021) note that enteric fermentation accounts for approximately 30% of global methane emissions. Hristov et al. (2015) demonstrated in a landmark trial that the methanogen inhibitor 3-nitrooxypropanol (3-NOP) persistently reduced enteric methane from dairy cows by about 30% with no adverse effect on milk production; the same group later characterised the underlying shifts in ruminal microbial gene expression (Hristov et al., 2022). Gruninger et al. (2021) reported additive effects in beef cattle, with 3-NOP alone reducing CH_4 by 28.2%, canola oil alone by 24.0% and the combination by 51.3%.

Macroalgal additives are more potent still. Indugu et al. (2024) provided a microbiome-informed mechanistic account of methane inhibition by *Asparagopsis taxiformis* in dairy cattle, with reductions reaching 80%, and Almeida et al. (2024) achieved 64%, 98% and 99% reductions at low, medium and high doses of *Asparagopsis* metabolites stabilised in canola oil. Hodge, Quille and O'Connell (2024) reviewed the wider additive landscape, and Aguilar-Pérez et al. (2020) reported up to 26% reduction from secondary plant metabolites such as tannins and saponins. Comparative efficacy across the productivity and mitigation literature is presented in Figure 4.

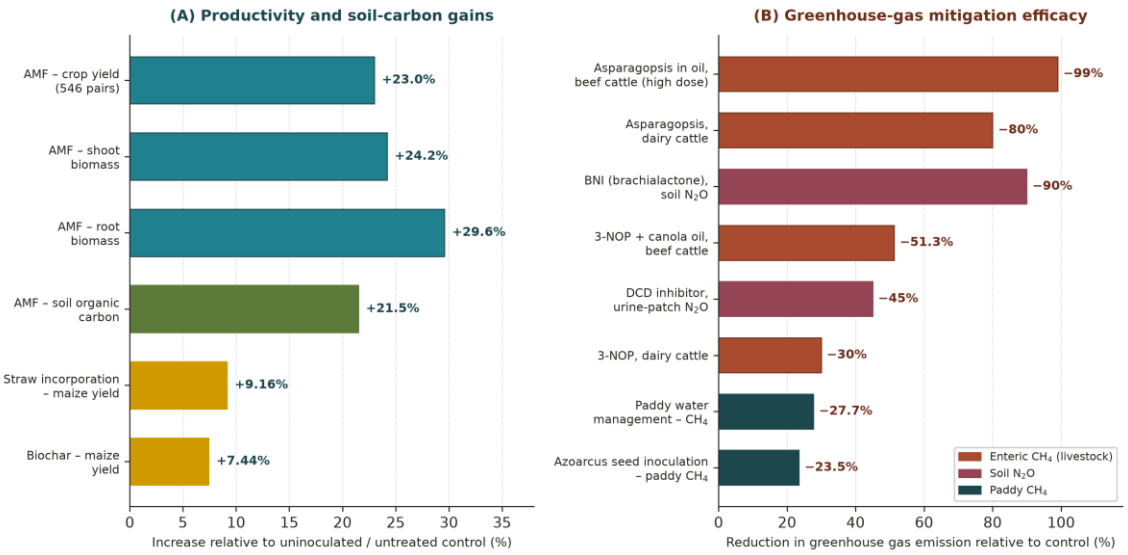

Figure4. Quantitative efficacy of microbial and microbially mediated interventions reported in the literature reviewed. Panel A summarises productivity and soil-carbon gains; Panel B summarises greenhouse-gas reductions. Values are means or maxima reported in the respective source studies and are not directly comparable across experimental systems

6. Microbial Pathways to Soil Carbon Sequestration

Understanding of soil carbon has shifted decisively from a chemical-recalcitrance model to a microbial one. Liang et al. (2019) quantified microbial necromass as a majority fraction of stable soil organic matter in many soils, and Miltner et al. (2021) formalised the conceptual link between necromass, soil processes and carbon turnover. Yang et al. (2025) position microbial carbon use efficiency (CUE) and necromass as the two master variables governing soil organic matter accumulation.

This reframing has practical consequences for CSA: management should aim to raise CUE and channel carbon into mineral-associated organic matter rather than simply increasing residue inputs. Ma et al. (2024) showed that CUE differs between particulate and mineral-associated pools, and Guo et al. (2024) linked enhanced CUE in

high-organic-matter soils to active microbial population dynamics and life-history strategy. Moorhead et al. (2024) established that resource limitation defines the global pattern of CUE, offering a basis for predicting where microbial carbon stabilisation will be most responsive to management. Sang et al. (2023) integrated community composition, biomass and necromass into a predictive framework for cropland soil organic carbon. Countervailing evidence exists, however: Grandy et al. (2022) found that fast-decaying litter enhanced soil carbon in temperate forests through pathways not explained by microbial physiological traits alone, and Angst et al. (2022) showed that earthworms act as catalysts in necromass stabilisation, indicating that faunal-microbial interactions matter. At the agronomic scale, Meng et al. (2022) reported maize yield increases of 9.16% from straw incorporation and 7.44% from straw-derived biochar in brown-earth soils, alongside changes in necromass carbon accumulation.

7. Microbial Biocontrol and Biopesticides

Climate change is expanding the geographic range and seasonal window of many crop pests and pathogens, increasing reliance on synthetic pesticides at precisely the moment when regulatory and residue pressures are tightening. Microbial biocontrol agents offer an alternative that is compatible with CSA objectives. Kumar et al. (2021) reviewed *Bacillus thuringiensis* and its Cry and Cyt toxins, still the most widely deployed microbial insecticide. Among fungal agents, *Trichoderma* dominates: Nowak et al. (2022) surveyed its current application status, Fadiji et al. (2023) provided a comprehensive treatment of *Trichoderma* species in plant disease biocontrol, and Chen et al. (2025) emphasised its dual role in disease suppression and growth promotion. Ijaz et al. (2024) reviewed eco-smart biocontrol strategies employing *Bacillus*, *Pseudomonas* and *Beauveria*. Adoption remains the bottleneck rather than efficacy: Manjunatha, Mawar and Kumar (2021) analysed the commercialisation and diffusion of bioformulations in Indian arid agriculture and identified inconsistent field performance, weak distribution networks and limited farmer awareness as the dominant barriers.

8. Enabling Technologies: Omics, Synthetic Communities and Machine Learning

Single-strain inoculants frequently fail in the field because they must compete with an established and highly diverse resident community. Synthetic microbial communities (SynComs), assembled from characterised isolates with complementary functions, are the leading response to this problem. Raaijmakers et al. (2024) reviewed strategies for tailoring functional SynComs, and Armanhi, Arruda and de Souza (2020) proposed a microbiome-to-traits design paradigm for improving crop resiliency. Koskella et al. (2024) provided a cross-systems methodological primer, while Jousset et al. (2024) framed SynComs as both a sandbox for hypothesis testing and a blueprint for soil health enhancement. Marotz et al. (2022) developed a reproducible and tunable synthetic soil community that makes controlled experimentation tractable.

Computational methods increasingly close the design-build-test-learn loop. Emmenegger et al. (2023) combined SynComs with machine learning to identify the community patterns most important for plant protection, an approach that converts high-dimensional microbiome data into actionable design rules rather than descriptive catalogues. Coupled with metagenomic and metatranscriptomic profiling of functional marker genes such as nifH, pmoA, mcrA and nosZ, these tools allow interventions to be targeted at specific biogeochemical steps rather than applied empirically.

9. Constraints, Regulation and Commercialisation

The gap between controlled-environment efficacy and field reliability remains the central obstacle to adoption, and the 2025 literature is notably candid about it. Poor rhizosphere competitiveness, competition from resident microbiota and cultivar- and site-specific responses all contribute to inconsistent outcomes. Shelf life compounds the problem: solid carrier-based inoculants typically retain

viability for only about six months below 30 °C and degrade rapidly under ultraviolet exposure, whereas liquid formulations containing cell protectants can remain viable for up to two years and tolerate temperatures as high as 55 °C. Advances in nanoformulation, freeze-drying, biofilm-based products and encapsulation are being pursued specifically to extend viability and improve establishment.

Regulation is the second structural constraint, and it is diverging across jurisdictions. In the European Union, Regulation (EU) 2019/1009, applicable from 16 July 2022, harmonised the market for EU fertilising products, establishing seven Product Function Categories, including PFC 6(A) for microbial plant biostimulants, and requiring qualifying microorganisms to appear on the CMC 7 positive list; compliant products may carry CE marking and circulate freely across the single market (European Commission, 2019). India regulates biofertilizers under the Fertiliser (Control) Order, 1985, amended in 2006 and 2009 to prescribe minimum viable counts of 1×10^7 CFU per gram of carrier material or 5×10^7 CFU per millilitre for liquid formulations, and further amended in 2024 to introduce a dedicated schedule for biostimulants (Government of India, 1985). By contrast, the absence of a harmonised federal definition of biofertilizer in the United States continues to impede market development. Commercially, the global biofertilizer market was valued at between USD 1.4 and 3.7 billion in 2024 depending on scope, with double-digit compound annual growth projected through the early 2030s (Grand View Research, 2024; & Global Market Insights, 2025) — substantial growth, but still a small fraction of the mineral fertilizer market.

10. Future Perspectives

Four priorities emerge from this synthesis. First, evaluation must move from single-season pot trials to multi-site, multi-year field networks with standardised protocols, so that effect sizes can be generalised rather than merely reported. Second, products should be matched to soil type, cropping system and climate rather than marketed as universal, with predictive models of the kind proposed by Moorhead et al. (2024) and Sang et al. (2023) guiding placement. Third, formulation science deserves investment commensurate with strain discovery, since viability during storage and transport is now a more binding constraint than microbial function. Fourth, monitoring, reporting and verification frameworks for microbially mediated mitigation need to mature before soil carbon and nitrous oxide benefits can be credibly monetised through carbon markets. Progress on the integration of stress-tolerance traits, mitigation function and yield stability within single SynComs — rather than trading these off — will determine whether microbial biotechnology becomes central or remains peripheral to CSA.

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All authors approved the final manuscript.

CONCLUSION

Microbial biotechnology now offers a coherent and evidentially substantial set of tools that act across all three pillars of climate-smart agriculture. On productivity, arbuscular mycorrhizal inoculation delivers average yield gains of around 23% under rainfed conditions and nitrogen-fixing bacteria can halve mineral nitrogen requirements without yield penalty. On adaptation, ACC deaminase, exopolysaccharide and osmolyte pathways confer measurable drought and salinity tolerance, with causal roles now confirmed genetically. On mitigation, the evidence is strongest of all: biological nitrification inhibition can reduce nitrous oxide by up to 90%, targeted paddy interventions lower methane by 17 to 80%, rumen additives suppress enteric methane by 30 to 99%, and

microbial necromass pathways stabilise soil carbon, with mycorrhizal management raising soil organic carbon by 21.5% on average.

The limiting factor is no longer biological plausibility but reliability at scale. Inconsistent field performance, short product shelf life, fragmented and divergent regulation, and weak farmer-facing distribution collectively explain why a technology with such strong mechanistic credentials still occupies a modest commercial position. Resolving these constraints is an engineering, regulatory and extension challenge as much as a scientific one. If it is met, the microbial layer of the agroecosystem — long invisible in climate policy — could become one of the most cost-effective instruments available for reconciling food production with climate stabilisation.

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