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Soil Microbial Activity and Its Association with Pepper Productivity

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Abstract To investigate the relationship between soil microbial activity and chili pepper yield, this study conducted field experiments and employed a combination of microbiological and agronomic analytical methods to systematically evaluate the characteristics of soil microbial activity under various management practices, as well as their impact on chili pepper growth and yield. The results demonstrated that soil microbial abundance, community structure, and enzyme activity all exhibited a significant positive correlation with chili pepper yield. Microorganisms enhance soil nutrient availability by facilitating the decomposition of organic matter and the transformation of nutrients, thereby bolstering the growth vigor and fruit-bearing capacity of chili pepper plants. Furthermore, soil microbial activity indirectly contributes to yield formation by improving soil structure and water-retention capacity. The study also revealed that different cultivation management practices—such as the application of organic fertilizers and the addition of microbial inoculants—can significantly modulate levels of microbial activity, thereby influencing chili pepper yield performance. Case studies further validated the potential application of optimized microbial management strategies in enhancing both the yield and stability of chili pepper production. These findings provide a crucial theoretical basis and practical guidance for high-yield chili pepper cultivation and soil health management.

Keywords Soil microbial activity; Chili pepper yield; Soil enzyme activity; Nutrient transformation; Soil health

1 Introduction

Pepper (*Capsicum* spp.) is a globally important vegetable and spice crop, valued for its economic returns, nutritional quality, and contribution to diversified farming systems (Morales-Manzo et al., 2023). Rapid expansion of pepper cultivation—especially under protected or continuous-cropping conditions-has intensified problems of soil degradation, nutrient imbalance, and microflora dysbiosis, ultimately reducing yield and fruit quality (Di et al., 2025). At the same time, there is growing recognition that soil health, particularly the activity and composition of soil microorganisms, underpins sustainable productivity and resilience in intensive pepper systems (Das et al., 2022; Wang et al., 2024). Understanding how soil microbial activity relates to pepper growth and yield is therefore critical for designing input strategies that maintain high productivity while reducing dependence on synthetic fertilizers and mitigating environmental impacts (Wu et al., 2025).

Soil microorganisms are central drivers of agroecosystem functioning, mediating nutrient cycling, organic matter turnover, and disease suppression, and thus strongly influencing crop performance. Reviews and long-term syntheses show that bacteria, fungi, and archaea regulate key processes such as mineralization of organic N and P, solubilization of otherwise unavailable nutrients, and maintenance of soil structural stability, all of which feed back to plant growth and yield (Yadav et al., 2021). In the rhizosphere, these communities respond sensitively to management practices such as fertilization regime, organic amendments, and biofertilizer application, and can be harnessed through microbial inoculants or microbial fertilizers to enhance nutrient uptake, stress tolerance, and yield (Li et al., 2024). Yet, despite substantial progress in microbial ecology, the quantitative links between soil microbial activity and pepper productivity under realistic field and greenhouse management remain insufficiently characterized, especially for different fertilization strategies and soil types (Morales-Manzo et al., 2023).

Within agroecosystems, soil microbial activity represents a key interface between plant roots, soil resources, and management inputs. Plant growth-promoting rhizobacteria (PGPR), arbuscular mycorrhizal fungi, and synthetic or assembled microbial communities have been shown to enhance pepper growth, root vigor, nutrient acquisition, and fruit yield by modulating the rhizosphere microbiome and associated enzymatic processes (Sini et al., 2024;

Lalkhumliana et al., 2025). Microbial and humic amendments can increase microbial biomass carbon, improve soil porosity and nutrient availability, and stimulate enzymatic activities, thereby improving soil health indicators and pepper performance relative to mineral fertilizer alone (Wu et al., 2025). More broadly, conceptual and review work emphasizes that plant-soil-microbe interactions form a tripartite system in which root exudates, microbial metabolism, and soil physicochemical conditions co-determine nutrient availability, pathogen pressure, and plant vigor, highlighting microbial activity as a sensitive and integrative indicator of soil function in crop systems.

Pepper yield formation is controlled by a combination of genetic, physiological, soil, and management factors that together shape biomass accumulation, reproductive development, and fruit set. Agronomic studies demonstrate that fertilization level and timing, the balance between mineral and organic or bio-based inputs, and the structure of rhizosphere microbial communities significantly affect photosynthetic capacity, dry matter accumulation, and yield components such as fruit number and size (Wang et al., 2025). Interventions that improve soil structure, nutrient availability, and microbial community composition—such as biochar plus N fertilizer, microbial organic fertilizers, or seaweed-based biostimulants—have been shown to increase pepper yields by 20-40% or more, while simultaneously enhancing fruit quality traits like soluble sugars, vitamin C, and capsaicinoids (Zhang et al., 2025). Environmental drivers, including soil type, irrigation regime, and continuous-cropping intensity, further modify rhizosphere microbial biomass and activity, thereby indirectly shaping pepper productivity and its stability over time (Liu et al., 2020). Against this backdrop, systematically analyzing the association between soil microbial activity and pepper productivity can help identify microbial and soil indicators linked to high yield and quality, providing a basis for microbiome-informed fertilization and management strategies in pepper cultivation.

2 Theoretical Basis and Mechanisms of Action

2.1 Definition and evaluation indices of soil microbial activity

Soil microbial activity generally refers to the intensity of life processes of soil microorganisms, including growth, metabolism, and participation in soil biochemical cycles. It reflects how actively microbes transform organic matter and nutrients, and thus is central to soil biological fertility and ecosystem functioning (Bhattacharyya and Furtak, 2022; Thepbandit and Athinuwat, 2024). High microbial activity is usually associated with greater nutrient cycling rates, organic matter turnover, and resilience of the soil-plant system, while intensive, unsustainable farming can suppress activity and degrade soil quality (Meena and Rao, 2021).

Evaluation of soil microbial activity relies on biological and biochemical indicators that respond sensitively to management and environmental change. Common indices include microbial biomass carbon (MBC), basal and substrate-induced respiration, and key enzyme activities such as β-glucosidase, phosphatase, dehydrogenase and urease, which together indicate carbon turnover and nutrient cycling capacity. Ratios such as MBC/soil C and the metabolic quotient (qCO_2) are also used to infer efficiency and stress status of microbial communities, and have proven valuable as soil health indicators under contrasting land uses and management regimes (Meena and Rao, 2021).

2.2 Mechanisms of microbial involvement in nutrient cycling and soil fertility formation

Soil microorganisms drive the main biogeochemical cycles by transforming nutrients between organic and inorganic forms and regulating their availability to plants. In the rhizosphere, bacteria and fungi fix atmospheric nitrogen, decompose organic matter, mobilize or immobilize nutrients, and secrete phytohormones and osmoprotectants, thereby integrating C, N and P cycling with plant growth processes (Das et al., 2022). Metagenomic studies show that fertilization regimes alter the abundance of genes for N fixation, nitrification, denitrification and ammonium assimilation, with rhizosphere selection often exerting stronger control on overall N cycling than fertilization alone (Li et al., 2023).

Microbial communities also determine the efficiency of phosphorus and potassium use, underpinning soil fertility formation. Phosphate-solubilizing microorganisms and arbuscular mycorrhizal fungi secrete organic acids and phosphatases that release P from insoluble forms, while other functional groups mobilize K and contribute to biological soil crusts that stabilize C and nutrients (Bhattacharyya and Furtak, 2022; Pang et al., 2024). Long-term fertilization experiments reveal that organic and biofertilizers enhance genes involved in N degradation, dissimilatory nitrate reduction, and organic P mineralization, tightly coupling C, N and P cycles in ways that sustain nutrient stocks and improve soil fertility over time (Tang et al., 2023).

2.3 Pathways through which soil microorganisms influence crop yield

Microorganisms influence crop yield through direct nutritional effects, growth promotion, and protection from biotic and abiotic stresses. Plant growth-promoting rhizobacteria and related beneficial microbes fix N, solubilize P, produce siderophores to acquire Fe, and synthesize phytohormones such as auxins and cytokinins, which together enhance root development, nutrient uptake and biomass accumulation (Timofeeva et al., 2023). Rhizosphere microorganisms also suppress pathogens by producing antibiotics and lytic enzymes and by inducing systemic resistance, thereby improving plant health and yield potential under reduced chemical inputs (Hakim et al., 2021).

At the community and functional level, shifts in microbial networks and keystone taxa are closely linked to yield performance. Long-term fertilization trials show that specific bacterial and fungal families associated with N-cycling genes strongly contribute to crop yield, with rhizosphere selection shaping more yield-supportive N functional profiles than bulk soil (Li et al., 2023). Similarly, metagenomic analyses in perennial systems indicate that biofertilizer-enhanced Proteobacteria and Firmicutes carrying C, N and P cycling genes improve nutrient acquisition and support higher productivity, highlighting that managing microbial functional capacity is a key pathway to stabilize and increase crop yields (Du et al., 2023).

3 Materials and Methods

3.1 Overview of the experimental site and basic soil conditions

The field experiment was conducted in a continuous pepper (*Capsicum annuum* L.) production system located in a subtropical monsoon climate zone, characterized by warm temperatures and distinct wet and dry seasons, similar to pepper-growing regions in southwest and south-central China (Chen et al., 2024). Mean annual temperature and rainfall were approximately 14 °C-18 °C and 700-1,200 mm, respectively, providing favorable conditions for intensive vegetable cultivation under open-field management. The site had undergone several successive years of pepper cultivation, leading to typical continuous-cropping symptoms such as soil acidification, nutrient imbalance, and shifts in microbial communities associated with reduced yield and increased soil-borne disease risk (Mao and Jiang, 2021).

Prior to treatment application, composite soil samples (0-20 cm) were collected using an S-shaped five-point sampling method across each plot and homogenized to characterize baseline properties (Yongbin et al., 2025). Soils were air-dried, passed through a 2-mm sieve, and analyzed for pH (soil-water suspension), organic matter, total N, and available N, P, and K following standard chemical procedures comparable to those used in pepper intercropping and cover-crop studies (Gao et al., 2022). Initial soils were classified as loamy with slightly acidic to weakly acidic pH, moderate organic matter, and low to moderate available P and K, reflecting fertility constraints typical of intensively cropped pepper systems and providing a suitable background for testing fertilization and microbial regulation strategies (Mossie et al., 2024).

3.2 Experimental design and treatment settings

The experiment followed a randomized complete block design with three replicates, each plot planted with a commercial pepper cultivar at conventional spacing and management. Treatments were established to distinguish the effects of mineral fertilization, organic inputs, and microbial regulation on soil microbial activity and pepper productivity. A mineral-fertilizer control received locally recommended NPK rates, while integrated treatments combined NPK with microbial organic fertilizer containing plant growth-promoting rhizobacteria, and/or microbial inoculants (PGPR consortia, arbuscular mycorrhizal fungi) similar to those tested in bell pepper and continuous-cropping systems (Sini et al., 2024).

Additional treatments targeted soil chemical constraints and microecological regulation. Quicklime was applied alone or in combination with microbial organic fertilizer and inoculant in selected plots to adjust soil pH and indirectly influence microbial communities, following ranges comparable to 1,500-4,500 kg/ha used in continuous pepper systems (Zhang et al., 2024). In separate sub-treatments, biofertilizer or PGPR mixtures were applied as seedling root dips or soil drenches at transplanting, with or without organic fertilizer, to assess their capacity to modify rhizosphere microbiology and enhance yield as observed in greenhouse bell pepper and field biofertilizer-compost combinations (Sini et al., 2024). All plots received uniform irrigation, weed, and pest management to minimize confounding effects and to isolate responses to fertilization and microbial regulation (Figure 1).

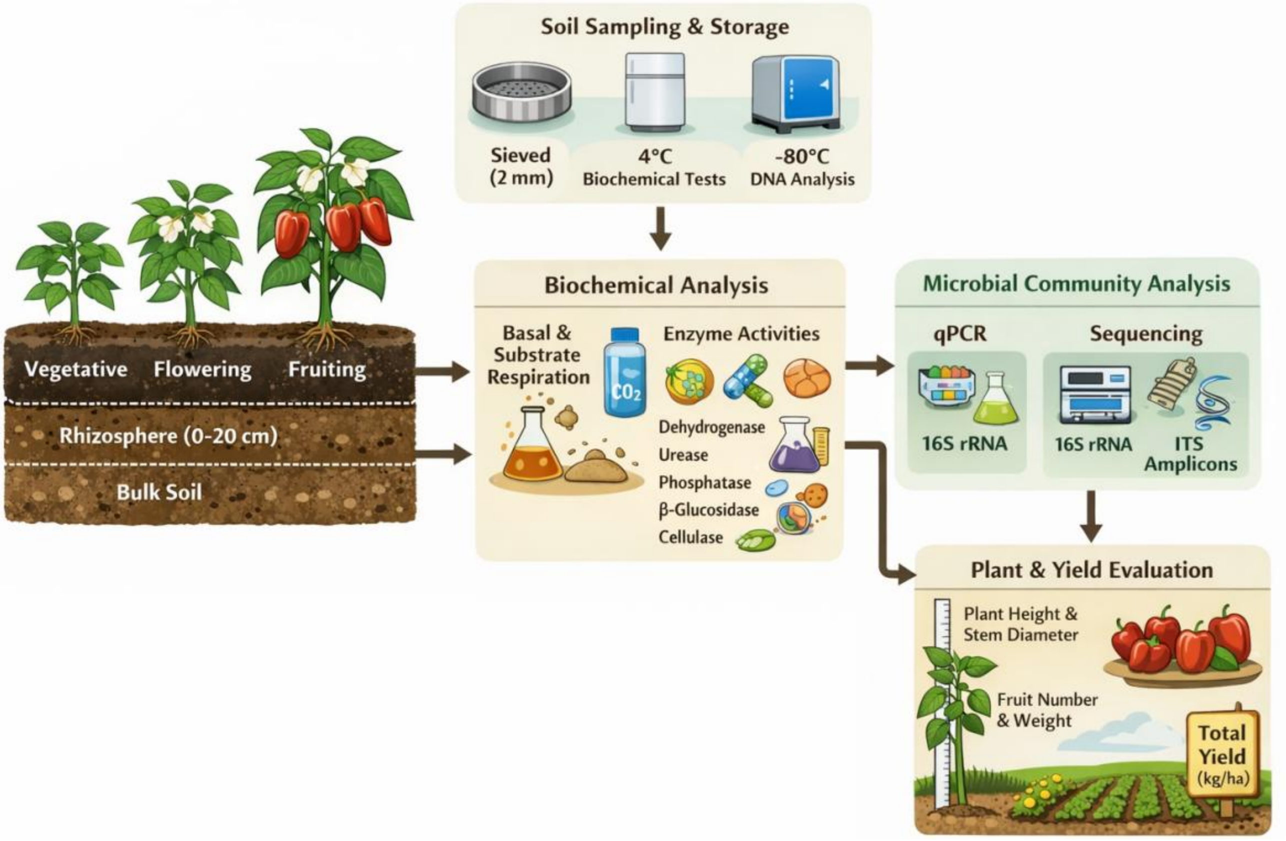

Figure 1 Schematic diagram of the framework for assessing soil microbial activity in pepper cultivation systems

3.3 Measurement methods for microbial activity and yield indices

Soil microbial activity was assessed using a combination of biochemical and molecular indicators. At key pepper growth stages (vegetative, flowering, fruiting), fresh soil samples were collected from the 0-20 cm rhizosphere and bulk zones, sieved (2 mm), and stored at 4 °C for short-term biochemical analyses or at -80 °C for DNA-based assays, following protocols used in pepper-maize intercropping and cover-crop experiments (Gao et al., 2022). Microbial biomass and activity were characterized by basal respiration and substrate-induced respiration, and by determining extracellular enzyme activities (e.g., dehydrogenase, urease, phosphatase, β-glucosidase, and cellulase) using colorimetric assays similar to those applied in red pepper fields treated with microbial agents and in multi-system microbial monitoring studies.

To complement functional indicators, microbial abundance and community profiles were obtained where relevant. Quantitative PCR targeting bacterial 16S rRNA genes and fungal ITS regions was used to estimate microbial gene copy numbers, while high-throughput sequencing of 16S rRNA and ITS amplicons characterized community composition and diversity in selected treatments, using workflows analogous to those employed in continuous-cropping and intercropping pepper systems (Chen et al., 2024). Pepper productivity was evaluated by measuring plant height, stem diameter, fruit number per plant, average fruit weight, and total yield per hectare at harvest, following standard agronomic procedures. Yield and quality responses to compost-based fertilization and microbial activity were interpreted using approaches similar to those that linked microbial biochemical function and enzyme activity ratios to bell pepper yield in urban and field systems (Zeiner et al., 2024).

4 Analysis of Soil Microbial Activity Characteristics

4.1 Changes in microbial abundance and community structure

Across treatments, microbial abundance in pepper rhizosphere soil responded strongly to management practices that altered nutrient supply and the soil microenvironment. In continuous pepper systems, the application of Trichoderma hamatum MHT1134 significantly increased overall microbial abundance compared with long-term monocropped controls, reversing the decline in total bacteria and fungi observed with increasing years of continuous cropping (Mao and Jiang, 2021). Similarly, adding microbial organic fertilizer, microbial inoculant, and quicklime in continuous pepper fields enhanced bacterial richness and co-occurrence network complexity relative to untreated soil, indicating a shift toward more functionally connected communities that support improved soil fertility and yield (Zhang et al., 2024).

Community composition at phylum and genus level also shifted under different biological and chemical inputs. In long-term continuous pepper fields, the relative abundance of pathogenic genera such as Fusarium and Gibberella increased, while beneficial taxa including Trichoderma and Chaetomium declined; introduction of MHT1134 reversed these trends, increasing beneficial fungi and restoring a more balanced community structure (Mao and Jiang, 2021). In pepper systems preceded by cover crops, bacterial abundance and community structure were significantly modified, with particular mixtures (e.g., wheat with legumes) enriching plant growth-promoting and pathogen-antagonistic genera such as Pseudomonas and Bacillus, alongside changes in pH and nutrient availability that further shaped rhizosphere assemblages (Chen et al., 2024).

4.2 Analysis of soil enzyme activity indices

Soil enzyme activities provided sensitive indicators of how fertilization and microbial regulation affected biological functioning in pepper fields. In red pepper receiving hairy vetch plus mineral N or livestock compost, dehydrogenase activity increased relative to sole chemical fertilizer or unfertilized control, reflecting stimulation of overall microbial oxidative metabolism, whereas urease activity was highest under chemical fertilizer, and β-glucosidase and phosphatase showed smaller treatment differences. In another red pepper field, application of a microbial consortium agent markedly enhanced dehydrogenase, urease, phosphatase, β-glucosidase, and cellulase activities, demonstrating that inoculated PGPR mixtures can substantially elevate multiple enzyme systems associated with C, N, and P cycling.

Biocontrol and remediation measures in continuous pepper systems further confirmed the tight linkage between enzyme activities and soil quality. In fields treated with Trichoderma hamatum MHT1134, activities of urease, dehydrogenase, acid phosphatase, catalase, sucrase (invertase), and acid protease were consistently higher than in untreated continuous-cropping soils, and redundancy analysis indicated that these enzymes, together with total N, available P, available K, and organic matter, strongly structured both bacterial and fungal communities (Mao and Jiang, 2021). More broadly, comparative studies emphasize that hydrolases such as β-glucosidase, phosphatase, and urease are robust soil quality indicators because they are operationally practical, highly sensitive to management, and tightly coupled to organic matter turnover and nutrient release for plant uptake (Figure 2) (Attademo et al., 2021).

4.3 Microbial diversity and functional group characteristics

Microbial diversity patterns in pepper fields were shaped by both cropping history and management inputs. Continuous cropping alone tended to reduce microbial abundance and diversity over time, with long-term monoculture favoring pathogenic fungi and narrowing community evenness, which is associated with soil sickness and declining yield (Chen et al., 2022). Interventions such as microbial organic fertilizer, inoculants, and quicklime increased bacterial diversity and fungal network complexity, while Mantel tests identified soil available nitrogen and bacterial diversity as key regulators of pepper growth and yield, underscoring the functional importance of maintaining diverse, well-structured communities (Romero et al., 2023).

Functional group analyses highlighted shifts between beneficial and deleterious taxa under contrasting management. In continuous pepper systems, Trichoderma and Chaetomium expanded following MHT1134 application, whereas Fusarium and Gibberella declined, indicating a transition from pathogen-dominated to biocontrol-enriched fungal assemblages with improved soil quality and disease suppression (Mao and Jiang, 2021). In cover-crop-pepper rotations, bacterial genera with documented plant-growth-promoting or pathogen-antagonistic traits (e.g., Pseudomonas, Bacillus) became more abundant in treatments involving wheat and legume mixtures, coinciding with higher pepper yields and altered soil pH, which emerged as a dominant driver of bacterial diversity and composition (Gao et al., 2022).

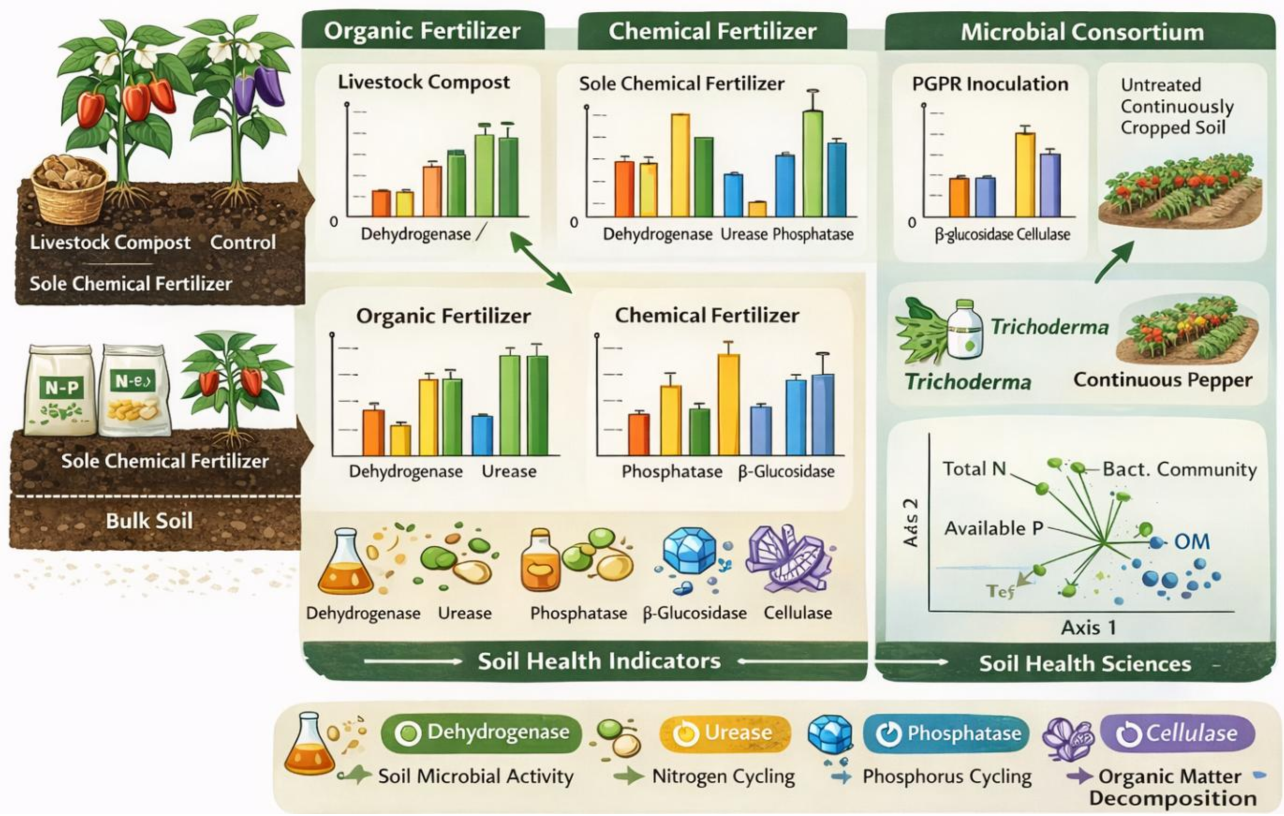

Figure 2 Soil enzyme activities and biological functioning in pepper fields

5 Impact of Soil Microbial Activity on Pepper Growth and Yield

5.1 Effects on pepper growth indices (plant height, leaf area, etc.)

Enhanced soil microbial activity is closely associated with improvements in pepper vegetative growth, including plant height, stem diameter, leaf area, and biomass accumulation. Application of effective microorganisms (EM) in continuous-cropping pepper increased plant height, stem diameter, leaf length, leaf width, and root length by 15%-35%, in parallel with higher soil enzyme activities and nutrient availability, indicating that biologically active soils support more vigorous canopy and root development (Liu et al., 2024). Similarly, integrating plant growth-promoting rhizobacteria (PGPR) with humic acid significantly increased plant height, branch number, and root length in pepper, and these gains coincided with higher microbial biomass carbon and available N, P and K, underscoring a functional link between microbial activity, soil fertility, and vegetative growth (Lalkhumliana et al., 2025).

Interventions that restructure the rhizosphere microbiome further demonstrate the growth-promoting potential of active microbial communities. Inoculation with a synthetic microbial community at the seedling stage increased shoot height, stem diameter, chlorophyll content, leaf number, root vigor, and total root length of pepper by roughly 20%-120%, while also increasing the Chao index of rhizosphere microbes and the abundance of key beneficial taxa positively correlated with growth indices (You et al., 2025). Biofertilizer treatments combining arbuscular mycorrhizal fungi (AMF) and PGPR similarly enhanced plant height, leaf number, and leaf area of poblano pepper, with co-inoculation increasing leaf area and dry biomass by more than 60% and improving gas-exchange traits, illustrating that microbially mediated improvements in resource acquisition and photosynthesis translate directly into superior vegetative growth (González-Mancilla et al., 2024).

5.2 Effects on yield components (number of fruits per plant, single fruit weight, etc.)

Higher soil microbial activity often manifests as favorable changes in yield components such as fruit number per plant, fruit size, and single fruit weight. In continuous-cropped pepper, combined application of microbial organic fertilizer, microbial inoculant, and quicklime significantly increased fruit diameter and length, with the optimal combination raising yield by about 30% over the control and highlighting the role of nutrient-enriched, microbially active soils in supporting larger fruits (Zhang et al., 2024). EM application in Xinjiang pepper systems increased fruit width and single fruit weight by roughly 5% and 43%, respectively, while simultaneously elevating soil nutrient contents and enzyme activities, suggesting that microbially stimulated nutrient cycling enhances assimilate supply to developing fruits (Liu et al., 2024).

Microbial inoculants also modulate fruit set and per-plant yield through improved root function and nutrient uptake. In bell pepper, AM fungi and PGPR applied with moderate P fertilization increased early fruit formation, number of fruits per plant, fruit size, and individual fruit weight, particularly when a mixed inoculum of two AM species plus Pseudomonas fluorescens was used (Tanwar et al., 2021). Similarly, co-inoculation of AMF and PGPR in poblano pepper increased the number of flowers and dry biomass, while a broader microbial consortium in capsicum under protected cultivation raised the number of fruits per plant and single fruit weight, indicating that diversified, functionally active microbial consortia can enhance both reproductive initiation and fruit growth (González-Mancilla et al., 2024).

5.3 Effects on final yield and yield stability

At the whole-crop level, management practices that boost soil microbial activity and improve microbial community structure generally increase final pepper yield and can contribute to yield stability. In continuous pepper monoculture, the combined use of microbial organic fertilizer, inoculant, and quicklime produced the highest yield, nearly 30% above the untreated control, with Mantel analysis identifying soil available N and bacterial diversity as key regulators of yield, thereby directly linking microbial-driven nutrient dynamics and community traits to productivity (Zhang et al., 2024). EM-based management in Xinjiang increased total yield by about 75% relative to the control, alongside higher soil nutrient levels and enzyme activities and reduced pathogenic fungi, indicating that active, functionally diverse microbial communities support both high yield and healthier cropping environments (Liu et al., 2024).

Other microbial strategies confirm the yield benefits and hint at enhanced sustainability. Integration of PGPR and humic acid with recommended fertilization produced the highest pepper yields and improved fruit length and diameter, coinciding with maximum microbial biomass carbon and available macronutrients, suggesting that microbially mediated improvements in soil health underpin production gains (Lalkhumliana et al., 2025). Similarly, combining PGPR-based biofertilizer with agricultural-waste compost in pepper fields significantly increased yield and fruit quality while enhancing soil organic matter and available NPK after one season, and improved disease control, illustrating that systems with high microbial activity not only raise yields but also better maintain soil fertility and resilience over time.

6 Synergistic Interactions between Soil Microorganisms and Soil Physicochemical Properties

6.1 Relationship between microbial activity and soil nutrient availability

Microbial activity in the rhizosphere is tightly linked to the availability of key nutrients such as nitrogen (N) and phosphorus (P). Rhizosphere microorganisms fix atmospheric N, decompose organic matter, and mediate nitrification, denitrification, and mineralization, thereby converting unavailable forms into plant-available pools and directly supporting crop growth (Richardson et al., 2009; Bhattacharyya and Furtak, 2022). Global syntheses show that rhizosphere processes increase available N and P and enhance microbial biomass N and P and related enzymes, with effects strongly mediated by pH, fertilizer rate, and microbial biomass, underscoring how biological activity and soil chemistry co-regulate nutrient supply in agroecosystems (Cai et al., 2022).

Management practices that sustain microbial diversity and activity can regenerate soil biological fertility and improve nutrient cycling. Reviews highlight that plant growth-promoting rhizobacteria and arbuscular mycorrhizal fungi enhance macronutrient cycling, while root exudates shape microbial communities and nutrient mobility in the rhizosphere (Thepbandit and Athinuwat, 2024). Conversely, intensive, unsustainable farming reduces microbial biodiversity and disrupts C, N, and P cycling, leading to impaired nutrient availability and reduced capacity of soils to support productive, resilient cropping systems (Bhattacharyya and Furtak, 2022; Das et al., 2022).

6.2 Regulatory role of microorganisms in soil structure and water status

Soil microorganisms strongly influence aggregate formation and stability by producing polysaccharides, glomalin, and other binding agents that cement particles into water-stable aggregates. During vegetation restoration in degraded granitic red soils, increases in bacterial and archaeal abundance and diversity were positively correlated with mean weight diameter, geometric mean diameter, and the proportion of water-stable aggregates, with Actinobacteriota contributing most to aggregate stability and associated nutrient accumulation (Liu et al., 2024). Classic work further shows that transient (polysaccharides), temporary (roots, fungal hyphae), and persistent organic binding agents, largely microbially derived or mediated, control macro- and microaggregation and, in turn, soil physical structure.

Improved aggregation and organic matter input from roots and microbes modify rhizosphere hydraulic properties, affecting water retention and movement. In annual ryegrass, higher microbial biomass, β-glucosidase, dehydrogenase, and glomalin concentrations in the rhizosphere were associated with greater soil organic carbon, lower readily dispersible clay, higher porosity, and enhanced water retention across matric potentials compared with bulk soil (Batista et al., 2024). Broader reviews confirm that by enhancing aggregate stability, porosity, and organic matter decomposition, microorganisms improve water infiltration and retention and buffer plants against hydric and edaphic stresses in agricultural soils (Das et al., 2025).

6.3 Coupling effects within the microorganism-soil-crop system

The microorganism-soil-crop system operates as a coupled network in which roots, microbes, and soil physicochemical properties co-determine nutrient cycling and plant performance. Rhizosphere zones, enriched with root exudates, create favorable habitats for diverse microbial communities that fix N, solubilize P and K, produce phytohormones, and form biological soil crusts, thereby enhancing nutrient mobility, soil protection, and crop resilience (Bhattacharyya and Furtak, 2022; Thepbandit and Athinuwat, 2024). Meta-analyses show that rhizosphere effects on N and P cycling are particularly strong in vegetable systems, where elevated microbial biomass and enzyme activities translate into higher available N and P, directly linking microbial processes to intensive crop production (Cai et al., 2022).

Plant traits and management also feed back to regulate microbial activity and nutrient flows. Experiments with species differing in resource-use strategies demonstrate that plants with higher photosynthesis and rhizodeposition accelerate soil N cycling via rhizosphere priming, increasing N uptake and supporting faster growth, while legumes enhance this feedback through N fixation (Henneron et al., 2020). Reviews emphasize that such plant-soil-microbe feedbacks, mediated by root exudates, microbial functional groups, and soil physical and chemical conditions, are central to soil biological fertility and should be harnessed through microbial inoculants and regenerative practices to improve crop productivity and sustainability (Bhattacharyya and Furtak, 2022; Das et al., 2022).

7 Case Study: Analysis of the Relationship between Soil Microbial Activity and Pepper Yield under Typical Planting Patterns

7.1 Planting patterns and management practices in the case study area

The case study focuses on typical intensive pepper systems where continuous monocropping has led to soil degradation, nutrient imbalance, and microflora dysbiosis, prompting the adoption of soil-improvement strategies. In one representative continuous-cropping system, 13 treatments combined different rates of microbial organic fertilizer, microbial inoculant, and quicklime to counteract acidification and restore soil function, all under locally conventional fertilization and irrigation regimes (Zhang et al., 2024).

In contrast, diversified planting patterns such as pepper-peanut and pepper-maize intercropping have been developed to alleviate continuous-cropping obstacles while maintaining high land-use efficiency (Wang et al., 2025). These systems use alternating pepper and companion rows with similar basal fertilization to monoculture, but rely more on biological regulation via root interactions, altered nutrient dynamics, and modified rhizosphere microecology to sustain productivity (Gao et al., 2022).

7.2 Comparison of microbial activity changes and yield data

Under continuous pepper with microbial amendments, combined application of microbial organic fertilizer, inoculant, and quicklime markedly increased soil available N, P, K, raised pH, and produced the most complex bacterial and fungal co-occurrence networks, indicating higher microbial activity and functional connectivity (Zhang et al., 2024). This treatment also delivered the highest yield, with pepper production increasing by about 30% compared with the untreated control, demonstrating a direct agronomic benefit of enhanced microbial functioning in a monoculture context (Figure 3) (Zhang et al., 2024).

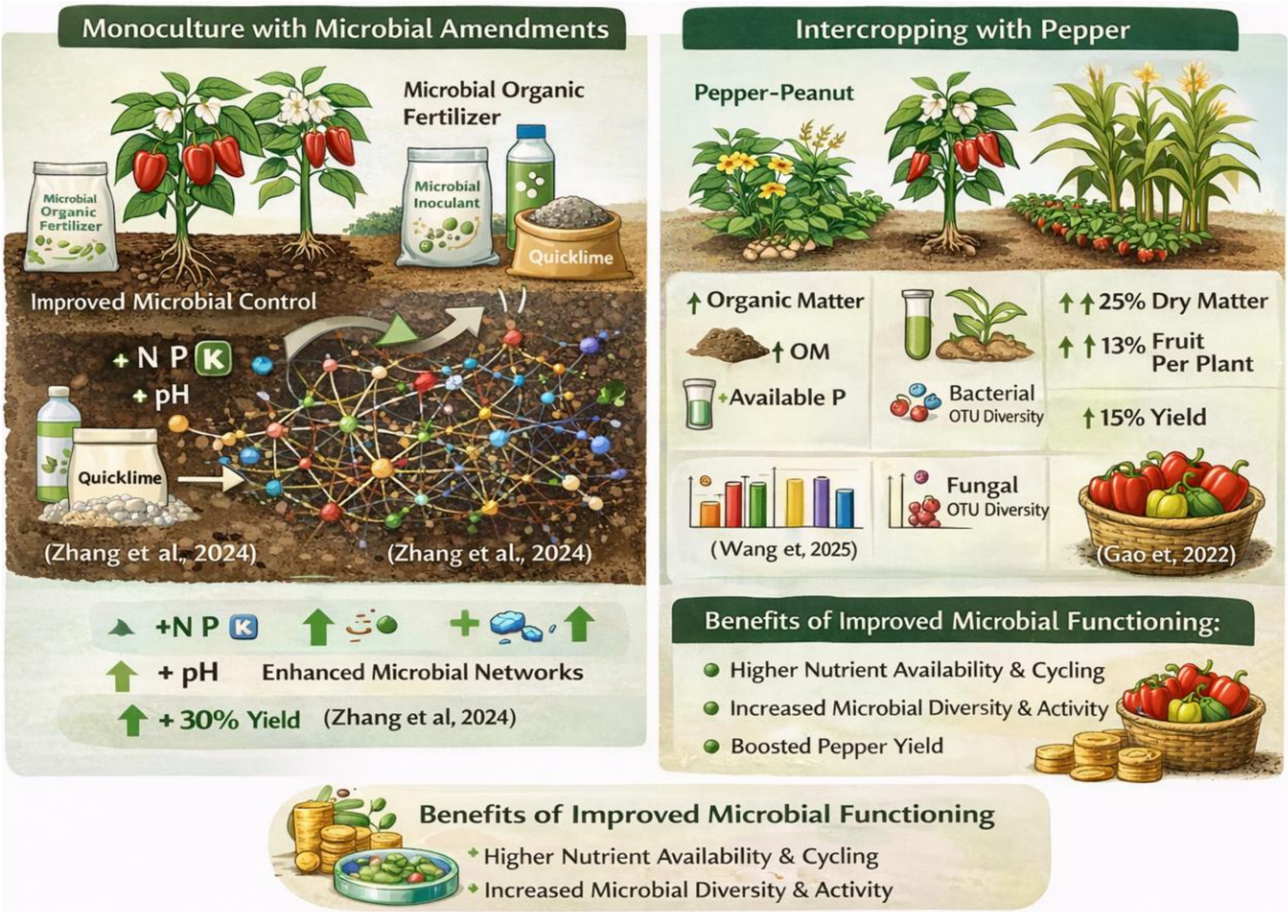

Figure 3 Soil microbial improvements and pepper productivity in monoculture and intercropping systems

In intercropping systems, pepper-peanut significantly increased pepper dry-matter accumulation by up to ~25%, fruit number per plant by ~10%-13%, and yield by 9%-15%, while raising soil organic matter, available P, urease and sucrase activities, and microbial OTU richness and diversity indices (Wang et al., 2025). Similarly, pepper-maize intercropping increased bacterial and fungal diversity, enriched beneficial taxa (e.g., Sphingomonadales, Nitrospira) and secondary metabolites, and elevated available P and K in rhizosphere soils, supporting improved nutrient cycling and a more active microbiome associated with higher yield (Gao et al., 2022).

7.3 Evaluation of microbial regulation strategies for enhancing yield

The continuous-cropping case shows that targeted microbial regulation through amendments is effective when treatment combinations are optimized. The best-performing mixture of microbial organic fertilizer, inoculant, and quicklime simultaneously improved nutrient availability, shifted bacterial communities toward higher diversity and network complexity, and maximized yield, with Mantel tests identifying soil available N and bacterial diversity as key drivers of pepper productivity. This indicates that managing both the chemical environment (pH, nutrients) and microbial community structure is essential for restoring yield in degraded monoculture soils (Zhang et al., 2024).

Diversified planting patterns act as in situ microbial regulation strategies by reshaping root-soil-microbe interactions without heavy external inputs. Pepper-peanut intercropping enhanced photosynthesis, increased beneficial Proteobacteria and Chytridiomycota, and formed a more stable microbial network, while pepper-maize intercropping enriched beneficial bacteria and rhizosphere metabolites that correlate with nutrient availability, together providing a biologically based route to higher and more sustainable yields (Wang et al., 2025). These case results suggest that combining microbial amendments in continuous systems with intercropping-based microbiome management offers a robust pathway to enhance pepper yield and resilience.

8 Conclusions and Outlook

Across pepper systems, soil microbial activity emerged as a central driver of plant growth, nutrient acquisition, and yield formation. Manipulating rhizosphere communities with synthetic microbial communities (SynComs), microbial organic fertilizers, and combined amendments consistently enhanced vegetative growth, root morphology, and yield by enriching beneficial taxa and functional pathways related to nutrient cycling and phytohormone synthesis. In continuous-cropping and greenhouse conditions, treatments that increased microbial diversity and network complexity also improved soil nutrient availability and reduced constraints associated with degraded soils, demonstrating that biologically active soils are foundational to pepper productivity.

These effects operate through coordinated changes in soil chemistry, biology, and plant traits. Co-application of organic materials (straw, biochar, insect residual streams) and microbiome-targeted measures increased microbial biomass, shifted community structure toward beneficial groups, boosted enzyme activities, and improved soil physical properties, together explaining large yield gains in continuous cropping systems 54. At the same time, evidence that some commercial inoculants do not improve pepper growth or yield under field conditions highlights that microbiome interventions must be context-specific and supported by clear links between microbial responses, soil health, and plant performance.

Findings support prioritizing strategies that both supply substrates and directly engineer rhizosphere communities. Sustained or stage-specific SynCom inoculation, particularly when applied at seedling and early vegetative stages, markedly increases biomass, root activity, fruit quality, and yield while restructuring microbial networks and enriching nutrient-cycling and hormone-related functions, suggesting that continuous or well-timed applications are more effective than single inoculations. In continuous cropping, combined use of microbial organic fertilizer, inoculant, and pH-ameliorating amendments improves nutrient availability and microbial network complexity, yielding the largest gains in pepper yield and soil restoration.

Microbial regulation should be integrated with broader soil-management practices. Co-application of straw and biochar, or use of insect residual streams, simultaneously improves soil fertility, enzyme activities, and microbial diversity, while enriching beneficial bacteria and suppressing pathogens, leading to dramatic yield increases and better plant physiological status. Intercropping and optimized organic inputs can further enrich functional microbiota and favorable metabolites in the pepper rhizosphere, providing a systems-level route to enhance nutrient use efficiency and resilience with reduced dependence on high synthetic fertilizer inputs.

Future work should move from single-factor trials toward mechanistic, multi-scale understanding and design of microbiome-based interventions. Priority areas include defining core rhizosphere microbiomes of pepper across environments, elucidating rules of SynCom assembly and persistence, and linking specific microbial taxa, genes, and metabolites to nutrient fluxes and plant traits under realistic field variability. Integrating omics, metabolomics, and network analyses will be essential to unravel how management, soil type, and pepper genotype jointly shape microbiome function and to refine predictive models of microorganism-soil-crop coupling.

From an application perspective, there is strong potential to develop climate-resilient, microbiome-informed pepper production systems. Microbiome engineering and targeted SynComs could be combined with organic amendments, diversified cropping, and precision management to buffer peppers against drought, heat, and disease while maintaining high yields and reducing chemical inputs. Realizing this potential will require long-term, on-farm validation of microbial products, improved formulation and delivery to ensure colonization, and close collaboration among researchers, industry, and growers to translate microbiome knowledge into robust, economically viable technologies for sustainable pepper cultivation.

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Conflict of Interest Disclosure

The author affirms that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

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