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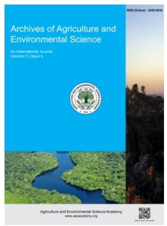

REVIEW ARTICLE

CrossMark

Rhizosphere microbial communities: Drivers of nutrient cycling, plant health, and soil fertility

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ABSTRACT

Soil microbial communities, particularly those inhabiting the rhizosphere, play a fundamental role in regulating nutrient cycling, plant health, and soil fertility within agroecosystems. The rhizosphere represents a biologically active microenvironment enriched with root exudates such as sugars, amino acids, and organic acids, which stimulate microbial colonization, metabolic activity, and complex plant–microbe interactions. These interactions drive essential biogeochemical processes, including nitrogen fixation, nitrification, denitrification, and nutrient mineralization, thereby sustaining soil productivity and ecosystem stability. Diverse microbial groups including nitrogen-fixing microorganisms, phosphate-solubilizing microbes, zinc-mobilizing bacteria and fungi, and mycorrhizal fungi enhance nutrient bioavailability by transforming nutrients into plant-accessible forms and improving nutrient uptake efficiency. This review presents the management practices strongly influence rhizosphere microbial composition and ecological network dynamics, with organic and no-till systems generally supporting more stable and complex fungal and bacterial interactions compared to conventional systems. Functional microbial consortia, particularly plant growth–promoting bacteria and indigenous bio-inoculants, contribute to soil fertility through nutrient mobilization, biofilm formation, and improved root architecture. Additionally, microbial colonization and signaling processes, mediated by root exudates and molecular communication, regulate both beneficial symbioses and pathogenic interactions in the rhizosphere. Environmental factors, host plant traits, and biotic stresses such as nematode parasitism further shape microbial community structure and functional pathways, including nitrogen fixation and pathogen-related mechanisms. Overall, a diverse and active soil microbiome enhances nutrient cycling, soil structure, and resilience to environmental stresses, reducing reliance on chemical inputs.

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INTRODUCTION

Soil represents one of the most complex and biologically rich environments on Earth, harboring an extraordinary diversity of microorganisms that collectively govern fundamental processes essential to ecosystem functioning and agricultural productivity. Among these, soil microbes constitute the most dynamic biological element of the soil system and are crucial for soil formation, nutrient transformation, plant growth, and ecosystem stability (Powlson *et al.*, 2001). Of particular importance is the rhizosphere the narrow zone of soil directly surrounding and influenced by plant roots which serves as a hotspot of intense microbial activity and intricate biological interactions. Microbial activity is most intense in this region, where nutrient-rich soil surrounds plant roots and creates conditions markedly different from root-free bulk soil (Hartmann *et al.*, 2009). Plant roots continuously release a diverse array of readily accessible organic carbon molecules, including sugars, amino acids, and organic acids, into this zone (Zhang *et al.*, 2014). The synergistic influence of abundant carbon availability and localized nutrient dynamics establishes a unique microenvironment that fosters significantly increased microbial population density and metabolic activity relative to bulk soil. Despite the recognized importance of the rhizosphere, the mechanistic complexity of plant–microbe interactions and their cascading effects on soil fertility and agroecosystem productivity remains incompletely understood. A wide range of soil microorganisms navigate concentration gradients of root exudates toward the root surface, resulting in an uneven and highly dynamic distribution of microbial communities throughout rhizosphere compartments. Beyond root exudates, additional abiotic factors such as rhizosphere pH further modulate microbial community composition and ecological interactions (Bravin *et al.*, 2009). Soil microbial communities are among the most prevalent and diverse biological assemblages in nature (Nemergut *et al.*, 2013), with a single gram of soil harboring a diverse collection of bacteria including actinomycetes, fungi, archaea, viruses, algae, and protozoa (Islam *et al.*, 2020; Sokol *et al.*, 2022). The rhizosphere is therefore regarded as one of the most intricate ecosystems on Earth, characterized by continuous and multidirectional interactions among plants, microbes, and soil (Goswami & Deka, 2022).

Microorganisms in the rhizosphere play a vital role in nutrient cycling, particularly within the nitrogen cycle, which encompasses four primary transformations: nitrogen fixation, nitrification, denitrification, and dissimilatory nitrate reduction to ammonium. These processes collectively maintain soil fertility and support sustainable plant productivity. Nitrogen-fixing microorganisms, including symbiotic, free-living, associative, and diazotrophic groups, play a fundamental role in enhancing soil nitrogen availability and plant growth (Table 1). Similarly, microbial zinc solubilization by rhizospheric bacteria and fungi improves zinc uptake and crop productivity, contributing to sustainable soil fertility management (Table 2). Beneficial microbial colonization of plant roots further represents an essential dimension of plant–microbe interaction, wherein bacteria respond to chemical signals released by roots, adhere to the root surface, and form biofilms regulated by specific transcriptional mechanisms (Arnaouteli *et al.*, 2021; Nie *et al.*, 2022; Ivanova *et al.*, 2023). The extracellular matrix of these biofilms shields microorganisms from environmental stress and plant defense responses, facilitating the establishment of stable and functionally active populations on root surfaces (Flemming *et al.*, 2023). However, the rhizosphere also serves as an arena for harmful interactions. Pathogenic microorganisms employ effector molecules to evade host immune responses and establish infection. For instance, *Phytophthora sojae* effectors Avr3b and CRN78 reduce reactive oxygen species accumulation by disrupting NADH availability and modifying aquaporin PIP2;2 (Ai *et al.*, 2021), while glycosylation of the virulence factor XEG1 enables pathogens to evade host proteases (Xia *et al.*, 2020). Root exudates such as rosmarinic acid, however, have been shown to suppress pathogenic biofilm formation, illustrating the dual regulatory role of root-derived chemical signals in governing both beneficial and harmful microbial colonization (Walker *et al.*, 2004). Upon successful colonization, certain microbes may further infiltrate internal plant tissues as endophytes, enabling even closer association with the host plant (Dudeja *et al.*, 2021; Mushtaq *et al.*, 2023).

Table 1. Dominant fungal groups and their ecological roles in soil networks across conventional, no-till, and organic.

Soil management system	Dominant fungal orders	Functional role / Influence on Network
Conventional	Sordariales, Agaricales	major influence on network structure and microbial interactions.
No-till	Sordariales, Cantharellales, Mortierellales	network stability and nutrient cycling under minimal disturbance.
Organic	Tremellales, Hypocreales, Glomerales, Paraglomerales, Diversisporales	Enhanced network complexity, promoted symbiosis, and supported soil fertility.

(Source: Banerjee *et al.*, 2019).

Table 2. Classification of nitrogen-fixing microorganisms with examples, fixation strategies, and agricultural importance.

Category of nitrogen-fixing microorganisms	Microorganisms	Mode of nitrogen fixation	Agricultural significance	Reference
Symbiotic nitrogen fixers	*Rhizobium sp., Frankia sp.*	Symbiotic association with plant roots (mainly legumes)	Improve nitrogen availability in soil and enhance plant growth	Debnath *et al.*, 2020
Free-living nitrogen fixers	*Azotobacter sp., Beijerinckia sp.*	Non-symbiotic nitrogen fixation in soil	Maintain soil nitrogen balance and support crop productivity	Ahemad & Kibret, 2014
Associative nitrogen fixers	*Azospirillum sp.*	Association with plant root surfaces	Promote plant growth and improve nitrogen uptake	Debnath *et al.*, 2020
Diazotrophic bacteria	*Klebsiella pneumoniae*	Biological nitrogen fixation through nitrogenase enzyme activity	Contribute to nitrogen cycling and soil fertility	Yoneyama *et al.*, 2019

Note: While symbiotic nitrogen fixers like *Rhizobium* demonstrate the highest contribution to plant nitrogen uptake, free-living and associative diazotrophs also play complementary roles in maintaining soil N balance. The effectiveness of these microorganisms can vary with soil type, crop species, and management practices, highlighting the importance of integrating microbial knowledge into sustainable agricultural strategies.

Understanding these relationships has become increasingly critical in the context of plant health management, soil remediation, and the development of sustainable agricultural systems (White *et al*., 1998; Verma *et al*., 2023; Torres-Farradá *et al*., 2024). Scientific advances including genetic engineering have further illustrated the potential of harnessing microbial functions to increase plant resilience by integrating beneficial microbial genes into crop plants (Ding *et al*., 2021; Reboledo *et al*., 2021). Understanding the phylum and genus-level structure, physiological activity, and functional roles of key microbial groups is therefore essential for elucidating the complex relationships among plants, soil, and microorganisms. Despite considerable progress in rhizosphere microbiology, several critical knowledge gaps persist. Most existing reviews address individual aspects of rhizosphere biology in isolation — focusing either on nutrient cycling, plant growth promotion, or pathogen interactions — without providing an integrated perspective that connects microbial community dynamics, functional diversity, and agricultural management practices within a unified framework. Furthermore, the influence of management systems such as organic, no-till, and conventional farming on the ecological network structure of rhizosphere communities, including fungal-bacterial interaction complexity and functional gene abundance, remains insufficiently characterized. The long-term ecological consequences of microbial bioformulations and engineered consortia on native soil microbiomes across diverse cropping systems also remain poorly understood. Additionally, the interplay between biotic stressors such as nematode parasitism and the functional trajectories of rhizosphere microbial communities including nitrogen fixation pathways has received limited systematic attention.
The present review aims to provide a comprehensive and integrated analysis of the structure, function, and agricultural significance of rhizosphere microbial communities. Specifically, it seeks to: (i) elucidate the roles of key microbial groups including nitrogen-fixing bacteria, phosphate-solubilizing microbes, zinc-mobilizing microorganisms, and mycorrhizal fungi in driving nutrient cycling and soil fertility; (ii) examine the mechanisms governing beneficial and pathogenic plant–microbe interactions in the rhizosphere; (iii) evaluate the influence of agricultural management practices on rhizosphere microbial community composition and ecological network dynamics; and (iv) identify future research directions including the application of multi-omics tools, climate-responsive microbial studies, and the engineering of tailored microbial consortia for sustainable agroecosystem management. By synthesizing current evidence across these dimensions, this review contributes a holistic perspective that bridges fundamental rhizosphere ecology with practical strategies for improving soil health and reducing dependence on chemical inputs in modern agriculture.

METHODOLOGY

Literature search strategy

In order to document the historical evolution, technical advancements, and emerging trends in rhizosphere microbial communities and their roles in nutrient cycling, plant health, and soil fertility, this review was carried out utilizing an organized and thorough literature survey strategy. Major scientific databases such as Web of Science, Scopus, PubMed, Google Scholar and publisher platforms like SpringerLink, Elsevier ScienceDirect, and Wiley Online Library were used to find peer-reviewed research papers, reviews, and reports. Rhizosphere microbiome, plant–microbe interactions, nutrient cycling, nitrogen fixation, phosphate solubilization, zinc mobilization, mycorrhizal fungi, plant growth–promoting bacteria, soil fertility, biofilm formation, root exudates, microbial consortia, agroecosystem productivity, organic farming, and multi-omics approaches were among the topics covered by the search queries, which were created using a combination of keywords and Boolean operators. In order to find more pertinent studies that were missed by the initial database search, reference lists of key papers were also manually searched.

Inclusion and exclusion criteria

Relevance to the conceptual, functional, and applied dimensions of rhizosphere microbiology and soil fertility management was considered when selecting publications. Studies were included if they provided theoretical or experimental insights into the mechanisms underlying plant–microbe interactions and nutrient cycling processes; presented methodological or functional understanding of nitrogen fixation, phosphorus and zinc solubilization, or mycorrhizal symbiosis; examined the influence of agricultural management practices, environmental factors, or host plant traits on rhizosphere microbial community structure and activity; or contributed to the development of microbial bio-inoculants, functional consortia, or multi-omics approaches for sustainable soil fertility management. Priority was given to original research articles and reputable reviews published between 2001 and 2025, while older foundational studies were included where necessary to establish the theoretical basis of the field. Non-peer-reviewed sources, abstracts without full text, and studies with unclear methodologies were excluded unless they held significant historical importance.

Data extraction and synthesis

Microbial taxa and functional groups, mechanisms of nutrient mobilization, plant species and soil management systems studied, experimental conditions and field settings, molecular signaling and colonization pathways, and the agricultural significance of specific microbial interactions were the main focus of the systematic extraction of information from selected publications. To highlight recurrent mechanistic principles, methodological consistencies, and sources of variation across studies, the findings were qualitatively synthesized rather than through quantitative meta-analysis. Comparative tables summarizing the classification of nitrogen-fixing microorganisms, phosphate-solubilizing microbes, zinc-mobilizing bacteria and fungi, and dominant fungal groups across management systems were constructed to facilitate cross-study comparison and identification of trends relevant to sustainable agroecosystem management.

RHIZOSPHERE MICROBIAL INTERACTIONS AND ITS FUNCTION IN AGRICULTURE

The rhizosphere is a biologically active soil region influenced by plant roots, where complex plant–microbe interactions regulate soil processes and plant health. In contrast to bulk soil, plant roots produce nutrient-rich microenvironments that selectively attract microbial communities to establish unique rhizosphere microbiomes that are essential to ecosystem functioning and plant productivity. While the composition of fungal communities is mostly controlled by management approaches, rhizosphere microbiomes under conventional and organic systems may exhibit comparable diversity and network structure when compared to their respective bulk soils. NosZ abundance among nitrogen-cycling genes has been found to be higher in organic management systems, suggesting that agricultural methods are linked to functional changes in microbial communities (Schmidt *et al*., 2019). The intricate ecological networks in which soil microorganisms live include symbiosis, competition, predation, and other forms of interaction that affect microbial adaptation and ecosystem stability. Microbial populations in the rhizosphere and root endosphere can also be changed by biotic stressors such nematode parasitism. Studies comparing plants with and without root-knot nematode (RKN) infection have shown that host species, developmental stage, ecological niche, and parasitism significantly influence root-associated microbiota. Enrichment of bacterial groups including *Rhizobiales*, *Betaproteobacteriales*, and *Rhodobacterales* has been observed in nematode-parasitized roots. Functional pathways associated with bacterial pathogenesis and biological nitrogen fixation, including increased abundance of the *nifH* gene and NifH protein, were also reported in parasitized plant (Li *et al*., 2023). In contrast to beneficial microbial interactions, plant pathogens can suppress host immune responses through effector-mediated mechanisms. Active neutralization strategies involve direct regulation of plant immune systems by inhibiting the production of defense substances or secreting inhibitory molecules. For example, the effector AVRblb2 from *Phytophthora infestans* and Avh240 from *Phytophthora sojae* target plant defense proteases such as PLCP C14 and aspartic protease AP1, preventing their secretion and activation and thereby weakening plant defense responses (Bozkurt *et al*., 2011).

PLANT GROWTH-PROMOTING BACTERIA AND MICROBIOMES ROLE IN SOIL FERTILITY

Enhancing soil fertility, plant development, and sustained agricultural productivity are all influenced by soil microbial communities, especially plant growth-promoting bacteria (PGPB). Soil bacteria are frequently isolated in microbiological investigations by suspending formed colonies in sterile saline solution for additional characterisation following incubation. Such investigations help in identifying beneficial microorganisms that can be used as biofertilizers for sustainable soil resource management. Indigenous multifunctional bio-inoculant microbes act as key components of plant growth–promoting microbiomes by mobilizing nutrients, enhancing microbial interactions, and improving soil fertility through fermentation-derived formulations that support sustained crop productivity (Table 3). Recent studies have emphasized the importance of PGPB in enhancing soil biological activity, crop productivity, and the nutritional quality of agricultural products. However, continued research in this field is necessary to provide farmers with reliable information on the biological functions and agricultural benefits of these microorganisms. To give farmers accurate knowledge on the biological roles and agricultural advantages of these microbes, more research in this area is required. In particular, it has been acknowledged that using phosphate-solubilising bacteria in conjunction with mineral or organic fertilisers is a successful integrated strategy for boosting soil fertility and increasing fertiliser use efficiency, improving phosphorus availability in soil (Table 4).

Table 3. Phosphate-solubilizing and phosphorus-mobilizing microorganisms: Mechanisms and impacts on soil fertility and crop productivity.

Category	Microorganisms	Mechanism of phosphorus availability	Agricultural significance	Reference
Phosphate-solubilizing bacteria (PSB)	*Bacillus*, *Pseudomonas*, *Rhizobium*, *Burkholderia*, *Achromobacter*, *Agrobacterium*, *Micrococcus*, *Acetobacter*, *Flavobacterium*, *Erwinia*	Production of organic acids, proton release, and chelation of inorganic phosphorus	Improve phosphorus availability and enhance plant growth	Kalayu, 2019; Alori *et al*., 2017
Phosphate-solubilizing fungi	Various soil fungi capable of solubilizing phosphate in vitro and in soil–plant systems	Organic acid production and mineral dissolution	Increase phosphorus availability and nutrient uptake	Bouizgarne, 2022
Bio-inoculant microorganisms	Indigenous multifunctional PGP microbes	Fermentation-based bio-inoculant production and nutrient mobilization	Improve soil fertility and crop productivity	Vassileva *et al*., 2022
Phosphorus-mobilizing microorganisms	Microbial P-mobilizers in soil	Transport of soluble phosphorus toward plant roots	Enhance nutrient accessibility in the rhizosphere	Nacoon *et al*., 2020
Mycorrhizal fungi (P-mobilizers)	Arbuscular mycorrhizal fungi	Symbiotic association and high-affinity phosphorus uptake mechanisms	Improve phosphorus absorption and plant growth	Parween *et al*., 2017
PSM effects on root morphology	PSM-associated microbes	Release of organic acids influencing root architecture	Increase root surface area, branching, and nutrient uptake efficiency	Fusconi, 2014
PSM contribution to nutrient cycles	PSM and diazotroph interactions	Improved phosphorus supply supporting biological nitrogen fixation	Enhance P-use efficiency and nitrogen fixation in legumes	Bargaz *et al*., 2018

Note: Phosphate-solubilizing microorganisms (PSM), including bacteria and fungi, play a central role in making soil phosphorus bioavailable through acidification, chelation, and mineral dissolution. Their effectiveness depends on microbial diversity, soil chemistry, and plant–microbe interactions. Integration of PSM with mycorrhizal fungi and diazotrophs can synergistically enhance both phosphorus and nitrogen nutrition, suggesting that microbial consortia, rather than single strains, may offer the most sustainable approach to improving crop productivity and soil fertility under diverse agricultural systems.

Table 4. Functional roles of zinc-mobilizing microbes in soil fertility and crop productivity.

Category	Microorganisms	Role in Agriculture	Mechanism of Zn Solubilization	Reference
Zinc-solubilizing bacteria (ZSB)	*Pseudomonas*, *Rhizobium*, *Bacillus*, *Azospirillum*, *Gluconacetobacter*, *Burkholderia*, *Serratia*, *Acinetobacter*, Cyanobacteria	Improve Zn availability and plant growth	Organic acid production, chelation, rhizosphere pH reduction	Mumtaz *et al.*, 2017
Zinc-solubilizing fungi (ZSF)	*Absidia*, *Penicillium*, *Paxillus*, *Hymenoscyphus*, *Oidiodendron*, *Suillus*, *Emericella*, *Beauveria*, *Trichoderma*	Enhance Zn uptake in plants	Dissolution of insoluble Zn compounds through microbial metabolites	Ladohia *et al.*, 2024
Rhizospheric Zn-solubilizing microbes	Various rhizosphere bacteria and fungi	Improve nutrient acquisition and crop nutrition	Chelation and mobilization of poorly mobile Zn in soil	Mumtaz *et al.*, 2017
Bacterial strains P29, P33, B40	Zn-solubilizing bacterial isolates	Improved maize biomass and micronutrient uptake	Zn solubilization from $ZnCO_3$ and ZnO	Goteti *et al.*, 2013
Wheat and sugarcane rhizosphere isolates	Zn-solubilizing microbial isolates	Enhanced wheat growth under pot conditions	Organic acid production and Zn mobilization	Kamran *et al.*, 2017

Note: Zinc-solubilizing microorganisms (ZSB and ZSF) play a crucial role in enhancing plant micronutrient uptake through organic acid production, chelation, and pH-mediated solubilization. While bacterial strains often act rapidly in the rhizosphere, fungal and mixed microbial communities can provide sustained Zn availability. Effectiveness is influenced by soil type, crop species, and environmental conditions, highlighting the importance of integrated microbial management strategies to optimize Zn nutrition and overall crop productivity.

In addition to microbial inoculation, plant traits and soil conditions can affect the composition and activity of rhizosphere microbial communities. Comparative studies of rhizosphere microbiomes across multiple plant species and environmental conditions have consistently demonstrated the strong influence of soil source on microbial community composition (Peiffer *et al*., 2013). In addition, plant characteristics collectively described as Microbiome Interactive Traits (MIT**)** such as root length, root biomass, root exudation patterns, and associated rhizosphere microbial communities play a key role in shaping plant microbiome interactions and regulating plant development (Zhao *et al*., 2024). Organic fertilization, which involves the application of plant- or animal-derived materials such as compost or manure, contributes organic matter to the soil and improves overall soil health (Lupatini *et al*., 2016; Krause *et al*., 2022; Su *et al*., 2022). According to reports, this technique improves the physicochemical characteristics of soil, increases microbial diversity, and increases soil enzyme activity. For example, organic cultivation has been associated with increased abundance of dominant bacterial groups such as *Proteobacteria* and *Acidobacteria*, as well as fungal groups including *Ascomycota* and *Basidiomycota* (Su *et al*., 2022).

FUNCTIONAL ROLES OF SOIL MICROBIOMES IN AGROECOSYSTEM PRODUCTIVITY

Soil microbial interactions are essential for sustaining and enhancing soil fertility as they regulate nutrient availability, decompose organic materials, and affect soil's physical and chemical characteristics. A recent review by Bhattacharyya & Furtak (2022) elucidates that soil microbes in the rhizosphere govern nutrient cycling processes, including nitrogen fixation, phosphorus mobilization, and carbon and nutrient mineralization, which directly affect the availability of soil nutrients to plants. The diversity of microorganisms, including bacteria and fungi, is crucial as it fosters functional redundancy and ecosystem multifunctionality. This allows multiple microbial species to concurrently perform processes such as decomposition, nutrient cycling, and pathogen suppression, collectively maintaining soil fertility (Chen *et al*., 2024). Beneficial microorganisms, including nitrogen-fixing bacteria (e.g., Rhizobium), mycorrhizal fungi, and phosphate-solubilizing microbes, augment plant nutrient absorption by transforming nutrients into bioavailable forms or by extending root access to phosphorus and water through symbiotic associations (Singh & Pathak, 2024). In addition to nutrient cycling, bacteria affect soil structure by creating soil aggregates and synthesizing organic molecules that adhere to soil particles, so enhancing aeration, water retention, and root penetration are essential factors for healthy soils. Additionally, individual microbial communities can influence soil responses to environmental factors such as micronutrient availability (e.g., manganese impacting phosphorus metabolic pathways) or seasonal fluctuations, linking microbial composition with soil fertility dynamics under different situations (Fatima *et al*., 2025).

FUTURE RESEARCH DIRECTIONS

Future studies on soil microbial interactions should concentrate on combining data from soil microbiomes with artificial intelligence and predictive models to enhance soil fertility assessment across various agricultural systems. Redundancy and resilience in microbial communities will help determine how soils maintain fertility under environmental stresses like drought or tillage (Iqbal *et al*., 2025). It's also crucial to comprehend how microbial populations react to climate change, including warming and modified precipitation, as these changes can have a significant impact on soil fertility and nutrient cycle. The engineering of customised microbial consortia to improve nutrient uptake, stress tolerance, and pathogen suppression is another crucial avenue that offers long-term substitutes for chemical fertilisers (Pandey & Saharan, 2025). The long-term ecological impacts of microbial bioformulations, such as their persistence and impact on native microbial communities over several cropping seasons, also require investigation (Pandey & Saharan, 2025). Furthermore, research should examine how complete microbial communities can be successfully included into fertility management and soil restoration, reducing disruption to already-existing soil ecosystems while increasing nutrient availability (Peddle *et al.*, 2025). High-resolution sequencing and multi-omics techniques can reveal unidentified microbial roles connected to soil fertility and nutrient cycling under various farming conditions (Xing *et al.*, 2025). Lastly, because microbial activity and nutrient cycling differ greatly with depth, studies should evaluate how agricultural management techniques affect microbial interactions across soil depths (Mo *et al.*, 2024). When taken as a whole, these paths will direct the creation of sustainable soil fertility management techniques that use microbial populations to boost agricultural productivity while lowering dependency on chemical inputs. Understanding how microbial communities respond to climate change, including warming and altered precipitation, is also critical, as these changes can strongly influence nutrient cycling and soil fertility Another important direction is the engineering of tailored microbial consortia to enhance nutrient uptake, stress tolerance, and pathogen suppression, providing sustainable alternatives to chemical fertilizers. Research is also needed to evaluate the long-term ecological effects of microbial bioformulations, including their persistence and influence on native microbial communities across multiple cropping seasons. In addition, studies should explore effective integration of whole microbial communities into soil restoration and fertility management, minimizing disturbance to existing soil ecosystems while enhancing nutrient availability.

Conclusion

In conclusion, a clearer understanding has been developed regarding how plant genotype, soil environment, and microbial communities together shape rhizosphere interactions. It is evident that the selection of rhizosphere microorganisms is not only influenced by plant genetics but is also strongly governed by the surrounding soil conditions and existing microbial populations. This highlights the importance of maintaining soil health as a foundation for establishing beneficial plant–microbe relationships. Furthermore, the careful selection of microbial strains adapted to specific environments can enhance plant resilience to stress, making it a promising approach in sustainable agriculture. However, the overall extent of rhizosphere influence remains a subject of ongoing discussion, particularly when considering the complexity of the plant holobiont and the role of extra-radical mycelium in arbuscular mycorrhizal associations. Future research integrating advanced tools such as genomics and metaomics will be essential to better understand these interactions. Such approaches can provide deeper insights into microbial functions, their contribution to biogeochemical cycles, and their role in ecosystem stability. Thus, by applying these emerging techniques, it becomes possible to further uncover the potential of soil microorganisms in improving plant productivity and supporting long-term ecosystem sustainability. Future research should focus on integrating multi-omics approaches, climate-responsive microbial studies, and engineered microbial consortia to optimize sustainable soil fertility management and agroecosystem productivity.

DECLARATIONS

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