International Journal of Botany Studies
www.botanyjournals.com
ISSN: 2455-541X
Received: 09-06-2026, Accepted: 09-07-2026, Published: 24-07-2026
Volume 11, Issue 3, 2026, Page No. 168-176

Plant–soil–microbiome networks: A systems perspective on ecosystem function, climate resilience, and sustainable agriculture

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DOI: https://doi.org/10.66856/ijbs.2026.11.3.11191

Abstract
This Paper identifies the plant-soil-microbiome complex as a holistic, interacting ecosystem, a crucial factor for ecosystem processes, improved plant production, and sustainable agriculture. As environmental and agricultural challenges continue to intensify, scientists are placing greater emphasis on understanding how plants interact with soil microbial communities, recognizing their importance in maintaining ecosystem stability, soil fertility, and global food security. Although considerable progress has been made in characterizing individual plant–microbe and soil–microbe relationships, a comprehensive systems-level understanding of their interconnected networks remains limited. A synthesis of recent breakthroughs in plant-soil-microbiome networks, using ecological, molecular, and systems biology approaches, to investigate how these interactions regulate nutrient cycling, plant growth, stress responses, soil properties, and ecosystem sustainability. It further explores the application of high-throughput sequencing, metagenomics, metatranscriptomics, metabolomics, network analysis, artificial intelligence, and remote sensing in deciphering the structure and function of these complex biological networks. The review points out those microbial inoculants play an important role in the development of stress (biotic and abiotic) tolerance, carbon capture and storage, sustainable nutrition, and resilience of ecosystems towards global changes in climate. Notwithstanding the much advancement in the research field, data availability, functional verification of such populations, and the scaling up from lab to field has posed limitations. The review concludes that integrating ecological network theory with emerging computational and multi-omics approaches provides a comprehensive framework for advancing climate-resilient agriculture, improving ecosystem sustainability, and supporting the development of next-generation precision agricultural systems. Future research should prioritize interdisciplinary collaboration and field-scale validation to facilitate the practical application of plant–soil–microbiome networks in sustainable crop production.

Keywords: Plant–soil–microbiome networks, Ecosystem function, Climate resilience, Sustainable agriculture, Systems biology

Introduction
Agriculture remains indispensable for supporting human populations and securing a stable food supply worldwide. Nevertheless, agricultural systems are under growing pressure from climate change, declining soil fertility, biodiversity loss, and the rising demand for agricultural production. These interlinked challenges threaten the sustainability and productivity of agriculture's future and create an environment of uncertainty for agricultural practices. However, The Food and Agriculture Organization (FAO) reports that agricultural land covers more than one-third of the Earth's terrestrial surface, emphasizing the need for effective management of these valuable resources. At the same time, a considerable proportion of the world's soils has experienced moderate to severe degradation as a result of erosion, nutrient exhaustion, salinity, and unsustainable farming and land-use practices. The deterioration of soil health not only limits agricultural output but also weakens ecosystem functions, reduces resilience to environmental change, and poses serious challenges to future food security [1].

Among Earth's natural resources, soil is indispensable for maintaining ecosystem processes and supporting agricultural productivity. The vast majority of the global food supply, estimated at approximately 95%, depends on soil either directly through crop cultivation or indirectly through its contribution to agricultural systems, making soil health a cornerstone of food security. Beyond food production, soils regulate water cycles, recycle nutrients, store carbon, and support a substantial proportion of global biodiversity. More than 25% of the planet's biodiversity is found in soil ecosystems, making soil one of the most biologically diverse habitats on Earth [2].

Recent developments in plant biology have transformed our understanding of plants by demonstrating that they exist in close association with diverse microbial partners rather than as independent organisms. These assemblages of microorganisms, collectively known as the plant microbiome, comprise bacteria, fungi, archaea, protists, and viruses that colonize plant tissues as well as the surrounding soil. Among the various plant-associated habitats, the rhizosphere, the thin layer of soil directly affected by root activity, represents one of the most biologically active environments. Within this dynamic zone, plant roots and microorganisms engage in continuous exchanges of nutrients, metabolites, and chemical signals that regulate plant growth, nutrient acquisition, and overall ecosystem functioning [3]. The extraordinary diversity of this underground ecosystem is reflected in the microbial abundance of fertile soils, where a single gram can harbor approximately 10^8 to 10^9 microorganisms, highlighting the remarkable complexity and ecological significance of belowground microbial communities [4].

The functioning of terrestrial ecosystems depends on intricate interactions among plants, soil, and their associated microbial communities, which together constitute dynamic plant–soil–microbiome networks. These interconnected systems govern numerous ecological processes, including nutrient transformation, decomposition of organic residues, soil structure formation, carbon storage, water regulation, and the natural suppression of plant pathogens. Beneficial symbioses provide clear examples of these functions. In leguminous plants, Rhizobium bacteria establish root nodules that convert atmospheric nitrogen into forms that plants can utilize, thereby reducing dependence on synthetic nitrogen fertilizers. Likewise, arbuscular mycorrhizal fungi improve phosphorus availability in crops such as maize, wheat, and soybean by expanding the soil volume explored by roots and enhancing nutrient absorption [5]. In addition, plant growth-promoting rhizobacteria (PGPR), particularly members of the genera Pseudomonas, Bacillus, and Azospirillum, support root development, increase nutrient-use efficiency, and strengthen plant tolerance to both biotic and abiotic stresses. Collectively, these plant–microbe associations enhance agricultural productivity while promoting the resilience and long-term stability of ecosystem functions [6]. Moreover, the significance of plant–soil–microbiome networks has become increasingly apparent as agriculture faces the growing impacts of climate change. Environmental stresses such as rising temperatures, prolonged drought, soil salinity, flooding, and the spread of plant diseases are placing considerable pressure on agricultural productivity across the globe. Under these challenging conditions, beneficial soil microorganisms enhance plant resilience through multiple mechanisms, including improved water and nutrient acquisition, phytohormone production, and the activation of stress-response pathways. Beyond supporting plant health, soil microbial communities also regulate important biogeochemical processes by contributing to carbon sequestration and influencing greenhouse gas dynamics, thereby strengthening ecosystem stability and supporting climate change mitigation [7]. Consequently, understanding and utilizing the functional diversity of soil microbiomes has become a key approach for advancing climate-resilient, resource-efficient, and sustainable agricultural systems.

Understanding these complex interactions requires a systems perspective that integrates ecological network theory, microbial ecology, systems biology, and computational sciences. Rather than examining individual organisms in isolation, a systems approach focuses on the structure, connectivity, and dynamics of entire biological networks. Recent developments in metagenomics, metatranscriptomics, metabolomics, artificial intelligence, machine learning, and ecological network analysis have significantly enhanced the ability of researchers to characterize microbial communities and predict their functional roles within ecosystems. These technologies are transforming plant science by enabling the identification of keystone microbial taxa, functional interactions, and ecosystem-level responses to environmental change [8].

This review examines plant–soil–microbiome networks from a systems perspective and explores their roles in ecosystem function, climate resilience, and sustainable agriculture. It synthesizes current knowledge on the structure and functioning of these networks, discusses emerging analytical and computational approaches, highlights key applications in sustainable crop production, and identifies future research priorities for harnessing plant–soil–microbiome interactions in resilient agro-ecosystems.

Plant–Soil–Microbiome Networks: Concepts and Theoretical Frameworks

The concept of plant–soil–microbiome networks has fundamentally transformed our understanding of terrestrial ecosystems by recognizing that plants, soils, and microorganisms function as an integrated and dynamic biological system rather than as isolated entities. Studies of early plant-microbe interactions have predominantly investigated single symbiotic relationships rather than the microbiome as a whole. Much of this research concentrated on widely studied mutualistic partnerships such as the association of legume plants with Rhizobium species which are responsible for the fixation of atmospheric nitrogen, and that between plant roots and arbuscular mycorrhizal fungi (AMF) that increases uptake of nutrients and water. These seminal studies gave the first evidence for the molecular basis of the interactions that result in mutualism, and they laid the foundations for today's study of complexity in plant-soil-microbiome interactions [9]. Although these investigations significantly advanced knowledge of nutrient acquisition and plant growth, they often overlooked the complex interactions occurring among diverse microbial communities and their collective influence on ecosystem processes. The emergence of microbial ecology, systems biology, and ecological network science has shifted this perspective towards understanding the plant–soil–microbiome as a highly interconnected network in which biological, chemical, and environmental interactions collectively regulate ecosystem function and agricultural sustainability.

Plant–soil–microbiome networks are dynamic systems formed through the continuous interactions among three fundamental components: plants, the surrounding soil environment, and diverse microbial communities. Soil microorganisms comprise a diverse group of bacteria, fungi, archaea, protists, and viruses that occupy distinct ecological niches within the plant–soil system, including the rhizosphere, rhizoplane, endosphere, and bulk soil. Each of these microbial habitats supports unique communities that perform specialized functions necessary for plant growth, soil fertility, and overall ecosystem functioning. Among these niches, the rhizosphere is considered one of the most biologically active environments because it serves as the primary interface where plant roots and microorganisms interact, exchange nutrients, and communicate through a variety of biochemical signals. These dynamic interactions strongly influence microbial activity, nutrient cycling, and plant health. Fertile soils support exceptionally diverse microbial populations, with a single gram containing estimated 10^9–10^{10} bacterial cells, thousands of microbial taxa, extensive fungal networks, and abundant populations of protists and viruses [10]. Plants actively influence these microbial communities by allocating approximately 20–40% of the carbon fixed through photosynthesis to the rhizosphere in the form of root exudates. These secretions are a rich source of sugars, amino acids, organic acids, phenolic compounds, and other secondary metabolites that serve both as nutrients and as signaling compounds to specifically attract beneficial microorganisms and regulate microbial activity, community diversity, and composition in the rhizosphere [11].

Understanding the importance of plants-soil-microbiome networks: Plants and their soil-dwelling microbial inhabitants, and the numerous beneficial mutualistic relationships between them, are essential to plant and ecosystem health. The leguminous plants and rhizobium bacteria symbiosis, a widely accepted beneficial plant-soil-microbiome relationship that leads to biological nitrogen fixation (the natural conversion of atmospheric nitrogen to ammonia), naturally contributes nitrogen to soils and greatly decreases the demand for artificial nitrogen fertilizers. This mutualistic symbiosis, where microbes help plants and plants in return, is also present in other partnerships, such as the arbuscular mycorrhizal (AM) fungi that can colonize approximately 70% - 80% of all land vascular plants and whose hyphae reach far beyond the plants' root systems to help plants absorb P, H2O, and to improve their resilience to drought and poor soils [12].

Furthermore, plant growth-promoting rhizobacteria (PGPR), such as species within the Pseudomonas, Bacillus, and Azospirillum genera, promote plant growth through various mechanisms, including phytohormone production, phosphorus solubilization, and synthesis of siderophores, which increase the solubility of iron in the soil, as well as suppressing soil-borne pathogens and inducing plant defensive responses.

Through such beneficial partnerships, plant-soil-microbiome networks contribute to better plant growth, soil quality, ecosystem functioning and promote more sustainable agriculture systems, reducing reliance on synthetic chemicals in agricultural production systems.

Ecological network theory [13] provides the principal theoretical framework for understanding these complex biological interactions. Unlike conventional ecological approaches that examine organisms individually, network theory considers ecosystems as interconnected systems in which plants, microorganisms, soil properties, and environmental factors represent nodes linked through multiple ecological relationships. These relationships include mutualism, competition, commensalism, parasitism, and facilitation, all of which influence ecosystem functioning. Important network properties such as connectivity, modularity, nestedness, robustness, and functional repetition determine the firmness and resilience of microbial communities. Highly connected microbial networks generally exhibit greater resistance to environmental disturbances because multiple microorganisms perform similar ecological functions, allowing ecosystem processes to continue even when certain taxa decline. Particular attention has recently focused on keystone taxa, microbial species that disproportionately influence community organization and ecosystem processes despite their relatively low abundance. The identification of these keystone microorganisms has become a major objective in microbial ecology because of their possible applications in sustainable crop management and ecosystem restoration.

A systems biology [14] perspective further expands this conceptual framework by integrating biological interactions across molecular, cellular, organismal, and ecosystem scales. Rather than investigating individual genes or microbial species independently, systems biology seeks to understand how multiple biological components interact to generate emergent ecosystem properties such as nutrient cycling, carbon sequestration, disease suppression, and climate resilience. Current developments in the field of high-throughput sequencing and in metagenomics, metatranscriptomics, metaproteomics, metabolomics, and bioinformatics enable comprehensive descriptions of microbial diversity and functionality. Ecological network analysis, machine learning, and artificial intelligence tools can then be applied in conjunction with this data to elucidate microbial interaction networks, predict the ecosystem's response to environmental alterations, and identify the microbial drivers of soil health.

Several complementary ecological theories provide a foundation for interpreting plant–soil–microbiome networks. The holobiont theory considers plants and their associated microorganisms as a single functional unit whose collective genomes influence plant adaptation and evolution. Plant–soil feedback theory [15] explains how plants modify soil microbial communities through root exudation and litter inputs, while these altered microbial communities subsequently influence the growth and performance of future plant populations. Niche theory [16] proposes that microbial community assembly is largely determined by environmental conditions, resource availability, and species-specific functional traits, whereas neutral theory recognizes the contribution of stochastic processes such as dispersal limitation and ecological drift. Together, these theories explain the mechanisms governing microbial community assembly, ecosystem stability, and plant–soil interactions under changing environmental conditions.

Advances in plant–microbiome research have shifted the focus from simply describing microbial diversity to understanding microbial functions and applying this knowledge to address agricultural challenges. Emerging approaches, including the identification of core microbiomes, microbiome engineering, and the development of synthetic microbial communities (SynComs), are being investigated as innovative strategies to enhance crop performance, increase tolerance to environmental stresses, and rehabilitate degraded soils. At the same time, the integration of ecological network analysis with systems biology and multi-omics technologies has improved our ability to identify functionally important microbial consortia and unravel the complex interactions that govern plant–soil ecosystems. These interdisciplinary approaches provide a scientific foundation for developing microbiome-based technologies that support sustainable and resource-efficient agriculture. As climate change continues to reshape ecosystem dynamics, a deeper understanding of plant–soil–microbiome networks will be critical for strengthening agricultural resilience, preserving biodiversity, maintaining ecosystem functions, and ensuring long-term food and environmental security.

Ecological Functions of Plant–Soil–Microbiome Networks

Plant–soil–microbiome networks constitute the biological foundation of terrestrial ecosystems by linking plants, soil, and diverse microorganisms into an interconnected and dynamic system. Through these interactions, they drive key ecological processes, including nutrient transformation, soil development, carbon storage, water regulation, conservation of biodiversity, and the suppression of plant diseases, all of which contribute to ecosystem resilience and sustainable agricultural production. Healthy soils are indispensable for global food security, supporting an estimated 95% of worldwide food production while serving as habitats for nearly one-quarter of the planet's biodiversity and an extraordinary diversity of microorganisms [17]. From an ecological systems perspective, ecosystem functioning is determined not only by the richness of species present but also by the structure, connectivity, and functional interactions among microbial communities that collectively regulate soil processes and ecosystem performance.

Soil microorganisms play a critical role in sustaining biogeochemical cycles by regulating the transformation and movement of these major elements. They mediate most carbon, nitrogen, phosphorus, sulfur, and various other nutrients through cycling. Their metabolic activities drive processes such as organic matter decomposition, nutrient mineralization, biological nitrogen fixation, phosphorus mobilization, and the recycling of organic residues, thereby converting complex organic and inorganic compounds into forms that are readily absorbed by plants. Among the most important nitrogen-fixing microorganisms are the symbiotic genera Rhizobium, Bradyrhizobium, and Frankia, which establish close associations with host plants to supply biologically available nitrogen [18]. Furthermore, free-living diazotrophic bacteria, such as Azotobacter and Azospirillum, help to enrich the soil with nitrogen and improve nutrient availability in the agro-systems. Phosphorus availability is also increased by phosphate-solubilising microorganisms (Bacillus, Pseudomonas, Penicillium, Aspergillus, etc.), which produce organic acids and phosphatase that facilitate insoluble P into soluble P available to plants. In the ecosystem, these microorganisms play roles in nutrient use efficiency, sustainability and decreasing the use of synthetic fertiliser.

Plant–soil–microbiome networks also play a vital role in carbon cycling and climate regulation. Plants allocate approximately 20–40% of their photosynthetically fixed carbon belowground through root exudates and root residues, providing energy for rhizosphere microorganisms. These microbial communities regulate organic matter decomposition, nutrient mineralization, and soil organic carbon formation through extracellular enzyme activities. Arbuscular mycorrhizal fungi, particularly Glomus species, enhance soil carbon stabilization by improving soil aggregation through extensive hyphal networks and glomalin-related soil proteins. Consequently, these interactions contribute to long-term carbon sequestration while influencing emissions of carbon dioxide, methane, and nitrous oxide [19].

Beyond nutrient cycling, plant–soil–microbiome networks maintain soil health by improving soil structure, fertility, and biological activity. Microbial extracellular polymeric substances bind soil particles into stable aggregates, enhancing water infiltration, aeration, root penetration, and resistance to erosion. Soil microorganisms also regulate enzyme activities, nutrient retention, and organic matter decomposition, while shifts in microbial diversity often provide early indicators of changes in soil quality. Beneficial microorganisms further promote plant growth by producing phytohormones such as indole-3-acetic acid, gibberellins, and cytokinins, increasing nutrient acquisition through siderophore production and enzyme secretion, and improving tolerance to drought, salinity, heat, and heavy metal stress. These mechanisms have been widely demonstrated in crops including wheat, rice, maize, soybean, tomato, and chickpea [20].

Plant–soil–microbiome networks also provide important ecosystem services through biological control and disease suppression. Beneficial microorganisms such as Trichoderma, Pseudomonas, Bacillus, and Streptomyces suppress pathogens including Fusarium, Rhizoctonia, and Phytophthora by competing for resources, producing antimicrobial compounds, secreting lytic enzymes, and inducing systemic resistance in host plants. In addition, microbial communities interact through cooperation, competition, quorum sensing, metabolite exchange, and cross-feeding, forming complex ecological networks that regulate community assembly and ecosystem stability. Network characteristics such as connectivity, modularity, nestedness, robustness, functional redundancy, and the presence of keystone taxa enhance ecosystem resilience by ensuring that critical ecological processes continue despite environmental disturbances.

Climate Change, Ecosystem Resilience, and Microbiome Adaptation

Rising global temperatures, irregular precipitation patterns, prolonged droughts, floods, soil salinization, wildfires, and increasing atmospheric carbon dioxide concentrations are modifying the physical and chemical characteristics of soils. The above mentioned environmental changes not only affect plant development but also affect soil microorganisms regarding their species diversity, abundance and ecological interactions. Because plants and microbes have co-evolved over millions of years, even small changes in climate can disrupt their ecological relationships, leading to shifts in nutrient availability, community organization, and ecosystem stability. Consequently, understanding the response of plant–soil–microbiome networks to climate change has become a major research priority for predicting ecosystem responses and ensuring long-term agricultural sustainability.

Climate-induced environmental stress alters the composition of microbial communities through a process known as community turnover, in which stress-sensitive microorganisms decline while stress-tolerant taxa become dominant. Drought, for example, generally reduces microbial biomass and diversity while favoring drought-adapted bacterial groups such as Actinobacteria and certain Firmicutes, which possess physiological traits that enable survival under limited water availability. Conversely, prolonged flooding creates oxygen-deficient soils that promote anaerobic microorganisms while suppressing aerobic bacterial populations. Elevated temperatures accelerate microbial metabolism but may simultaneously increase organic matter decomposition, reducing soil carbon stocks over time. These shifts demonstrate that climate change does not simply reduce microbial abundance; rather, it reorganizes microbial communities according to their adaptive capacities and ecological functions [21].

Plant responses to climate stress further influence microbial community assembly. These alterations affect microbial recruitment by selectively favoring microorganisms capable of utilizing newly available substrates or tolerating stressful conditions. Consequently, microbial community assembly becomes increasingly dynamic under climate stress, involving continuous processes of species replacement, ecological succession, and adaptation. Such restructuring influences not only microbial diversity but also the complexity of interaction networks connecting plants, microorganisms, and soil environments [22].

From a network perspective, ecosystem resilience depends not only on the presence of beneficial microorganisms but also on the architecture of microbial interaction networks. Climatic disturbances frequently reduce network connectivity by disrupting interactions among microbial species, yet they may also increase modularity, allowing smaller groups of microorganisms to function relatively independently and preventing the spread of disturbances throughout the entire network. This process, often described as network rewiring, enables microbial communities to establish new ecological interactions that compensate for the loss of previous associations. Highly resilient ecosystems are therefore characterized by flexible interaction networks capable of reorganizing while maintaining essential ecological processes [23].

An important feature of resilient microbial communities is functional resilience, whereby ecosystem functions are maintained despite changes in community composition. This resilience arises from functional redundancy, meaning that multiple microbial taxa perform similar ecological roles. Consequently, if one microbial group declines because of environmental stress, other microorganisms can partially compensate for its ecological function, reducing the risk of ecosystem collapse. Moreover, keystone taxa, a disproportionately important role in maintaining network stability by connecting different microbial groups and facilitating communication within ecological networks. The persistence or loss of these highly connected microorganisms often determines the speed and extent of ecosystem recovery following climatic disturbances.

Emerging Technologies for Deciphering Plant–Soil–Microbiome Networks

Technological progress in molecular biology, systems biology, computational approaches, and bioinformatics has fundamentally reshaped research on plant–soil–microbiome networks, shifting the emphasis from descriptive studies to predictive, data-intensive analyses. Earlier investigations relied heavily on culture-based techniques, which revealed only a limited portion of soil microbial diversity because many microorganisms are difficult or impossible to cultivate under standard laboratory conditions. The introduction of high-throughput sequencing technologies, together with sophisticated computational and analytical methods, has enabled researchers to characterize microbial communities with far greater depth and accuracy [24]. These advances provide detailed insights into microbial diversity, functional capabilities, and the complex interactions occurring within plant–soil ecosystems. Consequently, modern omics technologies have greatly enhanced our understanding of how plant–soil–microbiome networks respond to environmental disturbances and have created new opportunities for developing sustainable and climate-resilient agricultural management strategies. However, Amplicon sequencing of bacterial 16S rRNA genes and fungal ITS regions provides detailed information on taxonomic diversity and community composition, whereas whole-metagenome sequencing reveals the functional genes involved in nutrient acquisition, stress tolerance, and microbial metabolism. Advances in long-read sequencing platforms have further improved genome assembly and facilitated the identification of previously unknown microorganisms, expanding knowledge of microbial diversity across agricultural and natural ecosystems [25].

Beyond taxonomic characterization, multi-omics technologies provide a comprehensive understanding of microbial functions and interactions. Metagenomics identifies the genetic potential of microbial communities, while metatranscriptomics examines actively expressed genes under specific environmental conditions. Metaproteomics reveals the proteins responsible for biological functions, and metabolomics characterizes metabolites involved in plant–microbe communication, nutrient exchange, and stress responses. Integrating these complementary datasets enables researchers to connect microbial diversity with ecosystem functions and identify key metabolic pathways that influence plant health and soil processes [26].

Ecological network analysis has emerged as an important computational approach for investigating the organization of plant–soil–microbiome systems. Rather than examining microorganisms individually, network analysis represents plants, microbes, and environmental variables as interconnected nodes linked through positive or negative interactions. Network metrics such as connectivity, modularity, centrality, nestedness, and robustness help identify highly connected keystone taxa that regulate community stability and ecosystem functioning. These approaches also reveal how microbial interaction networks reorganize under environmental disturbances, providing insights into ecosystem resilience and adaptation [27].

Artificial intelligence and machine learning are increasingly being incorporated into microbiome research to analyze large and complex datasets generated by sequencing and multi-omics platforms. Algorithms can identify hidden patterns in microbial communities, predict microbial interactions, classify soil health, and forecast ecosystem responses to climate change or agricultural management practices. Deep learning models are also being used to integrate environmental variables with microbiome data, supporting precision agriculture and evidence-based decision-making. As computational resources continue to improve, AI-driven approaches are expected to accelerate microbiome discovery and optimize microbial management strategies [28].

Emerging technologies such as single-cell genomics, spatial transcriptomics, and advanced microscopy are providing unprecedented insights into microbial organization at cellular and microscale levels. Single-cell sequencing enables the characterization of uncultured microorganisms without the need for laboratory cultivation, whereas spatial transcriptomics reveals how gene expression varies across different regions of the rhizosphere. Combined with stable isotope probing and high-resolution imaging techniques, these approaches improve understanding of microbial interactions within their natural environments and reveal functional relationships that cannot be detected using bulk analyses alone.

The integration of molecular biology, computational modeling, ecological network analysis, and artificial intelligence is driving a new era of predictive plant–soil–microbiome research. Future developments are expected to include digital twins of agro-ecosystems, real-time microbiome monitoring using environmental sensors, autonomous decision-support systems, and microbiome-guided crop management. These innovations will enhance the ability to identify beneficial microorganisms, design synthetic microbial communities, and develop climate-resilient agricultural systems. By combining advanced technologies with ecological theory and long-term field observations, researchers can move from describing microbial diversity to predicting and managing ecosystem processes for sustainable agriculture.

Applications of Plant–Soil–Microbiome Networks in Sustainable and Precision Agriculture

The growing understanding of plant–soil–microbiome networks has created new opportunities to transform agricultural systems from input-intensive production toward biologically driven and resource-efficient management. Conventional agriculture has relied heavily on synthetic fertilizers, pesticides, and intensive tillage to maximize crop yields. While these practices have increased food production, they have also contributed to soil degradation, biodiversity loss, nutrient imbalance, greenhouse gas emissions, and declining ecosystem resilience. Integrating plant–soil–microbiome knowledge into agricultural management offers a sustainable alternative by harnessing naturally occurring microbial processes to improve crop productivity, soil health, and environmental sustainability.

A major advancement in sustainable agriculture is the use of microbial bio fertilizers to improve nutrient availability and decrease reliance on synthetic fertilizers. Beneficial nitrogen-fixing microorganisms, including Rhizobium, Bradyrhizobium, Azotobacter, and Azospirillum, naturally enrich soils by converting atmospheric nitrogen into forms that plants can readily utilize. Likewise, phosphate-solubilizing bacteria such as Bacillus and Pseudomonas enhance phosphorus availability by transforming insoluble phosphate compounds into plant-accessible forms, thereby increasing nutrient-use efficiency. Arbuscular mycorrhizal fungi complement these processes by forming extensive hyphal networks that expand the effective root zone, facilitating greater absorption of phosphorus and water, particularly under nutrient-poor or drought-prone conditions. The incorporation of these beneficial microorganisms into integrated crop management practices can enhance fertilizer efficiency, reduce production expenses, minimize nutrient losses, and promote environmentally sustainable agricultural systems [29].

Plant–soil–microbiome research has also accelerated the development of biological crop protection strategies. Beneficial microorganisms such as Trichoderma, Bacillus, Pseudomonas, and Streptomyces suppress soil-borne pathogens through competition, antibiosis, enzyme production, and activation of plant defense responses. These biological control agents reduce disease incidence while minimizing pesticide use and associated environmental risks. In addition, microbiome-informed disease management promotes healthier soils and supports integrated pest management programs by strengthening naturally occurring microbial communities rather than relying exclusively on chemical interventions.

Advances in microbiome science are also supporting the development of microbiome engineering and synthetic microbial communities (SynComs). Instead of applying individual microbial strains, researchers are increasingly designing functionally complementary microbial consortia that perform multiple ecological roles simultaneously, including nutrient mobilization, stress mitigation, and pathogen suppression [30]. The concept of the core microbiome has further improved the selection of stable and beneficial microbial communities that consistently associate with particular crop species across diverse environments. These innovations provide opportunities to develop crop-specific microbial inoculants with improved field performance and long-term ecological stability.

The integration of microbiome research with precision agriculture represents another major advancement in sustainable farming. High-resolution soil sensors, remote sensing technologies, geographic information systems (GIS), unmanned aerial vehicles (UAVs), Internet of Things (IoT) devices, and satellite observations generate real-time information on soil moisture, nutrient availability, crop health, and environmental conditions [31]. When combined with microbiome datasets, these technologies enable site-specific management of irrigation, fertilization, and crop protection. Artificial intelligence and machine learning further enhance decision-making by identifying patterns in complex datasets, predicting microbial responses to environmental changes, and optimizing agricultural practices based on local soil and climatic conditions.

Emerging digital technologies are paving the way for data-driven microbiome management. Decision-support systems integrating multi-omics information, ecological network analysis, climate forecasts, and field observations can help farmers identify appropriate microbial inoculants, optimize fertilizer application, and anticipate disease outbreaks before visible symptoms appear. Predictive models and digital twins of agricultural systems are increasingly being explored to simulate interactions among crops, soil properties, microorganisms, and climatic variables, allowing management strategies to be evaluated before field implementation. Such approaches improve resource-use efficiency while reducing production risks and environmental impacts.

Current Challenges and Future Opportunities [32]

As research on plant–soil–microbiome networks continues to evolve, attention is shifting from fundamental discoveries toward practical applications in sustainable agriculture. This transition presents both significant challenges and promising opportunities. Resolving existing knowledge gaps, improving methodological consistency, and integrating emerging technologies will be crucial for translating microbiome research into scalable solutions that enhance agricultural productivity, ecosystem resilience, and environmental sustainability.

Current Challenges

1. Plant–soil–microbiome networks are highly dynamic systems in which microorganisms, plants, soil properties, and environmental factors interact simultaneously. Because these interactions vary with crop species, soil type, geographical location, and plant developmental stage, identifying universal ecological principles remains difficult. This biological complexity limits the accurate prediction of microbial network behavior and ecosystem functioning under different environmental conditions.

2. Variability in sampling strategies, DNA extraction protocols, sequencing technologies, laboratory procedures, and bioinformatics pipelines often results in inconsistent findings across studies. Moreover, integrating multi-omics datasets with environmental, agronomic, and climatic information presents considerable computational and analytical challenges. Establishing standardized protocols and robust analytical frameworks is therefore essential to improve data quality, reproducibility, and cross-study comparisons.
3. Although many microbiome-based technologies have demonstrated promising results under controlled experimental conditions, their performance in field environments is often inconsistent. Variations in soil characteristics, climatic conditions, indigenous microbial communities, and crop genetics can strongly influence their effectiveness. Comprehensive long-term field evaluations across diverse agro-ecosystems are required to validate their practical value and scalability.
4. Climate change introduces multiple environmental stresses, including elevated temperatures, prolonged drought, erratic rainfall, flooding, and increasing soil salinity, all of which influence microbial diversity and plant–soil interactions. These changing conditions create uncertainty regarding the long-term stability of microbial functions and complicate efforts to develop climate-resilient agricultural systems.
5. The large-scale implementation of microbiome-based agricultural technologies is limited by evolving regulatory requirements, inconsistent product quality standards, relatively high production costs, and limited awareness among farmers. Addressing these constraints through stronger regulatory policies, standardized quality assurance systems, and effective agricultural extension programs will be essential for wider adoption.

Opportunities

1. Recent progress in high-throughput sequencing and advanced multi-omics technologies has transformed the study of soil microbial communities by enabling detailed analyses of their diversity, community structure, and functional attributes. The combined application of genomics, transcriptomics, proteomics, and metabolomics provides a holistic understanding of the complex interactions among plants, soil, and microorganisms. This integrated approach uncovers the biological processes underlying plant–soil–microbiome relationships. It facilitates the development of innovative, sustainable agricultural practices to improve crop performance, soil fertility, and ecosystem resilience.
2. Artificial intelligence and machine learning have proved useful computational tools for making sense of massive biological datasets and finding patterns in microbial communities that are hidden from more established techniques. When fed into these advanced analytics, vast, multi-dimensional data can improve ecological forecasts, deliver better soil quality, and pave the way for smart farming by informing decisions with facts, not hunches.
3. Recent advances in microbiome engineering have created new possibilities for designing efficient microbial consortia with complementary and synergistic ecological functions. These synthetic microbial communities (SynComs) can improve nutrient uptake, strengthen plant resilience to both biotic and abiotic stresses, and suppress plant pathogen activity. As a result, they enhance crop productivity while reducing dependence on chemical fertilisers and pesticides, supporting more sustainable agricultural systems.
4. Modern digital farming tools, including but not limited to remote sensing, geographic information systems (GIS), uncrewed aerial vehicles (UAVs or drones), internet of things (IoT) platforms, and sophisticated soil sensing equipment, were coupled with research on microbiomes, thereby enhancing the accuracy of monitoring and management of crops in fields. The combination of digital tools with microbiome knowledge enables more prudent use of agricultural resources, reduces negative environmental externalities, and improves resilience to stresses from climate variability and climate-related extreme events, thereby promoting more climate-smart and resilient agricultural systems.
5. Future advances in plant–soil–microbiome research will rely on close collaboration among plant biologists, soil scientists, microbiologists, agronomists, bioinformaticians, engineers, policymakers, and industry stakeholders. Such multidisciplinary partnerships will accelerate scientific discovery, promote the translation of research into practical technologies, and the growth of productive, resilient, and environmentally sustainable agricultural practices.

Conclusion

Plant–soil–microbiome networks have emerged as a fundamental framework for understanding the functioning of terrestrial ecosystems by revealing the intricate relationships among plants, soil, microorganisms, and their surrounding environment. Contemporary research has moved beyond examining these components in isolation and now recognizes that ecosystem processes are driven by complex biological interactions operating across multiple spatial and temporal scales. This systems-oriented perspective has provided valuable insights into the mechanisms governing nutrient cycling, soil fertility, plant productivity, biodiversity conservation, and ecosystem resilience, thereby reshaping our understanding of ecosystem functioning.

Collectively, the results reviewed here illustrate the indispensable importance of plant–soil–microbiome interactions for maintaining ecosystem services and advancing environmentally sustainable agriculture. Advanced tools, including high-throughput sequencing, multi-omics, ecological network analysis, artificial intelligence, and computational modeling, have greatly expanded knowledge on soil microbial diversity, functional potential, and their ecological interactions. These novel approaches enabled the development of microbiome engineering, synthetic microbial communities (SynComs), and precision agriculture to improve soil fertility, augment crop productivity, increase resource efficiency, and strengthen agricultural systems' resistance to environmental stress. With increasing environmental concerns such as climate change, land degradation, loss of biodiversity, and increasing food demand, the application of microbiome knowledge to agricultural policy, sustainable agriculture, and land management will be critical to support food security and environmental sustainability in the coming years.

Despite these advances, several barriers continue to limit the large-scale implementation of microbiome-based technologies. The immense complexity of soil microbial communities, environmental heterogeneity, methodological variability, and the limited availability of long-term field validation remain significant obstacles to their widespread adoption. Addressing these challenges will require standardized experimental protocols, coordinated multi-location field trials, improved computational and bioinformatics frameworks, and stronger collaboration among researchers, farmers, policymakers, industry partners, and other stakeholders. Strengthening the translation of fundamental scientific discoveries into practical agricultural applications will be essential for developing reliable, scalable, and economically viable microbiome-based solutions.

Future research should prioritize uncovering the ecological and molecular mechanisms that regulate plant–microbe interactions, microbial network dynamics, ecosystem stability, and plant adaptation to environmental change rather than focusing solely on microbial diversity. The integration of systems biology, ecological network theory, multi-omics technologies, artificial intelligence, and long-term ecological monitoring will improve the identification of keystone microorganisms, enhance predictive models of ecosystem functioning, and support the development of climate-resilient agricultural strategies. Continued interdisciplinary collaboration among plant scientists, soil ecologists, microbiologists, agronomists, bioinformaticians, engineers, and policymakers will be critical for translating scientific knowledge into practical innovations that promote ecosystem restoration, sustainable land management, biodiversity conservation, and long-term global food security. Ultimately, a deeper understanding of plant–soil–microbiome networks will provide a scientific foundation for building resilient agricultural systems capable of meeting future environmental and food security challenges.

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