



Plant-microbe networks under climate change: molecular mechanisms, systems biology, and strategies for ecosystem resilience

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Received: 22 May 2026 / Accepted: 22 September 2026
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Abstract

The interplay between plants and their associated microbiomes is a critical determinant of ecosystem resilience under climate change. This review synthesizes current knowledge of plant-microbiome systems, focusing on the molecular mechanisms that govern synergistic interactions and on systems biology approaches to unraveling their complexity. We examine how these networks facilitate plant adaptation to drought, salinity, and extreme temperatures by modulating physiological responses, nutrient acquisition, and defense mechanisms. Multi-omics technologies (metagenomics, metatranscriptomics, metaproteomics, and metabolomics) enable holistic characterization of these interactions, supporting predictive modeling and targeted microbiome engineering. We explore synthetic microbial communities (SynComs) and bioinoculants as innovative solutions to enhance crop resilience and promote sustainable agriculture. Quantitative evidence demonstrates that plant growth-promoting rhizobacteria (PGPR) inoculation under drought stress increases yield by 56% and root biomass by 61% relative to drought-stressed controls, with multi-strain consortia increasing shoot biomass by 70% compared with 28% for single strains, while field trials show approximately 50% reduction in efficacy relative to controlled conditions (22% vs 45% yield increase), highlighting the critical translation gap. Key challenges include inconsistent field performance, formulation stability, commercial viability (>40% product failure rate), and regulatory fragmentation. Future directions integrating digital twins, AI-driven predictive analytics, and synthetic biology offer important opportunities. This review provides a framework for harnessing plant-microbiome systems to foster climate-resilient agriculture and ensure food security.

Keywords Climate resilience · Molecular mechanisms · Multi-omics · Nutritional exchange · Plant-microbe symbioses · Systems biology

1 Introduction

Global climate change presents an unprecedented challenge to natural and agricultural ecosystems, with rising temperatures, erratic precipitation, and increasing frequency of extreme weather events profoundly impacting plant growth, productivity, and survival (Ipbes 2019; Pörtner et al. 2022). These shifts threaten global food security and contribute to biodiversity loss, disrupting ecological balances and essential ecosystem services (Newbold et al. 2015). Traditional agricultural practices and conventional conservation strategies are often insufficient to address these interconnected stresses, necessitating innovative, integrative approaches that leverage natural ecological processes, particularly plant-microbe associations.

Symbiosis, the intimate association between two or more organisms, has been recognized as a fundamental

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driver of plant evolution, adaptation, and ecosystem functioning (Vandenkoornhuyse et al. 2015). The plant microbiome, comprising bacteria, fungi, archaea, and viruses residing in the rhizosphere, phyllosphere, and endosphere, acts as an extension of the plant's own genetic and physiological machinery—often referred to as the plant's “second genome” (Vandenkoornhuyse et al. 2015; Berendsen et al. 2012). Symbiotic associations, including nitrogen-fixing rhizobia, arbuscular mycorrhizal fungi, and plant growth-promoting rhizobacteria, enable plants to access essential nutrients, tolerate environmental stresses, and defend against pathogens (Boyno et al. 2025). These partnerships are products of co-evolution over millennia, shaped by molecular recognition, reciprocal regulation, and metabolic integration that have enabled plants to colonise diverse and challenging environments.

In this rapidly evolving environmental context, the plant-microbiome system has emerged as a highly promising area of research, offering profound and nuanced insights into how plants adapt, survive, and even thrive under otherwise adverse conditions (Berg et al. 2020). This intricate microbial community acts as a crucial, often indispensable, extension of the plant's own genetic and physiological machinery. Indeed, it is frequently referred to as the plant's “second genome” due to its fundamental role in mediating critical plant functions such as overall health, efficient nutrient acquisition, enhanced stress tolerance (both biotic and abiotic), and robust disease resistance (Vandenkoornhuyse et al. 2015). The symbiotic and often mutualistic relationship between plants and their associated microbes is a product of co-evolution over millennia, a partnership that has demonstrably enabled plants to colonize and flourish in diverse and frequently challenging environments, from arid deserts to saline soils and nutrient-poor landscapes.

Despite growing recognition of the plant microbiome's importance, a significant gap persists in understanding how molecular-level interactions translate into ecosystem-scale resilience under real-world climate stress (Trivedi et al. 2020). While individual pathways and microbial functions have been well characterised (Fu and Dong 2013; Glick 2015), integrative structures linking molecular mechanisms to ecosystem outcomes remain underdeveloped, hindering predictive modelling and scalable solutions. This review critically synthesises current knowledge across molecular, physiological, and ecosystem scales, explicitly addressing three key questions: (i) What molecular mechanisms govern plant-microbe communication under climate stress? (ii) How can multi-omics and systems biology approaches advance predictive understanding? (iii) What are the translational barriers to deploying microbiome-based solutions in agricultural systems? We systematically explore the molecular mechanisms of plant-microbe communication, including signalling

pathways, hormonal crosstalk, and metabolic exchanges (Sect. 2). We then examine how multi-omics technologies and systems biology enable holistic characterisation of these interactions, supporting predictive modelling (Sect. 3). The review discusses microbiome engineering strategies, including SynComs and bioinoculants, as approaches for enhancing plant resilience (Sect. 4), and evaluates the broader ecological impacts on soil health, nutrient cycling, and carbon dynamics (Sect. 5). Finally, we address translational challenges, ethical considerations, and future directions (Sects. 6 and 7). By integrating insights across molecular, physiological, and ecosystem scales, this review provides a framework for understanding and harnessing plant-microbiome interactions to foster climate-resilient agriculture.

2 Molecular mechanisms of plant-microbe communication under stress

The ability of plants to perceive and respond to environmental stressors is intricately linked to their interactions with associated microbial communities. This section explores the sophisticated molecular mechanisms that govern plant-microbe communication, particularly under abiotic (e.g., drought, salinity, heat) and biotic (e.g., pathogen attack) climate stresses. These interactions involve a complex exchange of signaling molecules, metabolites, and genetic information that collectively modulate plant physiological adaptation and defense responses (Berendsen et al. 2012).

2.1 Signaling pathways and hormonal crosstalk

Plant hormones, including auxins, cytokinins, gibberellins, abscisic acid (ABA), salicylic acid (SA), jasmonic acid (JA), and ethylene (ET), mediate stress responses and plant-microbe interactions through complex crosstalk networks (Musilova et al. 2016). Microbes can produce or modulate these hormones, influencing root architecture, nutrient uptake, and systemic resistance. For instance, plant growth-promoting rhizobacteria (PGPR) synthesize auxins that promote root elongation, thereby enhancing drought tolerance (Glick 2015). Under stress, ABA accumulates and triggers stomatal closure, but beneficial microbes can modulate ABA signaling to balance water conservation with growth (Egamberdieva et al. 2019). The SA and JA/ET pathways are crucial for defense against biotrophic and necrotrophic pathogens, respectively. Beneficial microbes can prime these pathways, leading to an enhanced defense capacity through Induced Systemic Resistance (ISR) or Systemic Acquired Resistance (SAR), and enabling faster responses to subsequent stress (Pieterse et al. 2003; Van Loon and Bakker 2006).

2.2 Microbial recruitment and assembly under abiotic stress

Plants actively shape their rhizosphere and endosphere microbiomes by secreting root exudates, which are complex mixtures of organic acids, sugars, amino acids, and secondary metabolites (Sasse et al. 2018). The composition of these exudates changes significantly under abiotic stress, serving as selective cues that recruit specific microbial taxa capable of conferring stress tolerance. For example, under drought stress, plants may release higher amounts of specific sugars or amino acids that favor the growth of drought-tolerant microbes capable of producing exopolysaccharides (EPS) to improve soil water retention or synthesizing osmoprotectants (Naylor 2018).

Salinity stress also alters root exudation patterns, promoting the enrichment of halotolerant microbes that can help plants mitigate salt toxicity. These microbes may produce enzymes that degrade reactive oxygen species (ROS), facilitate ion sequestration, or synthesize phytohormones that alleviate salt-induced growth inhibition (Glick 2010). The dynamic nature of microbial recruitment under stress highlights a sophisticated co-adaptation strategy in which plants actively select their microbial partners to enhance survival in challenging environments.

2.3 Molecular basis of induced systemic resistance (ISR) and systemic acquired resistance (SAR)

ISR and SAR represent two distinct but often overlapping plant defense mechanisms that can be triggered by microbial interactions. SAR is typically induced by localized pathogen infection and provides broad-spectrum, long-lasting resistance throughout the plant, often mediated by SA signaling (Fu and Dong 2013). ISR, on the other hand, is commonly triggered by beneficial microbes (e.g., PGPR) colonizing the roots and provides enhanced resistance against a range of pathogens and sometimes abiotic stresses, often involving JA/ET signaling pathways (Van Loon and Bakker 2006).

The molecular basis of ISR involves the recognition of specific microbe-associated molecular patterns (MAMPs) by plant pattern recognition receptors (PRRs). This recognition initiates a signaling cascade that leads to the transcriptional reprogramming of defense-related genes, without necessarily activating direct antimicrobial responses. Instead, ISR primes the plant's immune system, allowing for a faster and stronger defense response upon subsequent pathogen attack. Recent studies have revealed that long non-coding RNAs (lncRNAs) play critical roles in modulating plant defense responses; for instance, specific lncRNAs regulate cell wall defense genes to confer resistance against *Verticillium*

wilt in cotton, highlighting the complexity of regulatory networks underlying plant immunity (Zhang et al. 2022). This molecular priming is a crucial aspect of how beneficial microbes contribute to plant resilience under biotic stress, which can be exacerbated by climate change (Zamioudis and Pieterse 2012). Table 1 summarizes the major signaling molecules involved in plant-microbe interactions under abiotic and biotic stress.

2.4 Molecular recognition and specificity in symbiotic associations

The establishment of beneficial plant-microbe symbioses begins with molecular recognition events that determine partner specificity. PRRs perceive microbial-associated molecular patterns MAMPs, initiating signalling cascades that distinguish beneficial symbionts from pathogens (Zamioudis and Pieterse 2012). On the microbial side, small regulatory RNAs (sRNAs) play critical roles in signal-responsive regulation, enabling bacteria to sense environmental changes and modulate gene expression for adaptation to host-associated niches (Yi et al. 2026). In legume-rhizobia symbiosis, Nod factors produced by rhizobia are recognised by specific LysM receptor-like kinases (e.g., NFR1 and NFR5 in *Lotus japonicus*), triggering root hair curling, infection thread formation, and nodule organogenesis (Oldroyd 2013). Similarly, arbuscular mycorrhizal fungi (AMF), belonging to the phylum Glomeromycota, establish symbioses with approximately 80% of terrestrial plants (Boyno et al. 2025; Smith and Read 2008). Recognition of AMF involves the perception of Myc factors including lipochitooligosaccharides and short-chain chitin oligomers by plant receptors such as CERK1 and LYK9, activating the common symbiosis signalling pathway (CSSP) that regulates both nodulation and mycorrhization (Gobbato 2015). Recent reviews highlight that AMF species within Glomeraceae are more effective in disease protection, whereas those in Gigasporaceae are more proficient in promoting plant growth (Trejo et al. 2016). The model fungus *Rhizophagus irregularis* is widely studied, but species such as *Funneliformis mosseae*, *Rhizophagus clarus*, and *Gigaspora margarita* offer distinct benefits and warrant further investigation (Behera et al. 2025).

2.5 Co-adaptation and mutual regulation in symbiotic partners

Co-adaptation between symbiotic partners involves reciprocal regulation of gene expression and metabolic pathways. In nitrogen-fixing symbioses, the plant supplies dicarboxylic acids (primarily malate and succinate) as carbon sources to bacteroids, while rhizobia provide fixed nitrogen

Table 1 Key Molecular Signaling Molecules and Their Roles in Plant-Microbe Interactions

Signaling Molecule/Class	Origin	Primary Role in Plant	Role in Symbiosis	Symbiosis-Specific Mechanism
Nod Factors	Rhizobia	Root hair curling, infection thread formation	Recognition and specificity in legume-rhizobia symbiosis	Perceived by LysM receptors (NFR1/NFR5); activates common symbiosis signalling pathway (Oldroyd 2013)
Myc Factors	AM Fungi	Hyphal branching, root colonisation	Recognition and specificity in arbuscular mycorrhizal symbiosis	Perceived by CERK1/LYK9 receptors; activates CSSP (Boyno et al. 2025)
Auxins	Both	Cell elongation, root development	Microbes produce auxins to promote root growth, enhancing nutrient/water uptake	Modulates root architecture for symbiont colonisation (Glick 2015)
Cytokinins	Both	Cell division, shoot development	Microbes modulate cytokinin levels, influencing plant growth and stress tolerance	Regulates nodulation and symbiotic development (Musilova et al. 2016)
Strigolactones	Plant	Shoot branching, root development	Promote AM fungal branching and hyphal growth	Plant-derived signals attracting AM fungi (Gutjahr 2013; Parniske 2008)
Abscissic Acid (ABA)	Plant	Stomatal closure, stress response	Microbes can modulate ABA signalling to balance water conservation and growth	Coordinates stress responses with symbiotic outcomes (Egamberdieva et al. 2019)
Salicylic Acid (SA)	Plant	Defense against biotrophic pathogens	Involved in SAR priming by beneficial microbes, enhancing defense	Regulates defence-suppression required for symbiosis establishment (Pieterse et al. 2003)
Jasmonic Acid (JA)	Plant	Defense against necrotrophic pathogens, herbivory	Involved in ISR priming by beneficial microbes, enhancing defense	Mediates trade-offs between symbiosis and defence (Van Loon and Bakker 2006)
NCR Peptides	Plant	Bacteroid differentiation	Drive endoreduplication and terminal differentiation of bacteroids	Plant-derived signals controlling symbiotic nitrogen fixation (Kondorosi et al. 2013)
Dicarboxylic Acids	Plant	Carbon source for bacteroids	Provide carbon skeletons for nitrogen fixation	Nutritional exchange: plant supplies malate/succinate in exchange for fixed N (Udvardi and Poole 2013)
Flavonoids	Plant	Pigmentation, UV protection	Root exudates recruit beneficial microbes (e.g., <i>Rhizobium</i>)	Induce Nod gene expression in rhizobia; recruit AM fungi (Naylor and Coleman-Derr 2018)
Siderophores	Microbe	Iron chelation	Microbes produce siderophores to acquire iron, making it available to plants	Nutritional exchange: iron provision in exchange for carbon (Berendsen et al. 2012)
Exopolysaccharides (EPS)	Microbe	Biofilm formation, water retention	Microbes produce EPS to improve soil structure and water retention	Aid in root colonisation and biofilm formation (Naylor and Coleman-Derr 2018)
Osmoprotectants	Microbe	Cell protection under osmotic stress	Microbes produce compounds like proline, glycine betaine to protect plant cells	Stress mitigation: enhances plant tolerance to drought/salinity (Glick 2010)
Lipochitooligosaccharides	Both	Nodulation, mycorrhization	Symbiotic signalling molecules activating CSSP	Foundational signalling molecules in both rhizobial and mycorrhizal symbioses (Oldroyd 2013)

as ammonium in exchange (Udvardi 2013). This nutritional exchange is tightly regulated: plant oxygen homeostasis via leghemoglobin maintains microaerobic conditions for nitrogenase activity, while bacteroid differentiation involves plant-derived nodule-specific cysteine-rich (NCR) peptides that drive endoreduplication and terminal differentiation (Kondorosi et al. 2013). In mycorrhizal symbioses, plants allocate up to 20% of photosynthetically fixed carbon to fungal partners, receiving phosphorus, nitrogen, and water in return (Smith and Read 2008). The mutual regulation extends to stress responses, where symbionts modulate plant hormone signalling to balance growth and defence (Pieterse

et al. 2014). Co-evolutionary trajectories have shaped these partnerships, with evidence for reciprocal selection on signalling molecules and receptor specificity across diverse plant lineages. Table 2 further discusses the symbiosis specific mechanisms in relation to recognition, specificity, and mutual recognition.

2.6 Nutritional exchange and metabolic integration

The metabolic exchange between symbiotic partners represents a defining feature of mutualistic associations. In nitrogen-fixing symbioses, the plant provides amino acids

Table 2 Symbiosis-specific mechanisms through recognition, specificity, and mutual regulation

Symbiosis Type	Recognition Mechanism	Specificity Determinants	Mutual Regulation	Nutritional Exchange	Co-adaptation Features
Legume-Rhizobia	Nod factor perception by LysM receptors (NFR1/NFR5)	Structural variations in Nod factors; receptor polymorphisms; NCR peptide diversity	Plant supplies dicarboxylic acids; rhizobia provide fixed N; hormonal signalling coordination	Dicarboxylic acids (malate, succinate) ↔ ammonium/ amino acids	NCR-driven bacteroid differentiation; leghemoglobin for O ₂ homeostasis (Oldroyd 2013)
Arbuscular Mycorrhizal	Myc factor perception by CERK1/LYK9	Myc factor structural variations; strigolactone signaling	Plant supplies up to 20% fixed carbon; fungi provide P and N; reciprocal signalling	Sugars (hexoses) ↔ phosphate, nitrogen, water	Common symbiosis signaling pathway (CSSP); phosphate transporter regulation (Parniske 2008; Smith and Read 2008)
PGPR Associations	MAMP perception by PRRs; ISR priming	Variable; less stringent than biotrophic symbioses	Microbes produce phytohormones, osmoprotectants; plant regulates root exudation	Organic acids, sugars ↔ phytohormones, antimicrobials	ISR priming; root architecture modulation (Pieterse et al. 2003; Zamioudis and Pieterse 2012)
Ectomycorrhizal	Fungal effector recognition	Species-specific; host ranges vary	Plant supplies carbohydrates; fungi provide N and P; stress tolerance	Sugars ↔ nitrogen, phosphorus, water	Extensive hyphal networks; soil aggregation; drought tolerance (Smith and Read 2008)
Epiphytic/Endophytic	MAMP perception; niche-specific colonisation	Plant exudate composition; host genotype	Microbe-produced secondary metabolites; plant regulation of colonisation	Sugars, amino acids ↔ vitamins, phytohormones, stress metabolites	Tissue-specific colonisation; defence priming (Sasse et al. 2018; Compant et al. 2019)

(e.g., aspartate, glutamate) and dicarboxylic acids to bacteroids, which are metabolised to support nitrogenase activity (Yadav 2020). The fixed nitrogen is exported to the plant as ammonium or amino acids, with transport across symbiosome membranes mediated by specific transporters (Udvardi 2013). In AMF symbioses, the fungal partner delivers phosphate, nitrogen, and water to the plant via the symbiotic interface, while receiving up to 20% of photosynthetically fixed carbon (hexoses) in exchange (Smith and Read 2008). AMF enhance phosphorus uptake by extending hyphal networks beyond the root depletion zone and solubilising insoluble phosphates (Raj et al. 2025). Under drought stress, AMF not only enhance nutrient uptake but also improve plant water relations through direct water transfer via extraradical hyphae (Boyno et al. 2025). Recent metabolomic studies demonstrate that *R. irregularis* inoculation under heat stress triggers root-centred accumulation of amino acids (proline, asparagine) and organic acids, while under cold stress, it promotes shoot-centred sugar accumulation (sucrose, trehalose), stabilising cellular structures (Wang et al. 2026).

3 Multi-omics and systems biology of plant-microbiome networks

Understanding the intricate interactions within plant-microbiome systems, especially under the dynamic conditions of climate stress, necessitates a holistic approach that moves

beyond single-gene or single-species analyses. Multi-omics technologies, coupled with systems biology, are essential tools for unravelling the complexity of these networks, offering a comprehensive view of genetic potential, gene expression, protein activity, and metabolic outputs (Jansson and Hofmockel 2018). This integrated perspective is crucial for developing predictive perspectives and targeted interventions for ecosystem resilience.

3.1 Metagenomics, metatranscriptomics, and metaproteomics

Metagenomic sequencing of all genetic material from an environmental sample (e.g., soil, rhizosphere) provides a snapshot of the taxonomic diversity and functional potential (Förstner 2009). Under climate stress, metagenomic studies reveal shifts in community composition and enrichment of genes associated with adaptation to specific stressors, such as genes for osmolyte synthesis under salinity or water acquisition under drought (Delgado-Baquerizo et al. 2016). Metagenomic approaches have been instrumental in understanding the biogeography and community stability of endophytic diazotrophs in mangrove ecosystems, revealing how host species and environmental factors shape microbial community assembly and nitrogen-fixing potential (Hou et al. 2026). Metatranscriptomics focuses on sequencing all RNA molecules (mRNA, rRNA, tRNA), offering insights into active gene expression in both hosts and microbes under specific conditions (Zhang et al. 2021). This dynamic

approach identifies microbial genes involved in nutrient mobilization and defense priming, as well as plant genes that respond to microbial signals (Crawford et al. 2019). Metaproteomics studies proteins expressed by the entire microbial community and the plant host, providing direct evidence of biochemical processes at the plant-microbiome interface (Muth and Renard 2016). This reveals key enzymes, stress-response proteins, and signaling molecules that mediate interactions (Moshood et al. 2025). Metabolomics complements these approaches by comprehensively analyzing small-molecule metabolites (e.g., sugars, amino acids, organic acids, secondary metabolites) (Fiehn 2002). These metabolites are end products of cellular processes and play crucial roles in plant-microbe communication, nutrient exchange, and stress responses (Sasse et al. 2018).

3.2 Methodological advances in plant microbiome multi-omics

Recent methodological advances have addressed critical bottlenecks in plant microbiome multi-omics research. Host DNA contamination remains a major challenge in metagenomic sequencing of plant-associated microbiomes, as it obscures microbial genetic signatures and complicates accurate analysis. Wang et al. (2026) provided a comprehensive overview of current host DNA depletion strategies, including physical separation (filtration, gradient centrifugation), selective lysis, enzymatic treatments targeting plant cell walls, and advanced techniques such as targeted sequence capture with magnetic beads, methylation-based enrichment, and nanopore selective sequencing. Innovations such as CRISPR-Cas9 and chromatin immunoprecipitation-based host DNA depletion methods are proposed as novel approaches to address current limitations (Wang et al. 2026; Shi et al. 2022). Multi-omics integration has advanced significantly, with emerging approaches utilizing machine learning and network modeling to map inter-layer dependencies and predict system-level behavior. However, challenges persist due to data heterogeneity, normalization inconsistencies, and temporal misalignment (Albuja et al. 2026). Single-cell omics technologies, including single-cell RNA sequencing and integrated single-cell multi-omics, have enabled high-resolution profiling of microbial heterogeneity, shifting focus from population-averaged signals to cell-specific functional landscapes. These approaches have uncovered rare biosphere members and revealed niche-specific metabolic functions within rhizosphere systems (Kumar 2025).

3.3 Network analysis and predictive modeling of microbial consortia

The vast amount of data generated by multi-omics approaches necessitates sophisticated computational tools

for network analysis and predictive modeling (Popkes 2020). Systems biology integrates these diverse datasets to construct interaction networks that map the relationships between genes, transcripts, proteins, and metabolites within the plant-microbiome system (Rodriguez et al. 2019). These networks can reveal key hubs, regulatory pathways, and emergent properties that contribute to ecosystem resilience. Recent advances in artificial intelligence (AI) and machine learning have revolutionized predictive modeling in plant-microbiome research. A 2025 study demonstrated that machine learning models incorporating environmental factors and major microbial phyla could predict plant health status with 93% accuracy (Akinsemolu and Onyeaka 2025). Similarly, research on potato crops showed that predictive models developed using machine learning, high-throughput sequencing of seed tuber microbiomes, and drone imaging could forecast crop performance based on microbiome composition (Song et al. 2025). These models can identify the best microbial predictors of plant growth, enabling early intervention strategies. Ma, et al. (2025) comprehensively reviewed AI applications in rhizosphere microbiome research, identifying two complementary strategies: “outside-in” (SynCom design for crop enhancement) and “inside-out” (microbiome-assisted breeding of crop genotypes that recruit beneficial microorganisms). The review highlighted that AI can address three core challenges in SynCom design: selecting strains with complementary functions from soil microbial libraries; predicting inter-microbial interactions to avoid antagonistic effects; and optimizing community composition for specific environmental conditions (Ma et al. 2025).

Predictive modeling, often employing machine learning algorithms, uses these integrated datasets to forecast how plant-microbiome systems will respond to future climate scenarios or specific interventions (Opara et al. 2024). For example, models can predict the stability of microbial consortia at increasing temperatures or the efficacy of specific bioinoculants in enhancing crop yield under drought conditions. Such models are invaluable for guiding microbiome engineering efforts and developing climate-smart agricultural strategies.

3.4 Integrating molecular data with ecosystem-scale observations

The ultimate goal of multi-omics and systems biology in this context is to bridge the gap between molecular insights and ecosystem-scale outcomes. This involves integrating high-resolution molecular data with broader ecological observations, such as plant growth, biomass production, nutrient cycling rates, and biodiversity metrics (Singh et

al. 2025). Remote sensing technologies, including optoelectronic devices, can provide large-scale ecological data that, when combined with localized multi-omics data, offer a powerful foundation for understanding and managing ecosystem resilience.

This integrative approach allows researchers to identify molecular biomarkers of ecosystem health, predict ecosystem responses to climate change, and design targeted interventions that leverage plant-microbiome interactions for sustainable agriculture and environmental restoration. Figure 1 illustrates the multi-omics workflow in plant-microbiome research. Individual omics layers (metagenomics, metatranscriptomics, metaproteomics, metabolomics) provide complementary information on genetic potential, gene expression, protein activity, and metabolic outputs. Integration of these datasets through systems biology approaches enables the construction of interaction networks, the identification of regulatory hubs, and the development of predictive models to guide microbiome engineering and enhance ecosystem resilience. Table 3 provides an overview of various multi-omics tools and their specific applications in plant-microbiome research.

Despite the promise of multi-omics integration, significant technical limitations persist. Data integration remains challenging, with each platform generating complex, non-overlapping datasets that are difficult to reconcile (Jansson et al. 2023). The lack of standardized workflows and reproducible pipelines severely hampers meta-analyses (Fadiji et al. 2025). As emphasized by (Kimotho and Maina 2024), current approaches often fall short of achieving an integrated understanding. This recognition of limitations is essential for interpreting the literature and guiding future priorities.

3.5 Multi-omics data integration workflow

To provide readers with a clear understanding of how disparate multi-omics datasets are integrated, Fig. 2 presents a comprehensive schematic of the data integration workflow from sample collection through to translational applications. The workflow proceeds through four sequential stages. First, sample collection involves harvesting rhizosphere soil, root tissues, and plant exudates from experimental or field settings under defined climate stress conditions (e.g.,

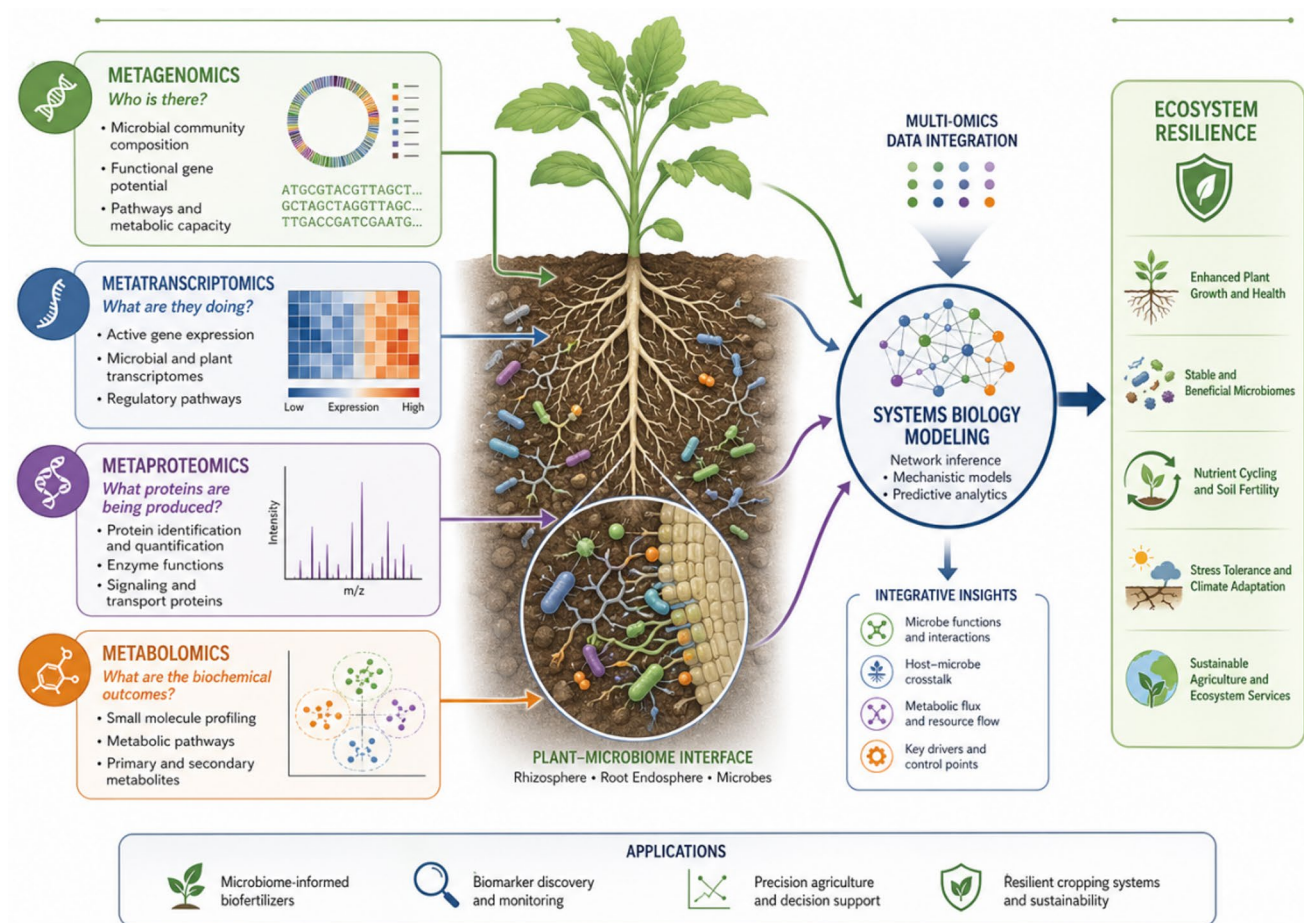


Fig. 1 Integrating multi-omics to understand and enhance plant-microbiome interactions

Table 3 Multi-omics tools and their applications in plant-microbiome research

Multi-Omics Tool	Information Provided	Key Applications in Plant-Microbiome Research	Advantages	Challenges	Representative Example(s)
Metagenomics	Genetic potential, taxonomic diversity	Identifying microbial taxa, functional genes (e.g., nutrient cycling, stress tolerance), community shifts under stress	Comprehensive view of genetic potential, discovery of novel genes/pathways	High data volume, functional annotation challenges, linking genes to active functions	Delgado-Baquerizo et al. (2016): identified microbial diversity drivers of multifunctionality in terrestrial ecosystems
Metatranscriptomics	Active gene expression, functional activity	Understanding microbial and plant responses to stress, identifying active metabolic pathways, host-microbe communication	Dynamic view of active processes, reveals real-time responses	RNA instability, high sequencing depth required, complex data analysis	Time-resolved tracking of microbial gene expression during drought in maize (Smith and Read 2008)
Metaproteomics	Expressed proteins, functional molecules	Direct evidence of biochemical functions, identifying key enzymes, stress response proteins	Direct insight into functional output, post-translational modifications	Low abundance proteins, complex sample preparation, database limitations	Martinez et al. (2023): cross-kingdom protein-protein interactions in rhizosphere
Metabolomics	Small-molecule metabolites, biochemical outputs	Identifying signaling molecules, nutrient exchange, stress-induced metabolic changes, biomarkers	Direct measure of physiological state, reflects phenotype	High chemical diversity, analytical challenges, compound identification	Schimmel and Schaeffer (2012): carbon flow mapping using stable isotope tracing
Systems Biology	Integrated networks, predictive models	Unraveling complex interactions, predicting system behavior, identifying regulatory hubs	Holistic understanding, predictive power, guides targeted interventions	Requires robust computational tools, integration of heterogeneous data, model validation	Chen et al. (2024): integrative multi-omics revealed drought tolerance network in wheat

drought, salinity, heat). Second, multi-omics data generation produces four complementary data layers: metagenomics (taxonomic diversity and functional gene potential), metatranscriptomics (active gene expression profiles), metaproteomics (expressed functional proteins), and metabolomics (small-molecule metabolites and biochemical outputs). Third, computational integration and systems biology modelling employs network analysis and machine learning algorithms to reconstruct interaction networks, identify regulatory hubs and biomarkers, and develop predictive models of system behaviour. Fourth, translational applications

leverage these integrated insights to guide targeted interventions, including SynCom design, bioinoculant development, and precision agricultural practices, ultimately contributing to enhanced ecosystem resilience under climate stress (Jansson and Hofmockel 2018; Rodriguez et al. 2019; Picard et al. 2021).

This integrated framework addresses a critical bottleneck in plant-microbiome research: reconciling heterogeneous datasets across different omics platforms. As emphasised by recent reviews, successful integration requires standardised workflows, consistent metadata reporting, and reproducible

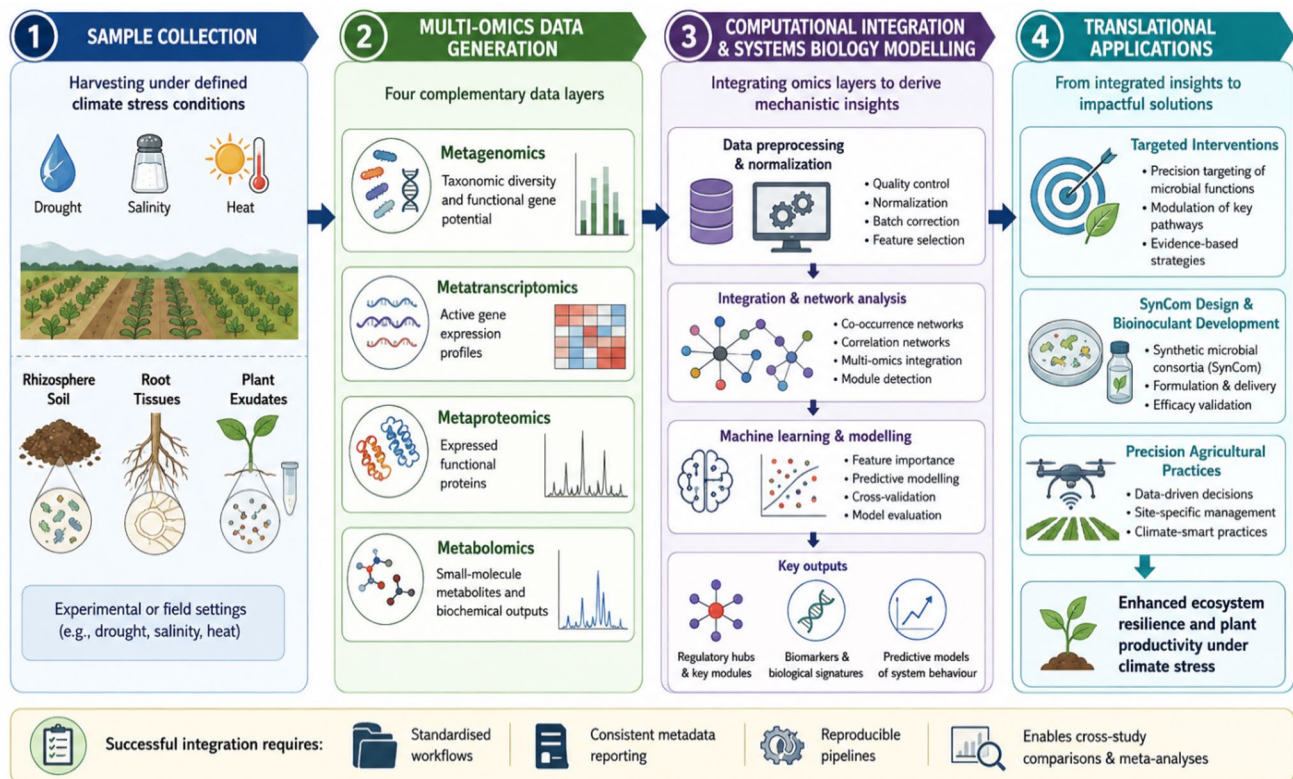


Fig. 2 Multi-omics data integration workflow for plant-microbiome research

pipelines to enable meaningful cross-study comparisons and meta-analyses (Singh et al. 2025; Pedrinho et al. 2026).

3.6 System biology of symbiotic networks

Systems biology approaches have illuminated the complexity of symbiotic interactions by integrating multi-omics data into predictive models of partner communication and metabolic integration (Rodriguez et al. 2019; Singh et al. 2025). Network analyses have identified regulatory hubs and keystone genes in both partners, revealing conserved modules for symbiotic signalling and stress responses (Ghag 2024; Lerner et al. 2026). For example, integration of transcriptomic and metabolomic data from *Medicago truncatula*-*Sinorhizobium meliloti* symbiosis identified regulatory networks coordinating nodulation and nitrogen fixation, with key transcription factors (e.g., NIN, NF-YA1) acting as master regulators of symbiotic development (Kapoor 2025; Rozas et al. 2022). Similarly, meta-analyses of mycorrhizal transcriptomes have revealed conserved gene expression signatures across diverse plant species, including phosphate transporters and stress response genes (Gutjahr 2013). Emerging applications of single-cell and spatial transcriptomics are enabling resolution of symbiotic interactions at cellular resolution, revealing heterogeneity in plant and microbial responses across infection zones (Wang et

al. 2026). Systems biology is also being applied to understand the ecological consequences of symbiosis, including impacts on ecosystem resilience and carbon dynamics under climate stress.

4 Microbiome engineering and synthetic communities (SynComs)

The profound understanding gained from multi-omics and systems biology approaches has enabled a new era of targeted interventions: microbiome engineering. This field aims to rationally design and manipulate microbial communities to enhance desirable plant traits, particularly resilience to climate stress, and improve agricultural sustainability (Wankhade et al. 2025). A key strategy within microbiome engineering is the development and application of Synthetic Microbial Communities (SynComs).

4.1 Design principles for SynComs

SynComs are defined as mixtures of microorganisms, typically bacteria and fungi, assembled to perform specific functions within a plant host or its environment (Han 2024). Unlike traditional bioinoculants, which often rely on single strains or undefined consortia, SynComs are

designed with a deliberate understanding of microbial interactions and their collective impact on plant phenotypes. The design principles for effective SynComs involve several critical considerations: selecting strains that collectively provide a broad range of beneficial functions (e.g., nutrient solubilization, phytohormone production, pathogen suppression, stress mitigation) that are complementary and non-redundant (Martins et al. 2023); ensuring that the selected strains can co-exist, interact synergistically, and establish themselves within the target environment without antagonistic effects. This often involves considering their metabolic capabilities, growth rates, and niche preferences (Johns et al. 2016); while some microbes are generalists, many exhibit host specificity. Designing SynComs that are compatible with the target plant species and its genetic background can enhance their efficacy and persistence (Pascale et al. 2020); selecting strains that can tolerate the specific abiotic stresses (e.g., drought, salinity, heat) prevalent in the target environment, ensuring their survival and functionality under challenging field conditions (Compant et al. 2019); and rigorously screening strains to ensure they are non-pathogenic to plants, animals, and humans, and do not pose any environmental risks (Lerner et al. 2026).

Recent studies have significantly advanced SynCom design through functional trait-based approaches and high-throughput screening. Jing et al. (2024) reviewed common principles in designing functional SynComs and proposed a multidimensional strategy integrating high-throughput experimental assays with computational genomic analyses of microbial functional capabilities, moving beyond taxonomy-based selection toward function-informed community assembly. Similarly, a 2026 study developed a cube-based screening strategy using 135 quinoa-associated bacterial isolates, identifying a nine-isolate SynCom (SCDY1) that promoted *Arabidopsis* growth under salinity stress by modulating oxidative stress, phenylpropanoid biosynthesis, and glutathione metabolism pathways (Dangjarean et al. 2026). This traceable framework demonstrates how systematic screening can discover functional consortia from large bacterial collections while preserving isolate-level contribution data.

Furthermore, Yamazaki et al. (2025) established a predictive approach integrating plant phenotyping, microbial genomics, and machine learning to optimize SynCom design in tomato. Testing over 800 SynCom–temperature combinations, an Elastic Net regression model trained on plant biomass data accurately predicted the performance of unseen SynComs, with prediction accuracy plateauing at approximately 5% of all possible combinations. Incorporating genomic features significantly improved model

performance, whereas microbiome compositional data alone were not informative (Yamazaki et al. 2025; Folorunso et al. 2026). The model-informed SynCom enhanced plant growth in field trials and improved heat stress tolerance under controlled conditions. Multi-omics analyses identified *Sphingobium* sp. enrichment linked to host plant metabolite (e.g., tomatine) and stress-responsive gene expression (Yamazaki et al. 2025).

The process often begins with isolating diverse microbes from climate-resilient environments or healthy plants, followed by extensive functional screening in controlled settings to identify strains with desired traits. These selected isolates are then assembled into consortia, with careful consideration of their interactions, before being formulated for field application. Figure 3 illustrates the SynCom development pipeline. (1) Isolation of diverse microbial strains from climate-resilient environments or healthy plants; (2) Functional screening in controlled settings to identify strains with desired traits (e.g., stress tolerance, nutrient solubilisation, phytohormone production); (3) Assembly into consortia with consideration of functional complementarity, ecological compatibility, and host specificity; (4) Formulation and field deployment for enhanced crop resilience under climate stress.

4.2 Bioinoculants and their role in enhancing crop resilience

Bioinoculants, which include single strains or simple mixtures of beneficial microorganisms, have been used in agriculture for decades to improve soil fertility and plant growth. With advancements in microbiome engineering, the development of next-generation bioinoculants, including SynComs, is becoming more sophisticated (Nehra and Choudhary 2015). These advanced bioinoculants are essential drivers in enhancing crop resilience to climate stress through various mechanisms:

Many bioinoculants, such as nitrogen-fixing bacteria (*Rhizobium*, *Azotobacter*) and phosphate-solubilizing microorganisms, enhance the availability and uptake of essential nutrients, reducing the need for synthetic fertilizers and improving plant vigor under nutrient-limited conditions (Vessey 2003). Bioinoculants can mitigate the effects of abiotic stresses by producing osmoprotectants, exopolysaccharides (EPS), or phytohormones that help plants cope with drought, salinity, and heat stress. They can also induce systemic tolerance mechanisms in plants (Glick 2012). Beneficial microbes can suppress plant pathogens through direct antagonism (e.g., antibiotic production, competition for resources), induction of systemic resistance (ISR), or by modifying the plant's immune system (Lugtenberg 2009). This reduces reliance on chemical

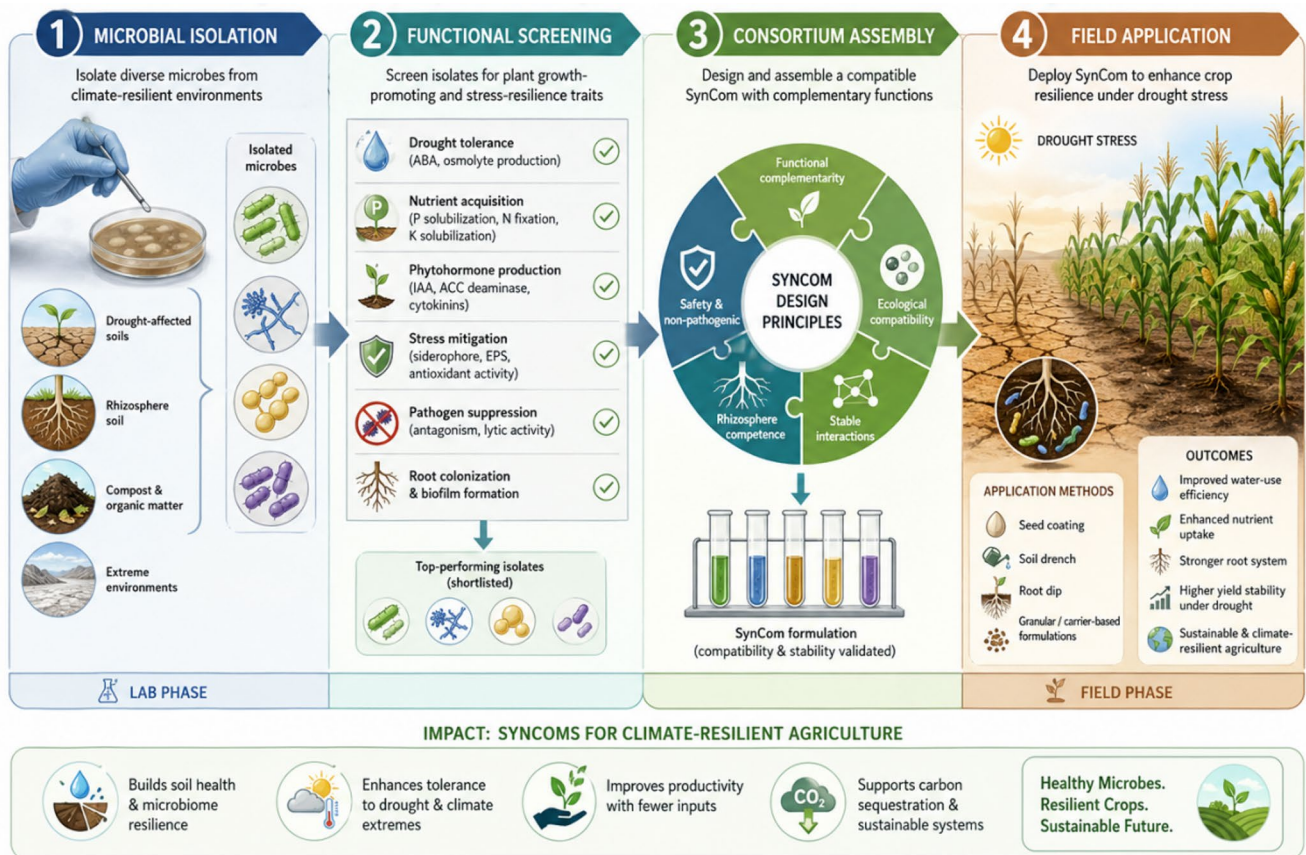


Fig. 3 From microbes to climate-resilient crops: design and deployment of synthetic microbial communities (SynComs)

pesticides, contributing to healthier ecosystems. Bioinoculants improve soil structure, aggregate stability, and organic matter decomposition, fostering a healthier soil microbiome and enhancing overall soil fertility and water retention capacity (Rillig and Mummey 2006).

Recent meta-analyses have provided robust quantitative evidence for the efficacy of bioinoculants. A comprehensive meta-analysis across corn, wheat, soybean, chickpea, cereals, and legumes evaluated the effects of plant growth-promoting rhizobacteria (PGPR) on biomass production, yield, and nutrient uptake under drought conditions (Satognon et al. 2026). Improvements in shoot nutrient concentrations were substantial, with nitrogen concentration rising by 24%, phosphorus by 44%, and potassium by 28%. Under drought conditions, root biomass increased by 61% and yield by 56% compared with drought-stressed controls. Crop group significantly moderated responses, with legumes exhibiting stronger responses than cereals, with shoot biomass increasing by 79% in legumes compared with 30% in cereals. Multi-strain consortia outperformed single-strain inoculants, increasing shoot biomass by 70% compared with 28% for single strains. Furthermore, consortia combining taxonomically distinct phyla (Firmicutes and Proteobacteria)

proved more effective than those composed of closely related taxa (Satognon et al. 2026).

A 2025 meta-analysis on *Trichoderma* spp. inoculation under abiotic stress demonstrated that *Trichoderma* presence resulted in increased plant biomass in both aerial and root parts, along with enhancement of photosynthesis-related parameters under all stress conditions. Specifically, positive effects were observed in chlorophyll fluorescence, stomatal conductance, chlorophyll a, and relative water content under salinity stress; in stomatal conductance and relative water content under drought; and in chlorophyll a and chlorophyll b under heavy metals exposure (dos Santos et al. 2025). Field validation of PGPR seed coating in potato demonstrated that PGPR increased plant height and stem diameter by 10.89% and 34.46%, respectively, compared with chemical coating, and elevated SPAD values and net photosynthetic rate at flowering by 20.22% and 32.22%, respectively. At maturity, potato aboveground, root, and tuber dry matter increased by 31.27%, 44.21%, and 41.88%, respectively, compared with chemical coating. Nitrogen and phosphorus translocation to tubers increased by 17.13% and 50.48%, respectively, with the best-performing composite formulation achieving a 38.9% higher yield compared with other treatments (Hu et al. 2025).

4.3 Case studies of successful microbiome engineering in the field

While the complexity of field environments poses significant challenges, several recent successful case studies demonstrate the potential of microbiome engineering:

Drought tolerance in maize SynComs derived from drought-tolerant microbial strains have shown promising results in enhancing water-use efficiency and yield in maize under limited irrigation (Aamir et al. 2026). These consortia often include bacteria capable of producing ABA-modulating enzymes or EPS. Recent field trials across multiple locations in sub-Saharan Africa demonstrated that a four-strain SynCom increased maize yield by 18–22% under moderate drought conditions (Aamir et al. 2026).

Salinity mitigation in rice Engineered microbiomes, particularly those enriched with halotolerant PGPR, have been shown to reduce sodium uptake and improve growth in rice cultivated in saline soils, offering a sustainable solution for agriculture in salt-affected areas (Kumawat et al. 2023). A study across 15 salt-affected fields in South Asia reported that halotolerant SynCom application reduced sodium content in rice shoots by 35% and increased grain yield by 27% compared with untreated controls (Kumawat et al. 2023). Ninkuu et al. (2025) further demonstrated that a quinoa-derived SynCom (SCDY1) promoted *Arabidopsis* growth under salinity stress through modulation of oxidative stress and phenylpropanoid biosynthesis pathways.

Predictive SynCom design in tomato Yamazaki et al. [72] demonstrated a predictive framework for SynCom optimization using machine learning, testing over 800 SynCom–temperature combinations. The model-informed SynCom enhanced tomato plant growth in field trials and improved heat stress tolerance under controlled conditions, validating the translational potential of AI-guided design [72].

PGPR seed coating in potato A two-year field experiment demonstrated that PGPR seed coating increased soil nitrate-N and available P by 16.29% and 17.29%, respectively. Plant height and stem diameter increased by 10.89% and 34.46% compared with chemical coating, while tuber yield increased by 38.9% with the best-performing composite formulation. Nitrogen and phosphorus accumulation in tubers increased by 66.74% and 55.25%, respectively (Hu et al. 2025).

Climate-smart biofertilizers A 2026 review on SynComs for climate-smart biofertilizers highlighted that rationally designed SynComs can enhance plant tolerance to drought,

flooding, extreme temperatures, and physical disturbance through complementary microbial mechanisms, including ACC deaminase production, osmoprotectant supply, and microbially induced calcite precipitation for soil structural integrity (Verma et al. 2026).

These examples underscore the translational potential of microbiome engineering, translating laboratory insights into practical applications that contribute to climate-resilient agriculture. However, challenges remain in ensuring the consistent performance and persistence of engineered microbiomes across diverse environmental conditions. Table 4 compares microbiome engineering strategies, highlighting their approaches, advantages, and limitations.

5 Impact on soil health and ecosystem functions

The plant-microbiome system is a cornerstone of soil health, profoundly influencing biogeochemical cycles, soil structure, and the overall functionality of terrestrial ecosystems. Under the increasing pressures of climate change, understanding and harnessing these interactions are critical to maintaining and enhancing ecosystem services vital to both natural and agricultural landscapes (Bardgett and Van Der Putten 2014).

5.1 Nutrient cycling and carbon sequestration

Microbial communities in the soil are the primary drivers of nutrient cycling, transforming essential elements like nitrogen (N), phosphorus (P), and potassium (K) into forms accessible to plants. Nitrogen fixation, carried out by free-living and symbiotic bacteria (e.g., *Rhizobium* in legumes), converts atmospheric nitrogen into ammonia, a crucial step in the global nitrogen cycle (Giller and Cadisch 1995). Similarly, phosphate-solubilizing bacteria and fungi release inorganic phosphate from soil minerals, making it available for plant uptake. Soil ecological stoichiometry entails the balance of carbon, nitrogen, and phosphorus which synchronously regulates nutrient concentrations and ratios in terrestrial and aquatic ecosystems, with microbial communities playing a central role in mediating these stoichiometric relationships (Liu et al. 2023). These microbial processes are highly sensitive to environmental conditions, and climate stressors such as drought or elevated temperatures can disrupt microbial activity, leading to reduced nutrient availability and impaired plant growth (Dubey et al. 2019). AMF play a particularly important role in carbon sequestration. They transfer plant-derived carbon to soil aggregates through several mechanisms: (i) production of

Table 4 Microbiome Engineering Strategies for Enhancing Symbiotic Outcomes

Strategy	Approach	Symbiotic Mechanism(s) Enhanced	Advantages	Limitations	Key Applications	Representative Example(s)
Traditional Bioinoculants	Single strain or simple mixture of beneficial microbes	Nutritional exchange (N, P, K); stress tolerance (osmoprotectants, phytohormones)	Easy to produce, relatively low cost, established market	Limited functional diversity, inconsistent field performance, lack of ecological compatibility	Nitrogen fixation, phosphate solubilization, general plant growth promotion	<i>Rhizobium</i> inoculants for legumes; <i>Azotobacter</i> for cereals (Nosheen et al. 2021)
Synthetic Microbial Communities (SynComs)	Rationally designed mixtures of defined microbial strains	Multi-faceted: recognition priming, nutritional exchange, co-adaptive regulation, stress mitigation	Targeted functions, enhanced robustness, improved predictability, synergistic effects	Complex design and assembly, high cost, regulatory hurdles, ecological establishment challenges	Enhanced stress tolerance, disease suppression, improved nutrient use efficiency, bioremediation	ML-designed SynCom enhanced tomato heat tolerance; quinoa-derived SynCom for salinity mitigation (Yamazaki et al. 2025)
CRISPR-based Genome Editing of Microbes	Direct genetic modification of microbial genomes to enhance beneficial traits	Recognition (enhanced MAMP production); nutritional exchange (improved N fixation/P solubilisation); stress tolerance	Precise control over microbial functions, creation of novel traits	Public perception concerns, regulatory challenges, off-target effects, limited to culturable microbes	Enhancing nutrient cycling, increasing stress tolerance, improving biocontrol efficacy	EcCMC engineered bacterium for enhanced N-fixing colonisation (Ghag 2024)
Phage Therapy	Use of bacteriophages to selectively target and eliminate pathogenic bacteria	Protection of symbiotic partners; maintenance of symbiotic interfaces	Highly specific, self-replicating, effective against antibiotic-resistant strains	Narrow host range, potential for phage resistance, regulatory approval	Biocontrol of bacterial plant pathogens, reducing disease burden	Phage-based biocontrol of bacterial wilt in tomato (Hjeljord and Tronsmo 1998)
Host Genetic Engineering for Microbiome Recruitment	Modifying plant genes to selectively recruit beneficial microbes	Recognition (enhanced exudation of attractants); specificity (modulated receptor specificity); co-adaptation	Long-term solution, integrated into plant genome	Complex genetic engineering, time-consuming, public acceptance	Enhancing plant-microbe symbiosis, improving nutrient uptake, boosting stress resilience	Plants engineered for enhanced flavonoid exudation to recruit specific PGPR

glomalin-related soil proteins (GRSP), stable glycoproteins that bind soil particles into aggregates and contain recalcitrant carbon that persists for decades (Singhn et al. 2025); (ii) physical enmeshment of organic matter by hyphae, promoting micro-aggregate formation (Yusuf et al. 2025); and (iii) hyphal exudation of low-molecular-weight compounds that stimulate microbial activity and carbon stabilisation (Musilova et al. 2016). AMF hyphae can reduce CO₂ and N₂O emissions from residue-affected soils, contributing to greenhouse gas mitigation (Boyno et al. 2025). Quantitative estimates suggest that AMF-mediated GRSP accounts for a substantial fraction of stable soil organic carbon in agricultural systems.

The plant-microbiome system plays a significant role in carbon sequestration in addition to nutrient provision. Plants fix atmospheric CO₂ through photosynthesis, and a substantial portion of this carbon is allocated to the roots and subsequently released into the soil as exudates, fueling microbial growth. Soil microbes, in turn, process organic matter, thereby forming stable soil organic carbon (SOC) (Jansson et al. 2023). Healthy, diverse microbiomes enhance the efficiency of carbon cycling and promote the

long-term storage of carbon in soils, thereby contributing to climate change mitigation. In alpine grassland restoration, SOC increased progressively with restoration time, reaching levels 72.6% higher in topsoil and 171.3% higher in subsoil compared with unrestored conditions. Vegetation recovery increased labile carbon inputs, stimulating microbial growth and accelerating the “microbial carbon pump” turnover, thereby promoting amino sugar accumulation and glomalin-related soil protein-driven soil aggregation (Deng et al. 2025). Research on mixed forest plantations demonstrated that soil microbial functional groups enhance carbon storage by regulating readily oxidizable carbon and particulate organic carbon content, with bacterial diversity and composition having more positive effects on soil organic carbon than fungal communities (Chen et al. 2024).

Climate stress, however, can alter plant carbon allocation patterns and microbial decomposition rates, potentially impacting the soil’s capacity for carbon sequestration (Schimel and Schaeffer 2012). In ¹³C pulse labeling experiments, drought decreased the transfer of labeled assimilates relative to irrigation treatments, with greater reduction of assimilate incorporation by fungi (−85%)

than by gram-positive (−43%) and gram-negative bacteria (−58%). This suggests that fresh rhizodeposits are predominantly used for osmoregulation or storage under drought, at the expense of new cell formation. Two weeks after rewetting, ^{13}C enrichment in microbial membranes was greater in previously dry than in continuously moist soils, indicating high resilience of belowground carbon allocation and rhizosphere communities to drought (Gao et al. 2024). The use of bioinoculants and SynComs can contribute to GHG mitigation by reducing synthetic fertilizer requirements (and associated N_2O emissions from fertilizer application), enhancing nitrogen use efficiency, and promoting carbon sequestration through improved soil aggregation and organic matter stabilisation. Studies have reported that PGPR inoculation can reduce N_2O emissions by 15–30% through enhanced plant nitrogen uptake and reduced soil nitrate availability, though this effect is highly dependent on soil type and management practices (Lopez et al. 2025; Gao et al. 2024).

5.2 Soil structure and hydrological dynamics

Microbes are instrumental in shaping soil physical properties, particularly soil structure and water retention capacity. Fungal hyphae and bacterial exopolysaccharides (EPS) act as glues, binding soil particles into stable aggregates (Rillig and Mummey 2006; Ali et al. 2024). These aggregates improve soil aeration and water infiltration and reduce erosion, creating a more favorable environment for plant roots and microbial life. Well-structured soil is more resilient to drought because it can hold more water and facilitate its movement to plant roots. Climate change-induced changes in precipitation patterns, leading to more frequent droughts or intense rainfall events, underscore the importance of microbial contributions to soil structure (Kumar et al. 2026). Research on Fiber Bragg Grating (FBG) sensors has shown promise in monitoring soil physical properties, including aggregation forces and hardness, which are directly influenced by microbial activity and organic matter content (Abdulraheem et al. 2025a). These optoelectronic devices can provide real-time, high-resolution data on soil dynamics, offering insights into how plant-microbiome interactions modify the soil environment. For instance, the presence of certain microbial communities can enhance soil aggregation, which FBG sensors could detect as changes in mechanical properties, thereby providing a quantifiable link between microbial activity and soil health (Abdulraheem et al. 2025b).

5.3 Microbiome-mediated ecosystem resilience

The collective impact of plant-microbiome interactions extends to the overall resilience of ecosystems. A diverse and functionally rich microbiome provides redundancy

and plasticity, allowing ecosystems to better withstand and recover from disturbances caused by climate change (Wagg et al. 2014). For example, in the face of pathogen outbreaks exacerbated by a changing climate, a healthy soil microbiome can offer a natural biocontrol buffer, reducing disease incidence and preventing widespread plant mortality. Similarly, in nutrient-poor environments, a robust microbial community can ensure a continuous nutrient supply, supporting plant productivity even under suboptimal conditions. Microbiome-mediated resilience is not limited to individual plant health but scales up to influence community structure and ecosystem stability. By enhancing the fitness of dominant plant species or facilitating the establishment of new species, microbiomes can help maintain biodiversity and ecosystem function in a changing world. Figure 4 illustrates the conceptual diagram showing how plant-microbiome interactions contribute to ecosystem resilience under drought, salinity, heat, and pathogen pressure. Beneficial microbes enhance plant stress tolerance through multiple mechanisms, including phytohormone modulation, osmo-protectant production, nutrient mobilisation, and pathogen suppression, collectively maintaining ecosystem functions and stability under climate extremes. Table 5 summarizes the conditions of the plant-associated microbiome in relation to major ecosystem services, highlighting the impact of climate stress on these functions and the mechanisms by which microbiome-mediated resilience is achieved.

6 Translational research from laboratory to field

While laboratory studies have elucidated symbiotic mechanisms, translating these insights to field applications requires addressing environmental complexity, formulation stability, and regulatory frameworks (Trivedi et al. 2020; Bashan et al. 2010). Field efficacy of microbial inoculants is approximately 50% of that observed under controlled conditions (45% vs. 22% yield increase), with commercial failure rates exceeding 40% within three years of market introduction (Aminov 2011). Advanced monitoring technologies, including remote sensing, wireless sensor networks, and portable sequencing, are emerging tools for assessing symbiotic performance in situ (Pedrinho et al. 2026; Abdulraheem et al. 2023). However, the core challenge remains understanding and predicting symbiotic outcomes across diverse environmental contexts.

6.1 Challenges in scaling-up laboratory breakthroughs

Translating promising laboratory results into effective field applications is often hampered by several factors.

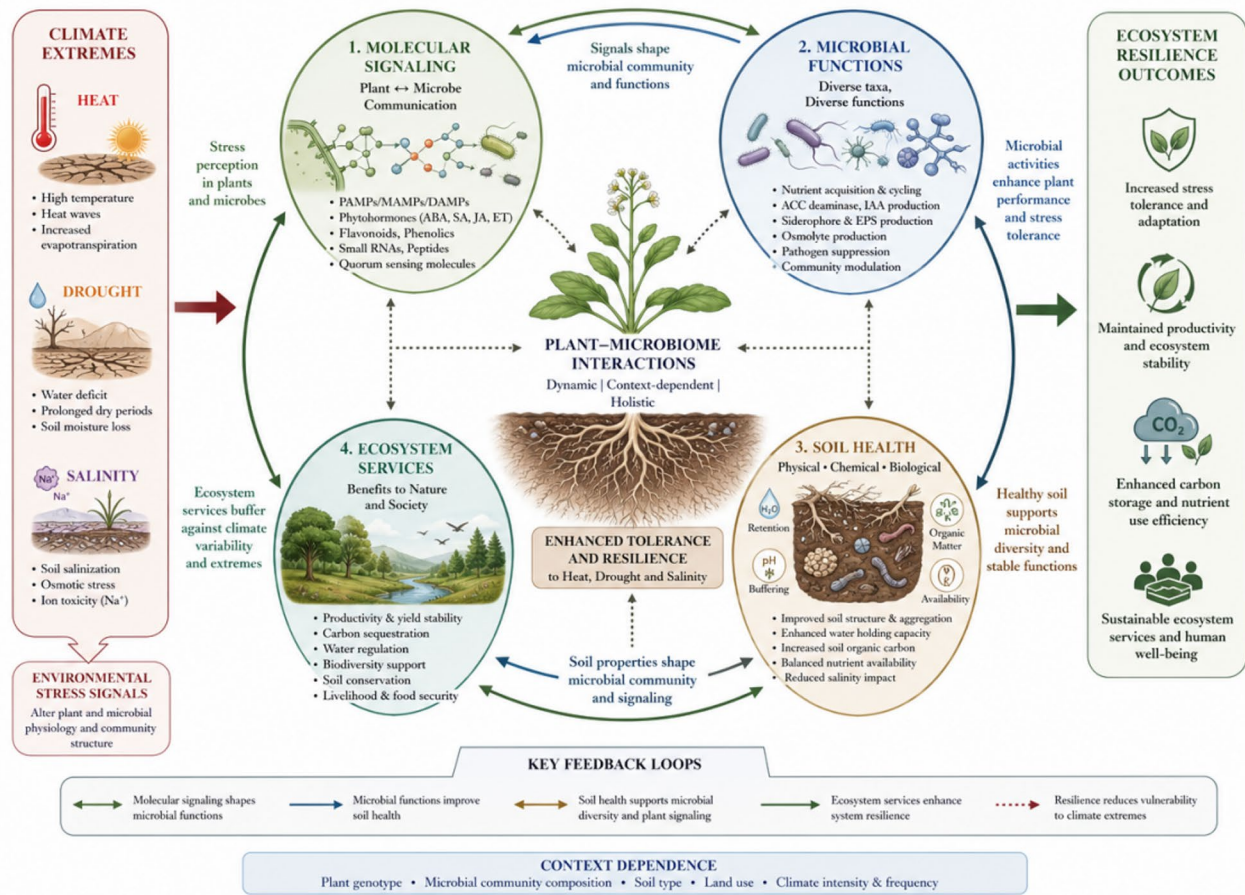


Fig. 4 Plant-microbiome interactions drive ecosystem resilience under climate extremes

Environmental complexity, including fluctuating temperatures, moisture levels, soil types, and nutrient availability, can significantly affect the survival, establishment, and functionality of introduced microbes (Trivedi et al. 2020; Walter et al. 2018). Microbial community dynamics in native soil are highly diverse and resilient, and introduced microbes compete with established communities for resources and niches, leading to unpredictable persistence and activity (Leite et al. 2022). Host-microbe-environment interactions are highly context-dependent; a beneficial interaction observed in controlled settings may not manifest similarly in the field due to genetic variations in plant cultivars, differences in soil properties, or the presence of other biotic factors (Malgioglio et al. 2022). Formulation and delivery of stable, cost-effective formulations for bioinoculants and SynComs that can withstand storage, transport, and field application remains a significant hurdle, with many products showing <10% viable cell recovery after 6 months of ambient storage (Bashan et al. 2010). The regulatory framework for introducing genetically modified microbes or novel microbial consortia raises concerns about regulatory oversight and public acceptance, necessitating robust safety assessments and clear guidelines (Kapoor 2025).

The documented field-scale failures and inconsistencies are further supported by a comprehensive evaluation of PGPR efficacy, which found that the median relative yield increase was 45% in growth chamber studies but declined to 22% in field trials, representing a reduction of more than 50% (Naqvi and Hasan 2026). Field trial success was highly dependent on experimental conditions: efficacy was higher in unfertilised soils compared with fertilised systems, and microbial consortia were significantly more effective than single species under stress conditions (Naqvi and Hasan 2026). Furthermore, the economic viability of microbial products is constrained by multiple factors. Production costs for high-quality SynComs remain substantially higher than for single-strain bioinoculants, with multi-strain formulation requiring additional quality control and compatibility (Adhikary et al. 2026). A 2025 industry analysis reported that while the global agricultural biologicals market is projected to reach USD 28.5 billion by 2030, the commercial failure rate for new microbial products exceeds 40% within the first three years of market introduction (Patel and Mandalia 2025). The 22% median yield increase observed in field trials does not always translate to consistent economic

Table 5 Microbiome impacts on key ecosystem services

Ecosystem Service	Microbiome Contribution	Impact of Climate Stress	Resilience Mechanism
Nutrient Cycling	Nitrogen fixation, phosphorus solubilization, nutrient mineralization	Disruption of microbial activity, reduced nutrient availability	Functional redundancy, stress-tolerant microbial strains, enhanced nutrient uptake by plants
Carbon Sequestration	Organic matter decomposition, humification, soil aggregate formation	Altered decomposition rates, reduced carbon input from plants	Stable soil aggregates, microbial production of recalcitrant carbon compounds
Greenhouse Gas Mitigation	N ₂ O reduction via enhanced N uptake, CH ₄ oxidation	Increased N ₂ O emissions under drought-rewetting cycles, altered CH ₄ flux	PGPR-mediated N ₂ O reduction (15–30%), methanotroph activity, improved N use efficiency
Water Regulation	Improved soil structure, enhanced water infiltration, reduced runoff	Increased drought frequency, altered precipitation patterns	Microbial EPS production, improved soil aggregation, enhanced plant water use efficiency
Disease Suppression	Biocontrol of pathogens, induced systemic resistance (ISR)	Increased pathogen virulence, altered host-pathogen interactions	Antagonistic microbes, ISR priming, competitive exclusion of pathogens
Pollution Remediation	Degradation of contaminants (e.g., pesticides, heavy metals)	Increased pollutant mobility, altered microbial degradation pathways	Microbial detoxification pathways, bioremediation potential of specific strains
Biodiversity Maintenance	Support for plant diversity, creation of diverse microbial habitats	Habitat loss, species shifts, reduced microbial diversity	Niche creation, facilitation of plant establishment, buffering against environmental fluctuations
Plant Productivity	Enhanced growth, stress tolerance, nutrient uptake	Reduced photosynthesis, impaired growth, yield losses	Phytohormone production, stress mitigation, improved resource acquisition

returns across seasons, particularly when product costs and seasonal variability are factored in. Adoption rates are further influenced by inconsistent field performance, limited

technical support, and uncertainty regarding cost-effectiveness relative to conventional inputs (Nosheen et al. 2021).

6.2 Field-based monitoring technologies

Overcoming field challenges requires sophisticated monitoring technologies providing real-time data on plant performance, microbial activity, and environmental conditions. Remote sensing and hyperspectral imaging—using satellite, drone, and ground-based systems—can monitor large agricultural areas, providing data on plant health, stress indicators, and vegetation indices that correlate with microbial interventions (Abdurraheem et al. 2023). Wireless sensor networks (WSNs) continuously monitor soil moisture, temperature, pH, and nutrient levels, integrating environmental data with plant physiological responses and microbial community analyses (Pedrinho et al. 2026). Fiber Bragg Grating (FBG) sensors offer high-resolution, real-time monitoring of soil physical properties, helping assess how microbiome engineering strategies impact soil structure and hydrological dynamics (Abdurraheem et al. 2025a). Portable ‘omics’ technologies—including advances in portable sequencing devices (e.g., Oxford Nanopore Technologies)—enable rapid, on-site metagenomic and metatranscriptomic analyses, allowing researchers to monitor microbial community shifts and gene expression patterns directly in the field (Khan et al. 2024). These technologies facilitate adaptive management strategies, allowing farmers and conservationists to adjust interventions based on real-time feedback from the ecosystem.

A critical assessment reveals that commercial inoculants frequently fail due to genotype-environment context dependency (Malgioglio et al. 2022). The “home-field-advantage” of resident native communities often outcompetes introduced formulations (Pedrinho et al. 2026). Despite reliability concerns, farmer adoption continues to grow rapidly—Brazilian farmers now use biological inputs on over 70% of the 81.5 million hectares in the 2024/2025 crop season (Pedrinho et al. 2026). This underscores that positive perceptions often outweigh statistical significance, highlighting the need for realistic expectations and product transparency (Nosheen et al. 2021).

6.3 Case studies of translational success

Despite the challenges, several successful translational efforts demonstrate the potential of plant-microbiome research: Commercial biofertilizers containing nitrogen-fixing bacteria or phosphate-solubilizing microbes are widely used globally, reducing reliance on chemical fertilizers and improving crop yields in various agricultural

systems (Glick 2012; Nosheen et al. 2021). Microbial-based biopesticides, often containing *Bacillus* species or *Trichoderma* fungi, are increasingly deployed to manage plant diseases and pests, offering environmentally friendly alternatives to synthetic chemicals (Fravel 2005). The long-standing success of *Rhizobium* inoculants for legume crops exemplifies effective microbiome engineering, significantly enhancing nitrogen fixation and productivity in agricultural fields worldwide (Lie et al. 1987). These successes provide a blueprint for future translational research, emphasizing the need for interdisciplinary collaboration, robust field validation, and the integration of advanced monitoring technologies to ensure the consistent performance and widespread adoption of plant-microbiome-based solutions.

Documented field failures provide critical lessons for improving translational success. A comprehensive meta-analysis found that PGPR efficacy in field trials (22% yield increase) was less than half that observed in controlled environments (45%), highlighting the profound impact of environmental variability. The analysis further revealed that soil type, fertilization regime, and the presence of abiotic stressors significantly moderated outcomes. This suggests that successful deployment requires careful matching of microbial products to specific environmental contexts rather than “one-size-fits-all” approaches. The economic implications of these inconsistencies are substantial. Factors contributing to failures included poor shelf-life, insufficient understanding of target environment conditions, and inadequate farmer support and training.

7 Challenges, ethical considerations, and future perspectives

While the potential of plant-microbiome systems to enhance ecosystem resilience under climate stress is immense, their widespread application is not without challenges. Addressing these technical, ecological, and ethical considerations is crucial for realizing the full promise of microbiome-based solutions.

7.1 Technical hurdles in data integration and field deployment

Data heterogeneity and integration Multi-omics datasets are vast and complex, originating from diverse platforms and experimental designs. Integrating these heterogeneous data types (genomic, transcriptomic, proteomic, metabolomic) to build comprehensive systems biology models

remains a significant computational and analytical challenge (Jansson and Hofmockel 2018; Picard et al. 2021).

Predicting microbial behavior in complex environments The behavior of microbes in controlled laboratory settings often differs from their performance in dynamic field environments. Factors such as soil type, pH, nutrient availability, and interactions with native microbial communities can drastically alter the efficacy of introduced microbes or engineered consortia (Yadav 2020). Developing robust predictive models that account for this environmental variability is essential.

Formulation and delivery of bioinoculants Ensuring the viability, stability, and effective delivery of bioinoculants and SynComs to the target plant or soil environment is critical. Current formulations may struggle with shelf-life, environmental stress (e.g., UV radiation, desiccation), and consistent establishment in the rhizosphere (Bashan et al. 2010).

High-throughput phenotyping Accurately assessing the impact of microbiome interventions on plant phenotypes in the field requires high-throughput phenotyping technologies. Integrating advanced sensors, robotics, and AI for automated data collection and analysis is vital for rapid evaluation of treatment efficacy (Abdulraheem et al. 2026).

7.2 Ecotoxicological and ethical implications of engineered microbiomes

The introduction of engineered microbes raises complex ecotoxicological and ethical questions that demand rigorous scrutiny and proactive governance. These considerations are paramount to ensure that the pursuit of enhanced agricultural productivity and ecosystem resilience does not inadvertently lead to unforeseen negative consequences for environmental health or societal well-being. A balanced approach is required, integrating scientific innovation with responsible stewardship and public engagement. Ecological impact and non-target effects introduced by microbes may displace native species, disrupt ecological networks, or alter critical ecosystem functions. Comprehensive environmental risk assessments and long-term monitoring are essential (Lerner et al. 2026). Furthermore, the potential for introduced microbes to become invasive or to persist beyond their intended functional lifespan needs careful consideration.

Horizontal gene transfer (HGT) from engineered microbes to native populations could spread novel traits, such as antibiotic resistance genes, virulence factors, or metabolic capabilities, into environmental or clinical settings (Aminov 2011). Biological containment strategies

(e.g., auxotrophy, suicide genes) and stringent risk assessment frameworks are required to minimize these risks. Also, public perception and acceptance of genetically modified organisms (GMOs) and engineered biological systems, including engineered microbiomes, vary widely across different regions and cultures. Negative perceptions, often fueled by misinformation, can impede technology adoption (Frewer et al. 2003). Transparent communication, proactive public engagement, and stakeholder involvement are crucial for building trust and social license. The regulatory frameworks designed for single GMOs are often inadequate for complex consortia (Ghag 2024; Rozas et al. 2022). Clear, science-based, adaptive regulatory guidelines are urgently needed to balance innovation with environmental and public safety. International harmonization is also critical for facilitating global research and deployment.

7.3 Future perspectives: digital twins, AI, and bio-integrated systems

The future trajectory of plant-microbiome research is poised for transformative advancements, driven by emerging technologies. Below, we critically distinguish between current achievements and future possibilities across key frontiers:

7.3.1 Digital twins of plant-microbiome systems

The Fermentwin project (INRAE DIGIT-BIO, 2024–2025) has demonstrated proof-of-concept by developing a digital twin that models and predicts microbial community behaviour during carrot juice fermentation through real-time sequencing. Yamazaki et al. (2025) showed that machine learning models trained on over 800 SynCom–temperature combinations could predict tomato plant biomass with mean $R^2 = 0.510$. However, current plant-microbiome digital twins remain largely descriptive, with significant hurdles including data heterogeneity, lack of standardised workflows, and difficulty linking molecular pathways to ecosystem-scale dynamics. The longer-term vision is a fully dynamic digital counterpart that integrates genomic regulatory networks, real-time soil sensor streams, and spatiotemporal weather inputs. Graph neural networks and the NOAH project (2026) aim to establish the first AI foundation model for crop microbiomes, trained on over 300,000 curated datasets to optimise crop performance. However, these remain aspirational and require explicit validation and cross-site field trials before they can guide real-world decisions.

7.3.2 AI-driven predictive analytics

Deep learning algorithms have successfully screened core rhizosphere strains for salt-alkali tolerance in rice, validated

through field trials. In SynCom design, Yamazaki et al. (2025) demonstrated that Elastic Net regression incorporating genomic features could predict SynCom performance, identifying microbial interactions—rather than individual strain effects—as the most important predictors of plant growth. Generative AI models (GANs) have achieved 25% improvement in predicting microbial diversity and 30% enhanced forecasting in low-data scenarios for soil health prediction. AI is expected to address three core SynCom design challenges: selecting strains with complementary functions, predicting inter-microbial interactions, and optimising community composition for specific environments. Physics-informed machine learning and transfer learning could improve generalisation across sites. However, the significant gap between controlled (45% yield increase) and field (22%) performance underscores that much work remains before AI predictions translate to reliable agricultural outcomes.

7.3.3 Synthetic biology and bio-integrated systems

Ghag (2024) developed a synthetic bacterium (EcCMC) engineered to express a surface-displayed artificial protein that enhances root colonisation of exogenous nitrogen-fixing bacteria in legumes. This addresses the bottleneck of low colonisation efficiency and rapid replacement by indigenous microbes—a limitation that currently compromises the contribution of nitrogen-fixing bacteria (≈ 200 million tons N/year to agriculture). This represents a successful application of synthetic biology to overcome a practical limitation. Long-term, synthetic biology could enable microbial strains with novel functions—enhanced carbon sequestration, improved nutrient cycling under extreme conditions, or on-demand biostimulant production. Bio-integrated sensing systems (plants engineered to report stress via optical signals) remain a longer-term vision. However, public perception, regulatory challenges, and off-target effects remain significant hurdles to deployment.

8 Critical analysis of current knowledge gaps, contradictions, and challenges

While the preceding sections have synthesized the substantial progress in plant-microbiome research, a critical evaluation of the field reveals significant knowledge gaps, conflicting findings, and methodological limitations that must be acknowledged to advance from descriptive ecology toward predictive, application-driven science (Berg et al. 2020; Trivedi et al. 2020). This section provides a systematic analysis of these challenges.

8.1 Conceptual and theoretical contradictions

A fundamental conceptual tension persists regarding the hologenome theory, which posits that the host and microbiota function as a single evolutionary unit (Vandenkoornhuyse et al. 2015). However, broader evolutionary analyses argue that holobionts need not be treated as primary units of selection, as microbial community members are often transient and environmentally acquired (Berg et al. 2020). This ambiguity has practical implications: if holobionts are valid evolutionary units, microbiome engineering should target co-adapted host-microbe combinations; if not, transient interventions may suffice but risk higher failure rates. Conflicting evidence also characterizes the effects of climate stress on microbiomes. While some studies report reduced diversity under stress (Dubey et al. 2019), a synthesis of 1,235 global change experiments found that abiotic stress primarily impacts rare microbial species rather than overall functionality and diversity (Kumar et al. 2026). These contrasting findings illustrate the complexity of predicting microbial responses to climate change and the importance of experimental duration and environmental context. Thermal stress responses also depend on the soil profile and aggregate structure, with macroaggregates better maintaining microbial functions than microaggregates. These contradictions underscore that simple “climate stress reduces microbial diversity” narratives are insufficient; responses are highly context-dependent.

8.2 Methodological limitations and bottlenecks

Despite considerable methodological and computational advances, integrating multi-omics data remains a major challenge. Each omics platform generates large, complex, and often non-overlapping datasets that are difficult to reconcile (Jansson and Hofmockel 2018). The lack of standardized workflows, metadata reporting, and reproducible pipelines across studies severely hampers meaningful meta-analyses and cross-study comparisons (Pedrinho et al. 2026). However, contrasting evolutionary analyses argue that holobionts need not be treated as primary units of selection, as microbial community members are often transient and environmentally acquired. This conceptual debate influences how microbiome engineering strategies are framed—whether targeting co-adapted host-microbe combinations (holobiont perspective) or deploying transient interventions (traditional perspective). As Kimotho and Maina (2024) emphasized, current approaches often fall short of achieving the integrated understanding they promise. Experimental duration fundamentally shapes conclusions about microbial resilience. Short-term studies may suggest functional recovery, whereas long-term studies (6+ months) frequently

report permanent legacy effects with no recovery of key processes such as N-cycling (Kumar et al. 2026). Most studies remain constrained to short timeframes due to resource limitations, potentially leading to incomplete conclusions. The immense spatial and temporal heterogeneity of soil environments makes representative sampling exceptionally challenging, yet this is rarely acknowledged in interpretations (Leite et al. 2022). Studies that sample small areas may lead to incorrect inferences about larger populations.

8.3 The discovery-to-deployment gap

Perhaps the most significant challenge is the persistent gap between laboratory discoveries and consistent field deployment (Trivedi et al. 2020; Langstroff et al. 2022). Commercial inoculants frequently fail due to genotype-environment context dependency, where formulations designed under specific conditions are likely to fail when environments or plant genotypes change (Malgiglioglio et al. 2022). Resident native microbial communities with “home-field-advantage” often outcompete introduced formulations (Pedrinho et al. 2026). A major unresolved issue is whether core taxa directly perform beneficial functions or primarily serve as keystone species facilitating functions performed by others (Compant et al. 2019).

Formulation and scaling Maintaining viability, functional stability, and consistency across production batches remains challenging, particularly for non-sporulating organisms and multi-member consortia (Bashan et al. 2010). Adoption by farmers is influenced by inconsistent field performance, limited technical support, and uncertainty about cost-effectiveness compared with conventional inputs (Nosheen et al. 2021). The regulatory landscape remains fragmented globally. Brazil and the USA have distinct approval frameworks, while the European Union separates microbial biostimulants from plant-protection products under distinct regulations (Rozas et al. 2022). The USA lacks a unified national framework, with overlapping EPA and USDA oversight creating inconsistencies (Lerner et al. 2026).

8.4 Fundamental knowledge gaps

Significant gaps persist in understanding of regulatory mechanisms, including cross-kingdom RNA interference, epigenetic inheritance of transgenerational microbiomes, specific host genetic loci that control microbial recruitment, and the precise role of microbial volatile compounds in mediating plant defense (Yadav 2020). These gaps persist mainly due to methodological barriers in validating molecular mechanisms in complex open-soil environments (Trivedi et al. 2020).

8.5 Priorities for advancing microbiome research

Addressing these challenges requires: (i) standardization of methodologies to enable cross-study comparison; (ii) extended experimental timeframes to capture temporal dynamics; (iii) integration of multi-omics with functional validation through advanced cultivation and synthetic biology; (iv) predictive frameworks accounting for Genotype $\times$ Environment $\times$ Microbiome interactions; (v) transparent field validation to build farmer confidence; and (vi) regulatory harmonization balancing innovation with biosafety.

9 Conclusion

The escalating climate crisis threatens plant health, agricultural productivity, and ecosystem stability worldwide. Plant-microbiome interactions have emerged as a critical frontier for developing innovative and sustainable solutions. This review has underscored the profound molecular dialogue between plants and their associated microbes, highlighting how signaling molecules, hormonal crosstalk, and metabolic exchanges orchestrate adaptation to abiotic and biotic stresses. Multi-omics technologies coupled with systems biology approaches are indispensable for dissecting these networks, enabling the identification of key functional genes, active pathways, and predictive biomarkers of ecosystem health. These advanced analytical capabilities are enabling a new era of data-driven insights into plant-microbiome dynamics. Microbiome engineering, particularly through Synthetic Microbial Communities (SynComs) and next-generation bioinoculants, offers targeted strategies to enhance nutrient acquisition, boost stress tolerance, and provide biocontrol against pathogens. These interactions maintain and improve soil health, facilitate nutrient cycling, and enhance carbon sequestration, directly contributing to climate change mitigation. However, translational challenges remain significant. Quantitative evidence reveals that field efficacy is approximately 50% lower than in controlled conditions, with commercial failure rates exceeding 40% within three years of market introduction. Future advances integrating digital twins, AI-driven predictive analytics, and synthetic biology hold promise for overcoming these barriers. Fostering climate-resilient agriculture requires an integrated, multi-technological approach that places plant-microbiome systems at its core, safeguarding biodiversity and ensuring food security in a changing climate.

Acknowledgements Appreciation is given to the South African Research Chairs Initiative in Sustainable Preservation and Agroprocessing Research, Faculty of Science, University of Johannesburg, South Africa, for the favorable environment for this study.

Author contributions Conceptualization: M.I.A., O.A.F.; Validation: M.I.A., and O.A.F.; Resources: M.I.A. and O.A.F.; Writing—original draft preparation, M.I.A., O.A.F.; Writing—review M.I.A., O.A.F., Editing, M.I.A., O.A.F., Supervision, O.A.F. All authors have read and agreed to the published version of the manuscript.

Funding Open access funding provided by University of Johannesburg. This work is partly based on research supported by the National Research Foundation of South Africa (Ref: SPAR231013155231).

Data availability No datasets were generated or analysed during the current study.

Declarations

Competing interests The authors declare no competing interests.

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