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Harnessing the greenhouse microbiome: Novel strategies to improve greenhouse crop productivity and resilience: A review

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Review Article

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ABSTRACT

Greenhouse agriculture has become a cornerstone of modern horticulture, enabling year-round production, efficient resource use, and resilience to climate variability. Globally, protected cultivation exceeds 500,000 hectares, achieving 15–30% higher yields than open-field systems. However, its sustainability is constrained by dependence on mineral fertilizers and pesticides, which degrade soil health and suppress beneficial microbial diversity. Harnessing the greenhouse microbiome offers a transformative pathway to improve nutrient cycling, enhance plant growth, suppress pathogens, and strengthen tolerance to abiotic stresses. Microbiome-based interventions such as biofertilizers, microbial stimulants, and biochar- or compost-enriched substrates can reduce fertilizer use by 20–40% while maintaining or increasing yield by 10–25%. This review synthesizes advances in microbial biotechnology and omics-based insights into plant–microbe interactions. It further discusses synthetic biology and host-mediated gene editing as tools to design resilient holobionts for controlled-environment systems. Integration with precision agriculture, through AI, sensor networks, and digital twins, enables real-time monitoring and traceability of microbial products. Overall, microbiome-driven greenhouse management can enhance productivity, reduce greenhouse gas emissions, and align profitability with sustainability goals, representing a key strategy for climate-smart and circular horticulture.

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1. Introduction

1.1. Greenhouse Agriculture in the Global Context

Greenhouse cultivation has emerged as a cornerstone of modern horticulture, contributing significantly to global food and nutritional security (Raza et al, 2025; Yusuf et al, 2025). In an era of rapid population growth, land degradation, and climate variability, greenhouse agriculture provides a strategic solution to ensure food availability, resource efficiency, and resilience to environmental stresses. By enabling year-round production, greenhouses enhance resource-use efficiency and ensure higher yields per unit area compared to open-field systems (Ahmed et al, 2024; Ahmed et al, 2023). Globally, more than 500,000 hectares are now covered under protected cultivation, with rapid expansion occurring in Europe, Asia, and the Middle East, where controlled environment agriculture (CEA) is increasingly being adopted to address the pressures of urbanization and climate variability (Yan et al, 2024). However, the success of greenhouse agriculture has historically relied on heavy inputs of mineral fertilizers and chemical pesticides (Arif et al, 2020; Compant et al, 2025). While these inputs ensure immediate productivity, their long-term impacts include soil degradation, reduced microbial diversity, and negative environmental externalities such as greenhouse gas emissions (Hu et al, 2017; Suman et al, 2022). Moreover, excessive chemical reliance disrupts beneficial microbial networks that underpin nutrient cycling and plant defense, leading to ecological imbalances even within controlled environments. Thus, there is a growing need to redesign greenhouse systems in ways that improve productivity while minimizing ecological costs (Ge & Wang, 2025; Ullah et al, 2025). Developing biologically driven production systems that integrate beneficial microbes, renewable substrates, and digital monitoring is now central to achieving climate-smart and circular greenhouse horticulture.

1.2. The Plant Microbiome as a Key Determinant of Crop Health

Plants are holobionts, relying not only on their genetic makeup but also on complex associations with microbial partners inhabiting the rhizosphere, phyllosphere, and endosphere (Trivedi et al, 2021). Collectively, these microbial consortia constitute the plant microbiome, which plays vital roles in nutrient acquisition, growth promotion, disease suppression, and resilience to abiotic stressors (Marco et al, 2022; Mitter et al, 2019). The plant microbiome is increasingly recognized as a dynamic "second genome" that co-evolves with its host, shaping plant physiology, immunity, and stress tolerance (Ge & Wang, 2025). In greenhouse systems, where plants are cultivated under high-density and often stressful microclimates, the stability and diversity of the microbiome become particularly critical (Khan et al, 2024; Pandey & Saharan, 2025). Beneficial microorganisms such as plant growth-promoting rhizobacteria (PGPR), arbuscular mycorrhizal fungi (AMF), and biocontrol agents like *Trichoderma spp.* have been shown to enhance crop performance while reducing dependence on synthetic agrochemicals (Collinge et al, 2022; Papadopoulou et al, 2025). Beyond conventional inoculation, advances in microbial ecology, metagenomics, and synthetic biology now allow the deliberate manipulation of these microbial assemblages to optimize plant performance in controlled-environment systems. Importantly, the semi-closed nature of greenhouses provides unique opportunities to intentionally manage and engineer microbial communities for enhanced plant growth (Li et al, 2024).

1.3. Current Challenges in Greenhouse Microbiome Management

Despite growing recognition of the plant microbiome's significance, several challenges hinder its practical implementation in greenhouse systems. A major limitation is the inconsistent performance of microbial inoculants, whose efficacy is strongly influenced by microclimatic conditions, substrate types, and management practices (Mitter et al, 2019; O'Callaghan et al, 2022). Second, the overuse of chemical fertilizers and pesticides in conventional greenhouse systems tends to suppress microbial diversity, limiting the establishment of beneficial consortia (Edlinger et al, 2022).In addition, most greenhouse microbiome studies have been conducted at small experimental scales, leaving major knowledge gaps in long-term field validation and cost-effectiveness for commercial operations (Ahmed et al, 2024; Barea, 2015). Moreover, growers often lack access to technical knowledge, affordable bioinoculant formulations, and decision-support tools that can guide precise microbiome management (Hamilton et al, 2023). These limitations underscore the need for integrative approaches that combine microbial biotechnology with advanced monitoring, modeling, and extension strategies (Ansabayeva et al, 2025; Misu et al, 2025). Bridging this gap requires cross-disciplinary integration of microbial science, data analytics, and policy support to mainstream microbiome management in greenhouse horticulture.

1.4. Rationale and Objectives of this Review

Given the dual need for enhanced productivity and sustainability, microbiome management offers a viable pathway to reduce reliance on chemical inputs while maintaining crop yield and quality in greenhouse systems. Over the past decade, advances in omics technologies, synthetic biology, and digital agriculture have provided unprecedented insights into plant–microbiome interactions (Thakur et al, 2023). These advances are gradually translating into innovations such as multi-species biofertilizers, microbial stimulants, and AI-driven monitoring systems (OYEDIRAN et al, 2025; Silva et al, 2025). However, despite this rapid progress, a comprehensive and integrative review focusing specifically on microbiome management within greenhouse systems, linking microbial ecology, technological innovations, and socio-economic aspects, remains largely missing in current literature.

The present article addresses this gap by systematically reviewing (i) the components and sources of the greenhouse microbiome, (ii) practical strategies for its management, including biofertilizers, growing media, and environmental control, (iii) specific applications across different horticultural crops, (iv) challenges and limitations, and (v) future directions, including the integration of AI, omics, and real-time microbiome monitoring. By addressing these dimensions, this review aims to establish a conceptual and practical framework for translating microbiome-based innovations from research into scalable and climate-resilient greenhouse production systems.

2. Components of the Greenhouse Microbiome and Their Sources

The greenhouse microbiome is a complex and dynamic consortium of microorganisms inhabiting different ecological niches of the production system, including the rhizosphere, phyllosphere, and growth substrates (Figure 1). These communities are shaped not only by plant genotype but also by external inputs such as seeds, irrigation water, and organic amendments (Compant et al, 2025; Nishisaka, 2025). Understanding the composition and sources of the microbiome is fundamental to designing management strategies that support plant health and productivity.

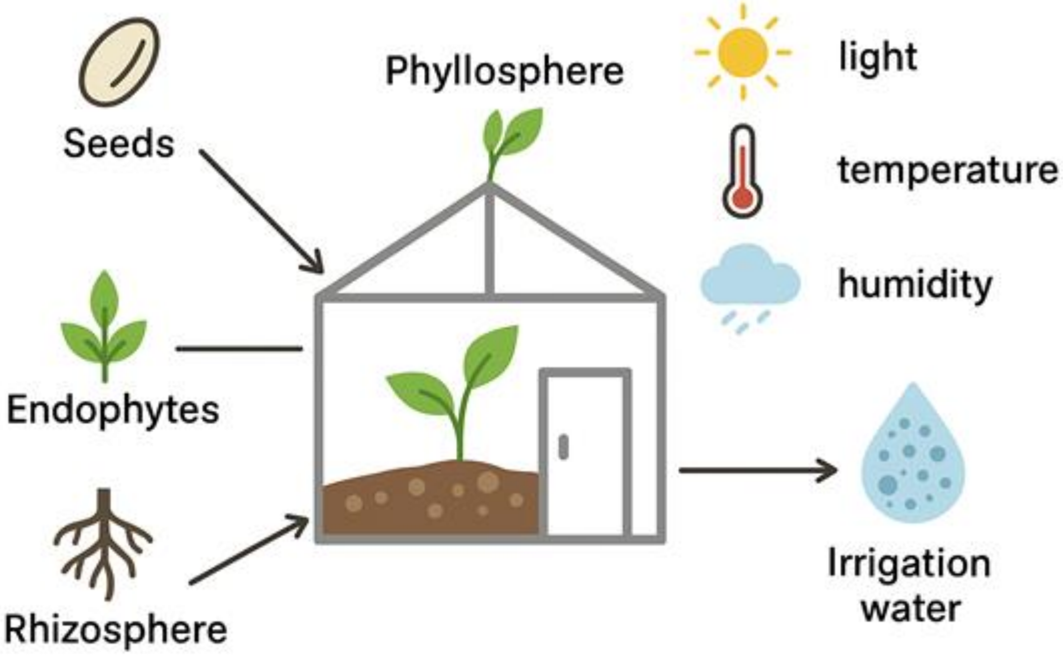

Figure 1 Components and sources of the greenhouse microbiome

2.1. Rhizosphere Microbiome

The rhizosphere, defined as the soil zone directly influenced by root exudates, harbors the most functionally significant microbial communities for plant growth. Root exudates, including sugars, amino acids, and secondary metabolites, act as chemical signals that selectively recruit beneficial microorganisms such as *Pseudomonas, Bacillus*, and *arbuscular mycorrhizal* fungi (AMF) (Cheng et al, 2020; Yuan et al, 2024). In greenhouse-grown tomato and cucumber, enriched rhizosphere populations have been shown to enhance nutrient solubilization (particularly phosphorus and iron) and improve resistance to root pathogens such as *Fusarium oxysporum* and *Ralstonia solanacearum* (Raza et al, 2025). However, due to artificial substrates and controlled irrigation regimes, the diversity of rhizosphere microbiota in greenhouses is often narrower than in open-field systems, making targeted inoculation strategies more relevant (Ge & Wang, 2025).

2.2. Phyllosphere Microbiome

The phyllosphere refers to the aerial parts of plants, mainly the leaf surface, which is colonized by bacteria, yeasts, and filamentous fungi. Despite being exposed to fluctuating environmental conditions such as humidity and light, phyllosphere microbiota contribute to foliar health through competitive exclusion of pathogens, production of antimicrobial compounds, and modulation of plant stress responses (Portal-Gonzalez et al, 2025;

Wang et al, 2025). In greenhouse ornamentals such as roses, beneficial leaf-associated bacteria (Methylobacterium, Sphingomonas) have been reported to delay senescence and improve post-harvest longevity (Khan et al, 2024). Moreover, foliar microbial inoculants applied as sprays can strengthen systemic resistance in crops against powdery mildew and downy mildew diseases (Thakur et al, 2023).

2.3. Substrate and Growth Media Microbiome

Artificial substrates such as rockwool, peat, coir, and perlite form the physical foundation of many greenhouse systems. These growth media are typically poor in indigenous microbial diversity, but their microbiological composition can be enriched through amendments like compost, vermicompost, and biochar (Ullah et al, 2025). Substrate-associated microbiota play a critical role in seedling establishment by supporting root colonization and protecting against soilborne pathogens. For example, tomato seedlings grown in biochar-enriched peat substrates demonstrated enhanced colonization by beneficial *Trichoderma spp*., which suppressed damping-off disease (Yang et al, 2023). Thus, the selection and management of growth media are crucial levers for shaping beneficial microbial communities in greenhouses (Table 1).

Table 1 Key microbial strains used in greenhouse vegetable crops (e.g., tomato, cucumber) and their effects

Microbial strain / group	Crop examples	Main effects	References
Pseudomonas spp. (PGPR)	Tomato, cucumber	Phosphate solubilization, siderophore production, ISR (Induced Systemic Resistance) activation	(French et al, 2021; Raza et al, 2025)
Bacillus spp.	Tomato, cucumber, pepper	Nutrient solubilization, phytohormone synthesis, pathogen suppression	(Ibáñez et al, 2023; Singh et al, 2022)
Trichoderma spp.	Tomato, cucumber	Biocontrol of Fusarium, improved root growth	(Collinge et al, 2022; Yang et al, 2023)
Arbuscular mycorrhizal fungi (AMF)	Tomato, cucumber	Improved nutrient uptake (P, Fe), drought tolerance	(Ullah et al, 2025; Yang et al, 2023)
Methylobacterium, Sphingomonas (phyllosphere bacteria)	Tomato, cucumber, ornamentals	Delay senescence, improve post-harvest quality	(Khan et al, 2024; Portal-Gonzalez et al, 2025)

2.4. Sources of Microbiomes in Greenhouses

Greenhouse microbial communities are continuously replenished from multiple sources (Table 1), which act as reservoirs for beneficial as well as pathogenic microorganisms:

Seeds: Seeds carry endophytic and epiphytic microbes that can establish early colonization of seedlings. Seed-associated microbes such as Enterobacter, Paenibacillus, and AMF spores have been shown to influence early root architecture and disease resistance (Li et al, 2025). In addition, seed coating and biological priming techniques can be employed to selectively enhance beneficial microbial colonization at germination.

Irrigation water: Hydroponic and fertigation systems can act as major microbial entry points. While untreated water may introduce pathogens like Pythium and Phytophthora, it can also serve as a carrier for beneficial bacteria if biologically treated (Thakur et al, 2023). Recent studies highlight that maintaining biofilm-forming beneficial microbes in irrigation systems can stabilize nutrient delivery and suppress pathogen proliferation.

Organic amendments: Compost, vermicompost, and manure-based inputs are rich microbial inocula, often containing consortia of decomposers and plant growth-promoting rhizobacteria (PGPRs) (Karimi et al, 2025a). However, variability in microbial composition requires standardization to avoid introducing opportunistic pathogens (Sun & Shahrajabian, 2023). Proper composting temperature control and post-processing screening are critical to ensure biosafety and consistency of introduced microbial populations.

Airflow and greenhouse surfaces: Although airflow in greenhouses is limited, microbial dispersal from ventilation systems, workers, and tools can significantly influence phyllosphere colonization patterns (Noman et al, 2021). Regular sanitation of greenhouse structures, coupled with the use of beneficial aerosolized inoculants, can help maintain a balanced phyllosphere microbiome.

2.5. Environmental Drivers of Microbiome Composition

The structure of microbial communities in greenhouses is highly sensitive to abiotic factors such as temperature, humidity, and light. Elevated humidity, for instance, promotes foliar fungal pathogens but can also favor beneficial yeasts with antagonistic activity (Ge & Wang, 2025). Similarly, temperature fluctuations regulate root exudation patterns, indirectly shaping the rhizosphere microbiome (Arif et al, 2020). Optimizing these environmental parameters not only benefits plant physiology but also steers microbial community assembly toward beneficial trajectories (Table 2).

Table 2. Sources of the greenhouse microbiome and their functional roles

Source	Key Microbial Groups	Functional Roles in Greenhouse Crops	References
Seeds	Endophytic bacteria, seed-borne fungi	Early colonization, disease suppression, seedling vigor	(Trivedi et al, 2021; Wankhade et al, 2025)
Rhizosphere	PGPR (*Pseudomonas, Bacillus*), AMF	Nutrient acquisition, growth promotion, systemic resistance	(Noman et al, 2021; Yan et al, 2024)
Phyllosphere	*Methylobacterium, Sphingomonas*, yeasts	Foliar pathogen suppression, abiotic stress tolerance	(Papadopoulou et al, 2025)
Growth Medium	Compost- and biochar-associated microbes	Enhanced microbial diversity, stable plant–microbe interactions	(Lastochkina et al, 2022)
Irrigation Water	Aquatic bacteria, introduced inoculants	Vehicle for inoculation, risk of pathogen dissemination	(O'Callaghan et al, 2022)
Environmental Factors	Condition-dependent microbial assemblages	Shaping community composition via humidity, light, temperature	(Ahmed et al, 2024)

3. Advances in Omics and Synthetic Biology for Greenhouse Microbiome Management

3.1. Multi-omics technologies in microbiome studies

Recent advances in genomics, transcriptomics, proteomics, and metabolomics have revolutionized our understanding of plant–microbiome interactions. These approaches allow for the identification of microbial diversity, functional pathways, and stress-response mechanisms in greenhouse crops. For instance, genomics provides insights into the taxonomic structure of rhizosphere communities, while metabolomics highlights secondary metabolites involved in plant growth and defense (Ferrocino et al, 2023; Rai et al, 2022; Sahoo et al, 2025) By integrating multi-omics data, researchers can model complex ecological networks that underpin plant health and productivity (Table 3).

Table 3. Applications of omics technologies in greenhouse microbiome research

Omics approach	Focus	Applications in greenhouse systems	References
Genomics	DNA-level characterization	Microbial community profiling, functional gene identification	(Ferrocino et al, 2023; Rai et al, 2022)
Transcriptomics	Gene expression analysis	Monitoring microbial activity under stress or nutrient variation	(Srikanth et al, 2025)
Proteomics	Protein-level profiling	Identifying enzymes in nutrient cycling, plant defense	(Sahoo et al, 2025)
Metabolomics	Metabolite profiling	Detection of plant–microbe signaling molecules and secondary metabolites	(Manna et al, 2025; Rai et al, 2022)
Multi-omics integration	Systems-level analysis	Linking microbial networks with plant health and yield traits	(Ge & Wang, 2025)

3.2. Synthetic biology and engineered microbial consortia

Synthetic biology enables the design of synthetic microbial communities (SynComs) with targeted functional traits, such as enhanced nitrogen fixation, phosphorus solubilization, or pathogen suppression. Engineered strains of Pseudomonas or Bacillus have already demonstrated promising results in greenhouse trials by improving nutrient uptake and disease resistance (Karmakar et al, 2025; Ke et al, 2021). Such approaches move beyond traditional single-strain inoculants toward tailored microbial consortia adapted to specific greenhouse environments. Recent advances have also involved the rational assembly of multi-functional SynComs combining bacteria, fungi, and cyanobacteria to perform complementary roles in nutrient cycling and stress mitigation. For example, co-cultures of *Azospirillum brasilense*, *Rhizobium leguminosarum*, and *Bacillus megaterium* have been engineered to improve nitrogen fixation efficiency and phosphorus bioavailability in leafy vegetables and tomato under controlled environments (Chaudhary et al, 2023). Engineered *Trichoderma harzianum* and *Pseudomonas fluorescens* strains expressing antifungal peptides or siderophore genes have shown enhanced suppression of soil-borne pathogens such as *Fusarium oxysporum* and *Rhizoctonia solani* (Cui et al, 2025). Synthetic biology tools such as CRISPR-Cas9 and gene circuit design are increasingly used to regulate metabolite production, quorum sensing, and stress response pathways, enabling precise control of interspecies interactions within SynComs (Li et al, 2024).

In addition to strain-level engineering, computational modeling and systems biology approaches are now used to predict community dynamics and optimize consortia design for specific crops and substrates. Machine learning-assisted SynCom design helps identify keystone taxa and minimize antagonistic interactions, increasing the stability and predictability of microbial performance under greenhouse conditions (Li et al, 2024). These innovations collectively mark a transition from empirical bioinoculant development toward intelligent microbiome engineering, where synthetic biology and data-driven tools jointly accelerate the development of robust microbial formulations tailored for climate-smart greenhouse systems.

3.3. Gene editing and host-mediated engineering

Gene editing tools like CRISPR/Cas9 allow precise modification of microbial genomes to enhance beneficial traits, as well as host-mediated engineering of plants to optimize interactions with symbiotic microbes. This dual strategy, modifying both microbes and their plant hosts, can strengthen the holobiont concept, resulting in crops with improved resilience under controlled-environment conditions (Clouse & Wagner, 2021; Thakur et al, 2023). Recent studies have demonstrated the use of CRISPR-based editing in plant growth-promoting rhizobacteria (PGPR) such as *Bacillus subtilis* and *Pseudomonas putida* to enhance ACC deaminase activity, phosphate solubilization, and stress-responsive metabolite production (Thankappan et al, 2024). Similarly, gene editing of *Rhizobium leguminosarum* and *Azospirillum brasilense* has improved nitrogen-fixing efficiency and colonization stability under greenhouse conditions (Baloglu et al, 2022). On the host side, CRISPR/Cas9-mediated modifications in tomato (*Solanum lycopersicum*) and cucumber (*Cucumis sativus*) targeting receptor-like kinases (RLKs) and root exudate pathways have enhanced microbial recruitment, leading to increased disease resistance and nutrient uptake (Thankappan et al, 2024). In addition, emerging host-microbiome co-engineering strategies aim to synchronize plant signaling networks with engineered microbes through synthetic promoters and quorum-sensing pathways.

Table 4. Applications of omics technologies in greenhouse microbiome research

Omics Approach	Focus	Application in Greenhouse Systems	Key References
Genomics	DNA-level characterization of microbial communities	Identification of rhizosphere and phyllosphere diversity; functional gene profiling	(Ferrocino et al, 2023; Rai et al, 2022)
Transcriptomics	Gene expression analysis	Monitoring active microbial functions under stress or nutrient changes	(Srikanth et al, 2025)
Proteomics	Protein-level profiling	Identifying enzymes involved in nutrient cycling and plant defense	(Sahoo et al, 2025)
Metabolomics	Metabolic products	Detection of plant–microbe signaling compounds and secondary metabolites	(Manna et al, 2025; Rai et al, 2022)

3.4. Integration with smart technologies

The convergence of omics data with artificial intelligence (AI), sensors, and digital twin modeling is paving the way for real-time monitoring and predictive management of greenhouse microbiomes (Table 4). By linking high-throughput sequencing with machine learning, it becomes possible to forecast shifts in microbial communities in response to environmental changes or management practices (Manna et al, 2025; Srikanth et al, 2025). This integration aligns with the paradigm of precision horticulture.

4. Practical strategies for microbiome management

Greenhouse systems allow for the precise manipulation of microbial communities to enhance plant growth, stress tolerance, and overall productivity. Several practical strategies have been developed and tested to optimize microbiome functionality, with emphasis on biofertilizers, growing media, environmental regulation, and microbial stimulants.

4.1. Use of biofertilizers

The application of microbial inoculants, particularly plant growth-promoting rhizobacteria (PGPR) such as Pseudomonas and Bacillus, and arbuscular mycorrhizal fungi (AMF), has been widely adopted in greenhouse horticulture (Table 5). These microorganisms promote nutrient uptake, phytohormone synthesis, and induce systemic resistance (ISR), thereby reducing pathogen incidence and enhancing plant vigor (Ibáñez et al, 2023; Khalid et al, 2025; Singh et al, 2022). Common application methods include seed dressing, soil drenching, and foliar spraying, each targeting specific stages of plant growth. Studies on tomato and cucumber cultivation have shown that microbial seed coating improves germination, root development, and early resistance to soil-borne pathogens (French et al, 2021; Rocha, 2020).

Table 5. Comparative overview of biofertilizer application methods in greenhouse systems

Application method	Description	Advantages	Limitations	References
Seed dressing / coating	Microbes applied directly on seed surface before sowing	Early root colonization, low inoculum requirement	Limited persistence, sensitive to storage conditions	(French et al, 2021; Rocha, 2020)
Soil drenching	Suspension of inoculants applied to root zone	Strong root–microbe interaction, effective against soil-borne pathogens	Requires repeated application, risk of leaching	(Ahmed et al, 2023; Singh et al, 2022)
Foliar spraying	Microbes or metabolites sprayed on leaves	Direct protection against foliar pathogens, ISR activation	Short persistence on leaf surface, dependent on humidity	(Papadopoulou et al, 2025; Thakur et al, 2023)
Root-zone inoculation in soilless substrates	Application of beneficial microbial consortia (e.g., Azospirillum, Pseudomonas, Trichoderma) to inert media such as perlite, cocopeat, or rockwool	Promotes root proliferation, nutrient uptake, and hormone balance under controlled conditions	Potential for biofilm clogging or uneven distribution in fertigation systems	(Chaudhary et al, 2023; Thankappan et al, 2024)
Hydroponic inoculation / nutrient solution enrichment	Introduction of microbial biofilms or soluble inoculants into hydroponic systems	Enhances root hair development, reduces root-browning, and improves stress tolerance in lettuce, cucumber, and tomato	High contamination risk if nutrient solutions are not properly sterilized	(Baloglu et al, 2022; Cui et al, 2025)

Note: While hydroponic inoculation shows promising potential for stimulating root proliferation and nutrient absorption, improper management may pose contamination risks. Therefore, periodic sterilization of nutrient solutions, use of biosafe strains, and controlled dosing are essential to ensure both efficiency and biosafety.

4.2. Enrichment growing media

Amendments such as compost, vermicompost, and biochar not only provide nutrients but also create niches for beneficial microbial populations (Karimi et al, 2025b; Karimi et al, 2024). Their integration enhances soil structure, water retention, and microbial diversity, leading to more resilient rhizosphere communities (Rahman et al, 2022; Rehman et al, 2023). Research indicates that combining organic amendments with biofertilizers results in a synergistic effect, increasing microbial stability and crop yield in greenhouse vegetables (Ahmed et al, 2023; Chaudhary et al, 2024). Furthermore, the deliberate selection of growing media with high microbial-holding capacity, such as peat-based substrates enriched with biochar, supports the persistence of beneficial microbes over the cropping cycle (Liang et al, 2025).

4.3. Integrated management of environmental factors

Environmental conditions within greenhouses significantly influence microbiome composition and functionality. Regulating temperature and humidity can favor the proliferation of beneficial microbial taxa while suppressing pathogens (Chen et al, 2023). For instance, maintaining moderate humidity reduces foliar pathogen incidence while enhancing the phyllosphere's beneficial microbial community. Additionally, the application of organic mulches has been shown to buffer temperature fluctuations and stabilize the rhizosphere, thus promoting microbial-mediated nutrient cycling (French et al, 2021; Liang et al, 2025).

4.4. Application of microbial stimulants

Beyond inoculants, microbial stimulants such as plant growth-promoting rhizobacteria (PGPR)-based biostimulants and chemical elicitors are increasingly used to enhance crop performance. PGPR formulations improve the availability of micronutrients like zinc and iron, supporting critical physiological processes in crops (Ibáñez et al, 2023; Singh et al, 2022). Furthermore, compounds that trigger induced systemic resistance (ISR), including microbial metabolites and plant-derived elicitors, fortify plant defense responses against both biotic and abiotic stresses (Afridi et al, 2022; Khalid et al, 2025). Application of such stimulants has been particularly effective in improving tomato flavor quality, cucumber nutrient uptake, lettuce high yield and quality values and post-harvest resilience of roses under greenhouse conditions (Ahmed et al, 2023; Demir et al, 2024; Peixoto et al, 2022; Tahiri et al, 2022). Collectively, these strategies represent a paradigm shift in greenhouse production, where microbiome-centered management replaces reliance on chemical inputs and fosters sustainable horticulture.

5. Special applications in horticultural crops

The application of microbiome management strategies in greenhouse horticulture is particularly relevant for high-value crops such as vegetables, ornamentals, and seedlings, where productivity, quality, and post-harvest performance are critical. Specific approaches tailored to each crop category can maximize the benefits of beneficial microorganisms. For instance, in greenhouse tomato production, inoculation with *Bacillus subtilis* and *Trichoderma harzianum* has been reported to enhance root growth, fruit yield, and lycopene content while reducing the incidence of *Fusarium wilt* (Chaudhary et al, 2023). In cucumber and pepper, microbial consortia containing *Pseudomonas fluorescens* and arbuscular mycorrhizal fungi (AMF) improved nutrient uptake efficiency and drought tolerance under controlled environments (Thankappan et al, 2024). Similarly, in ornamental crops such as chrysanthemum and gerbera, beneficial endophytic bacteria have been employed to improve flower color intensity, vase life, and stress resilience during post-harvest storage (Li et al, 2024).

5.1. Vegetable and summer crops

Vegetables such as tomato, cucumber, and pepper represent the cornerstone of greenhouse production worldwide. Microbiome-based strategies have demonstrated significant potential to enhance flavor, aroma, and shelf life by modulating plant metabolism and improving nutrient uptake efficiency (Abbas et al, 2023; Lastochkina et al, 2022). For example, inoculation with plant growth-promoting rhizobacteria (PGPR) improves the bioavailability of micronutrients and secondary metabolites, thereby enriching the nutritional profile of vegetables (Melini et al, 2023). Additionally, bio stimulants and microbial consortia have been shown to mitigate the decline in sensory quality associated with intensive cultivation, ensuring improved consumer acceptance (DAS et al, 2024; Sangiorgio, 2022).

5.2. Ornamental plants and cut flowers

In ornamentals such as roses, gerbera, and lilies, the microbiome plays a decisive role in prolonging post-harvest vase life and maintaining visual quality. Postharvest microbial deterioration is one of the primary causes of reduced shelf life; hence, the use of beneficial microbes and protective yeasts has gained traction to suppress spoilage organisms (He et al, 2024; Zaman et al, 2025). Studies have shown that inoculating cut flowers with microbial antagonists or applying microbial elicitors can significantly extend vase life while reducing reliance on chemical preservatives (Gupta & Dubey, 2018; Kumar et al, 2024). Such practices not only improve color stability and petal freshness but also align with eco-friendly post-harvest management (Malakar et al, 2023; Mishra & Dwivedi, 2015).

5.3. Seedlings and transplants

Strong seedlings with well-developed root systems are essential for successful transplanting in greenhouse crops. Microbiome management through root-associated inoculants, organic substrates, and grafting techniques enhances root vigor, nutrient acquisition, and tolerance to transplant shock (Pascual et al, 2018; Ronga et al, 2021). Biofertilizers combined with optimized growing media not only reduce nursery losses but also produce resilient seedlings capable of faster establishment after transplantation (Franco et al, 2011; Lee et al, 2010). For instance, microbial enrichment of nursery substrates has been reported to improve the performance of tomato and cucumber seedlings under abiotic stress, ensuring uniform growth and early flowering in commercial production systems (Kumari et al, 2023). Together, these specialized applications highlight the versatility of microbiome-based interventions across horticultural sectors, from enhancing vegetable quality to extending flower vase life and producing robust seedlings. Integrating these practices into commercial greenhouse systems holds promise for sustainable intensification of horticultural production.

6. Challenges and Limitations

Despite their promising role in sustainable agriculture, the application of microbial inoculants still faces several important challenges that hinder their large-scale adoption. Incompatibility with greenhouse and field conditions. One of the most significant limitations is the inconsistency of microbial performance under diverse environmental conditions. While certain strains may perform effectively in controlled laboratory settings, their activity often decreases when introduced to greenhouse or field conditions due to fluctuations in temperature, humidity, soil type, and interactions with native microbial communities. This incompatibility reduces the reliability of inoculants across different agroecological zones (Ghorui et al, 2024; O'Callaghan et al, 2022; Timmusk et al, 2017). High cost and technological complexity. The production of microbial inoculants requires advanced fermentation processes, quality control systems, and formulation strategies to ensure viability and shelf-life. These technologies not only demand substantial capital investment but also increase the final product cost. Furthermore, scaling up production while maintaining microbial efficacy presents additional technical and economic barriers (Fadiji et al, 2024; Leggett et al, 2011; Singh et al, 2025). Requirement of technical knowledge and management skills. Effective use of microbial inoculants relies on precise knowledge of microbial ecology, host–microbe interactions, and soil health parameters. Farmers often lack access to the necessary training or advisory services, which limits the successful integration of inoculants into farming practices. Moreover, the complexity of microbial community dynamics requires continuous monitoring and expert management, posing further challenges for adoption in smallholder and resource-limited systems (Bharti et al, 2025; Chernov & Semenov, 2021; Díaz-Rodríguez et al, 2025). In summary, the incompatibility with heterogeneous conditions, high production costs, and the need for specialized technical expertise remain critical barriers to the widespread application of microbial inoculants in sustainable agriculture. Overcoming these limitations will require interdisciplinary approaches, improved formulation technologies, and farmer-centered extension programs.

7. Challenges and Opportunities for New Frontiers and Technologies to Guarantee Food Production

The transition from conventional greenhouse management to microbiome-driven strategies presents both technical challenges and unprecedented opportunities. Despite advances, several barriers hinder the widespread application of novel microbial and digital technologies in greenhouse systems (Table 6, 7). First, incompatibility of microorganisms under diverse microclimatic conditions remains a limiting factor, as inoculants often fail to establish stable populations when environmental stressors such as temperature, humidity, and salinity fluctuate (Silva et al, 2025). Second, the cost and complexity of microbial inoculant production and formulation technologies, especially for engineered consortia or biofilm-based products, restrict adoption at a commercial scale (Otaiku et al, 2022; OYEDIRAN et al, 2025).

Table 6. Challenges and opportunities in adopting frontier technologies for microbiome management in greenhouse systems

Dimension	Challenges	Opportunities	References
Microbial inoculants	Difficulty of adaptation under variable greenhouse microclimates	Development of multi-species consortia and biofilm-based inoculants	(OYEDIRAN et al, 2025; Silva et al, 2025; Wankhade et al, 2025)
Production technology	High cost and complexity in large-scale formulation	Biofilmed biofertilizers and smart fermentation technologies	(Otaiku et al, 2022; OYEDIRAN et al, 2025)
Technical expertise	Limited grower knowledge in omics, microbiome engineering, and ISR activation	AI-guided training tools and real-time monitoring platforms	(Gillett David et al, 2025; Srikanth et al, 2025)
Monitoring systems	Lack of robust long-term field validation	Use of omics-based diagnostics, blockchain for traceability, and digital twins	(Bühler et al, 2024; Silva et al, 2025)
Sustainability	Risk of inconsistent performance across crops	Integration with circular economy frameworks and climate-smart agriculture	(OYEDIRAN et al, 2025)

Third, effective implementation requires advanced technical knowledge, including expertise in metagenomics, real-time monitoring, and microbiome engineering, which is often lacking among growers (Srikanth et al, 2025;

Wankhade et al, 2025). Opportunities. On the other hand, innovations in biotechnology, data science, and systems integration open new horizons. Omics-driven approaches combined with real-time sensors and blockchain technologies enable precise monitoring of microbiome functions and traceability of microbial products throughout the production chain (Silva et al, 2025; Srikanth et al, 2025). Bio filmed biofertilizers and synthetic microbial consortia offer opportunities to improve resilience, nutrient cycling, and stress tolerance in crops under greenhouse conditions (Gillett David et al, 2025; OYEDIRAN et al, 2025). Moreover, integrating digital twins and AI-based predictive models can facilitate decision-making and dynamic adjustment of crop management practices (Bühler et al, 2024).

Table 7. Expanded challenges and opportunities in greenhouse microbiome management

Dimension	Key challenges	Opportunities	References
Microbial inoculants	Inconsistent performance under variable greenhouse conditions	Development of SynComs and biofilm-based inoculants	(OYEDIRAN et al, 2025; Silva et al, 2025)
Production technology	High cost, technological complexity, short shelf-life	Smart fermentation technologies, decentralized production	(Fadiji et al, 2024; Leggett et al, 2011)
Technical expertise	Limited farmer knowledge in microbiome application	AI-based training tools, participatory extension models	(Hamilton et al, 2023)
Monitoring systems	Lack of robust field-scale validation	Integration of sensors, omics-based diagnostics, digital twins	(Srikanth et al, 2025)
Sustainability	Risk of ecological inconsistency across crops	Climate-smart integration, circular economy approaches	(Ge & Wang, 2025)

8. Socio-economic and Policy Perspectives

Socio-economic factors critically influence the uptake and scale-up of microbiome-based technologies in greenhouse horticulture. Production and formulation of high-quality microbial inoculants require advanced fermentation, quality-control systems, and cold-chain logistics, which increase unit costs and raise barriers to market entry (Fadiji et al, 2024; Leggett et al, 2011). Without mechanisms to de-risk early adopters, small and medium-scale growers may find the upfront investment for biofertilizers and monitoring tools prohibitive. Regulatory clarity and standardized certification are essential to ensure product quality, biosafety, and farmer confidence. The regulatory landscape for microbial inoculants, including mycorrhizal products and engineered consortia, remains fragmented across jurisdictions, complicating cross-border trade and commercialization (Ghorui et al, 2024). For engineered microbes and SynComs, robust risk assessment frameworks, post-market surveillance, and stewardship programs will be required to manage horizontal gene transfer and ecological risks (Gillett David et al, 2025; Silva et al, 2025). Traceability and transparent labelling, potentially supported by blockchain—can further strengthen market trust. Adoption also depends on accessible extension services, farmer training, and locally validated demonstrations. Knowledge gaps around application methods, timing, and integration with existing fertilization regimes limit consistent field performance (Bharti et al, 2025; Hamilton et al, 2023). Participatory trials, subsidized demonstration plots, and digital decision-support tools can accelerate learning cycles and build confidence among growers (Srikanth et al, 2025). Policy and market interventions can unlock commercialization pathways. Public investment in R&D and pilot-scale validation, targeted subsidies for early adopters, standardized certification and quality-control labs, and incentives for private–public partnerships (PPPs) will lower entry barriers and improve product reliability (Leggett et al, 2011). Decentralized production models (regional cooperatives or contract fermentation facilities) can reduce logistics costs and adapt formulations to local substrates and crops. Finally, integrating economic incentives with climate-smart objectives (e.g., carbon credits for practices that reduce N_2O emissions) can align private returns with public goods (Hu et al, 2017).

Key policy recommendations:

- Establish national certification and quality-control laboratories for microbial inoculants.
- Provide time-limited subsidies or cost-share mechanisms for early adopters and pilot farms.
- Support public–private partnerships for scalable production and regional distribution.
- Fund extension services and participatory on-farm trials to validate products locally.
- Develop regulatory frameworks and stewardship plans for engineered microbes and SynComs.
- Promote traceability and transparent labelling (blockchain-enabled where feasible) to build market trust.

Taken together, socio-economic and policy measures, alongside technical advances, are essential to translate microbiome innovations from research into reliable, scalable, and climate-smart greenhouse practices.

9. Integration with Precision Agriculture

The convergence of microbiome management with precision agriculture opens new opportunities for optimizing crop productivity, resource-use efficiency, and sustainability in greenhouse systems. Precision agriculture tools, including artificial intelligence (AI), sensor networks, remote imaging, and decision-support platforms, enable real-time monitoring of crop and microbiome dynamics, thus allowing proactive and adaptive interventions (French et al, 2021). AI and machine learning. By integrating multi-omics data with environmental and crop performance datasets, AI-driven models can identify microbial signatures linked to nutrient uptake, stress tolerance, or disease suppression (Manna et al, 2025). Predictive algorithms can forecast shifts in microbial communities under varying humidity, temperature, or substrate conditions, guiding timely applications of biofertilizers and bio stimulants. Sensor networks and IoT platforms. Advanced sensor technologies (e.g., soil moisture, nutrient probes, volatile organic compound detectors) enable continuous monitoring of plant and microbial activity within greenhouses. When linked with Internet of Things (IoT) platforms, these sensors provide high-resolution spatiotemporal data to guide microbial inoculation, irrigation, and fertilization strategies (Chen et al, 2023). Digital twin models simulate the interactions among crops, microbes, and greenhouse environmental factors, enabling growers to test “what-if” scenarios virtually before implementing management practices. This reduces risk and accelerates the adoption of microbiome-based interventions by providing transparent, evidence-based decision-making frameworks (Bühler et al, 2024). Blockchain and traceability. Blockchain-enabled systems can strengthen market trust by providing end-to-end traceability of microbial products, from production and formulation through application in greenhouses. Such traceability frameworks ensure compliance with biosafety standards, facilitate certification, and enhance consumer confidence in sustainably produced crops (Silva et al, 2025). Together, these precision agriculture tools complement microbiome-centered strategies by improving monitoring, prediction, and control. Their integration can transform greenhouses into adaptive, data-driven ecosystems, where microbial management is optimized in real time to enhance resilience, reduce chemical inputs, and align with climate-smart agriculture goals.

Conclusion

The integration of microbiome management into greenhouse agriculture offers a practical and scalable route to improve productivity while reducing environmental impacts. By promoting beneficial microbial communities, greenhouse systems can enhance nutrient-use efficiency, suppress pathogens, and increase resilience to abiotic stresses, outcomes that translate into economic and ecological gains for high-value horticultural production. To move from promise to practice, four priority areas require immediate attention: (1) product development, creation of cost-effective, shelf-stable and locally adapted microbial formulations; (2) mechanistic research, long-term field validation of SynCom stability, host–microbe specificity, and ecosystem-level effects; (3) digital integration, coupling real-time sensing, AI-driven decision support, and predictive models to optimize inoculation timing and environmental control; and (4) biosafety and governance, standardized certification, risk assessment frameworks, and stewardship measures to ensure safe deployment. Scientifically, the manuscript’s conceptual contribution is to frame microbiome management as a systems-level intervention that links molecular/omics insights and synthetic biology with precision horticulture and circular economy practices. Practically, adoption will depend on demonstrable agronomic benefits, reduced input costs, and accessible extension and supply chains. In summary, microbiome-centered greenhouse management can be both transformative and pragmatic: with targeted research, appropriate governance, and industry–grower partnerships, it can deliver resilient, low-carbon, and commercially viable horticulture at scale.

Conflict of interest

The authors declare no conflict of interest.

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