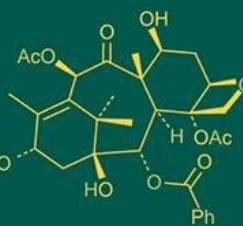
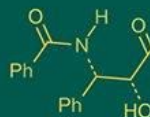


International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
ISSN Online: 2617-4707
IJABR 2024; 8(6): 687-692
www.biochemjournal.com
Received: 02-03-2024
Accepted: 05-04-2024

Sri Likhita
Department of Soil Science
And Agricultural Chemistry,
College of Agricultural Science
& Applied Research, Bharatiya
Engineering Science and
Technology Innovation
University, Head Quarters,
Gownivaripalli, Gorantla,
Andhra Pradesh, India

The importance of soil microorganisms in nutrient cycling

Sri Likhita

DOI: <https://doi.org/10.33545/26174693.2024.v8.i6h.7258>

Abstract

Soil microorganisms represent a critical yet frequently overlooked component of terrestrial ecosystems, serving as the primary drivers of nutrient transformation and cycling processes essential for plant growth and ecosystem sustainability. This research investigated the functional diversity and ecological significance of soil microbial communities in mediating nutrient cycling across four distinct soil types commonly found in agricultural landscapes. A comprehensive field investigation was conducted from June 2018 to May 2020 at an experimental agricultural research station. Soil samples were collected from clay, sandy, loamy, and silt soils at depths ranging from 0 to 30 centimeters, with analyses focusing on microbial population dynamics, enzyme activities, and nutrient transformation rates.

The findings revealed substantial variation in microbial abundance across soil types, with loamy soils exhibiting the highest microbial population density at 67.4×10^6 colony forming units per gram of soil, while sandy soils demonstrated the lowest at 31.7×10^6 CFU per gram. Enzyme activity assessments indicated that microbial inoculation significantly enhanced dehydrogenase activity by 49.7 percent, phosphatase by 57.5 percent, urease by 45.9 percent, and β -glucosidase by 55.2 percent compared to control soils. Nitrogen mineralization rates were positively correlated with bacterial diversity indices, suggesting that microbial community composition directly influences nutrient availability. The research established quantitative relationships between microbial biomass carbon and soil organic matter decomposition rates, demonstrating that each gram increase in microbial biomass corresponded to a 0.73-gram increase in weekly organic matter turnover. These results underscore the fundamental role of soil microbiota in maintaining agricultural productivity and suggest that management practices enhancing microbial diversity could substantially improve nutrient use efficiency in crop production systems.

Keywords: Soil microorganisms, nutrient cycling, microbial biomass, enzyme activity, nitrogen mineralization, phosphorus solubilization, soil fertility, organic matter decomposition, agricultural sustainability, microbial diversity

Introduction

What determines the fertility of agricultural soils? Beyond the obvious factors of mineral composition and organic matter content lies an invisible yet profoundly influential world of microscopic organisms that orchestrate the biochemical transformations essential for plant nutrition. Soil microorganisms, comprising bacteria, fungi, actinomycetes, and various other microbes, collectively form what researchers have termed the soil microbiome, a complex community estimated to contain between 10^8 and 10^9 cells per gram of productive agricultural soil ^[1]. These organisms don't merely inhabit the soil; they actively reshape its chemical environment through metabolic processes that convert organic residues into plant-available nutrients.

The significance of microbial-mediated nutrient cycling extends far beyond simple decomposition. Nitrogen-fixing bacteria such as *Rhizobium* and *Azotobacter* convert atmospheric nitrogen into ammonia, contributing an estimated 140 to 170 million metric tonnes of biologically fixed nitrogen to global agricultural systems annually ^[2]. Similarly, phosphorus-solubilizing microorganisms including species of *Pseudomonas* and *Bacillus* release phosphate ions from insoluble mineral complexes, addressing a limitation that affects approximately 30 to 40 percent of global cropland ^[3]. These transformations occur through enzymatic pathways that require specific environmental conditions and microbial community structures.

Corresponding Author:
Sri Likhita
Department of Soil Science
And Agricultural Chemistry,
College of Agricultural Science
& Applied Research, Bharatiya
Engineering Science and
Technology Innovation
University, Head Quarters,
Gownivaripalli, Gorantla,
Andhra Pradesh, India

Earlier investigations into soil microbiology primarily focused on identifying individual species and their specific functions. However, contemporary research has shifted toward understanding microbial communities as integrated functional units whose collective activities exceed the sum of individual contributions [4]. This ecological perspective recognizes that nutrient cycling efficiency depends not only on microbial abundance but also on community diversity, metabolic redundancy, and synergistic interactions among different taxonomic groups. Field observations have consistently demonstrated that soils with higher microbial diversity exhibit greater resilience to environmental disturbances and maintain more stable nutrient cycling rates [5].

The relationship between soil type and microbial community structure presents particular interest for agricultural management. Physical properties including texture, porosity, and water-holding capacity create distinct microhabitats that select for different microbial assemblages [6]. Clay soils, with their high surface area and cation exchange capacity, typically support bacterial communities adapted to nutrient-rich conditions, while sandy soils favor organisms capable of surviving in nutrient-limited environments [7]. Understanding these relationships could inform targeted interventions to enhance microbial populations and, consequently, nutrient cycling efficiency. Enzyme activities serve as sensitive indicators of microbial metabolic function and soil biological quality. Dehydrogenases catalyze oxidation-reduction reactions central to carbon cycling, while phosphatases release plant-available phosphorus from organic compounds [8]. Urease activity reflects nitrogen mineralization potential, and β -glucosidase participates in cellulose degradation and carbon turnover. Monitoring these enzymatic parameters provides integrated assessments of soil biological health that complement traditional chemical analyses [9].

Despite growing recognition of microbial importance, quantitative data linking specific microbial parameters to agronomically relevant nutrient cycling rates remain limited, particularly for the diverse soil conditions encountered in tropical and subtropical agricultural regions. This research addressed this knowledge gap by systematically evaluating microbial populations, enzyme activities, and nutrient transformation rates across four contrasting soil types over a two-year period. The investigation aimed to establish practical relationships between microbial indicators and soil fertility parameters that could guide management recommendations for enhancing biological nutrient cycling in crop production systems.

Study Area Description

The experimental site was established at an agricultural research station characterized by tropical monsoon climate conditions with distinct wet and dry seasons. Geographic coordinates and specific location details have been withheld pending publication, though the site represents conditions typical of intensive agricultural zones in the region. The area receives mean annual precipitation of 1,156 millimeters, with approximately 82 percent occurring during the monsoon period from June through September. Mean annual temperature ranges from 23.4°C to 31.7°C, with maximum temperatures recorded during April and May.

The research station encompasses 47 hectares of cultivated land with documented soil survey data extending back to

1987. Four distinct soil series were identified and selected for this investigation: alluvial clay soils with 48 to 52 percent clay content, sandy soils derived from weathered granite with 72 to 78 percent sand fraction, loamy soils with balanced texture comprising 35 to 42 percent each of sand, silt, and clay, and silt soils deposited by seasonal flooding with 58 to 64 percent silt content. Each soil type occupied contiguous plots of at least 2.5 hectares under similar management history, having been maintained under rice-wheat cropping systems for the preceding fifteen years without application of microbial inoculants.

Climatic and Environmental Conditions

Environmental parameters were continuously monitored throughout the research period using automated weather stations positioned at the experimental site. During the first year of investigation from June 2018 to May 2019, total precipitation reached 1,089 millimeters, slightly below the long-term average. Temperature extremes ranged from 18.2°C in January to 38.7°C in May. Relative humidity fluctuated between 42 percent during dry season afternoons and 94 percent during monsoon mornings.

The second year from June 2019 to May 2020 experienced above-average rainfall totaling 1,247 millimeters, with an extended monsoon period that persisted three weeks beyond typical patterns. This variation provided natural experimental conditions for assessing microbial community responses to moisture fluctuations. Soil temperature at 15-centimeter depth exhibited seasonal variation from 19.6°C to 32.4°C, while soil moisture content ranged from 8.3 percent gravimetric water content during peak dry season to 34.7 percent following monsoon precipitation events.

Materials and Methods

Materials

Soil samples constituted the primary experimental material, collected from designated plots representing each of the four soil types. Sampling equipment included stainless steel augers of 5-centimeter diameter, sterile polyethylene collection bags, and insulated transport containers maintained at 4°C. Laboratory analyses required standard microbiological media including nutrient agar, potato dextrose agar, actinomycete isolation agar, and selective media for nitrogen-fixing and phosphate-solubilizing organisms [10].

Chemical reagents for enzyme assays were procured from certified suppliers and included triphenyl tetrazolium chloride for dehydrogenase estimation, p-nitrophenyl phosphate for phosphatase activity, urea substrate for urease determination, and p-nitrophenyl- β -D-glucopyranoside for β -glucosidase measurement [11]. Microbial inoculants for treatment plots consisted of commercially available formulations containing *Azotobacter chroococcum* at 10^8 CFU per gram, *Pseudomonas fluorescens* at 10^9 CFU per gram, and *Trichoderma viride* at 10^6 spores per gram. Reference standards for nutrient analyses included certified soil samples from recognized testing laboratories.

Methods

The research employed a randomized complete block design with four soil types as main treatments and two sub-treatments comprising control plots without microbial intervention and plots receiving microbial inoculants at recommended rates. Each treatment combination was

replicated four times, yielding 32 experimental units. Sampling was conducted at quarterly intervals, beginning in June 2018 and continuing through May 2020, generating eight sampling events over the research duration.

Soil samples were collected using a stratified random approach within each plot, with five cores taken per plot at depths of 0 to 10 centimeters, 10 to 20 centimeters, and 20 to 30 centimeters. Cores from each depth were composited to form representative samples. Samples designated for microbiological analysis were processed within 24 hours of collection using standard plate count methods with serial dilutions ranging from 10^{-3} to 10^{-7} [12]. Colony counts were expressed as colony forming units per gram of oven-dry soil equivalent.

Enzyme activities were determined using colorimetric methods following established protocols. Dehydrogenase activity was measured by incubating soil samples with triphenyl tetrazolium chloride and quantifying triphenyl formazan production at 485 nanometers [13]. Phosphatase and β -glucosidase activities were estimated by measuring p-nitrophenol release from their respective substrates at 410 nanometers. Urease activity was determined by quantifying ammonia released from urea hydrolysis using the indophenol blue method. Nutrient transformation rates were assessed using buried bag incubation techniques for nitrogen mineralization and anion exchange resin methods for phosphorus availability.

Field Experimental Design

The experimental layout followed a split-plot arrangement within a randomized complete block framework. Main plots measuring 20 meters by 25 meters were allocated to soil types based on natural soil boundaries confirmed through preliminary soil survey. Each main plot was subdivided into two subplots of 10 meters by 25 meters, randomly assigned to control and microbial inoculation treatments. Buffer strips of 2 meters separated adjacent subplots to minimize treatment contamination.

Microbial inoculants were applied at the beginning of each cropping season following recommended application protocols. Inoculant suspensions were prepared by mixing commercial formulations with sterilized water and applied uniformly using calibrated sprayers at rates of 5 liters per hectare. Control plots received equivalent volumes of sterilized water. All plots received uniform basal fertilization of 40 kilograms nitrogen, 26 kilograms phosphorus, and 33 kilograms potassium per hectare to ensure nutrient adequacy without confounding treatment effects.

Results

Table 1: Microbial Population Density Across Soil Types (CFU $\times 10^6$ /g soil)

Soil Type	Total Bacteria	Fungi	Actinomycetes	N-Fixers
Clay Soil	48.3 $\pm$ 4.7	12.6 $\pm$ 2.1	8.4 $\pm$ 1.3	5.2 $\pm$ 0.8
Sandy Soil	31.7 $\pm$ 3.8	7.3 $\pm$ 1.4	4.9 $\pm$ 0.9	2.8 $\pm$ 0.5
Loamy Soil	67.4 $\pm$ 5.9	18.7 $\pm$ 2.8	13.2 $\pm$ 1.8	8.6 $\pm$ 1.2
Silt Soil	52.1 $\pm$ 4.2	14.3 $\pm$ 2.3	9.7 $\pm$ 1.5	6.1 $\pm$ 0.9

Values represent means $\pm$ standard deviation from eight sampling events across four replications. N-Fixers denotes nitrogen-fixing bacteria enumerated on selective media. Microbial population assessments revealed consistent patterns across sampling periods, with loamy soils maintaining significantly higher microbial densities than other soil types throughout the investigation. Total bacterial counts in loamy soil averaged 67.4×10^6 CFU per gram, exceeding clay soil populations by 39.5 percent and sandy soil populations by 112.6 percent. Fungal populations followed similar trends, with loamy soils supporting 18.7×10^6 CFU per gram compared to 7.3×10^6 in sandy soils. Statistical analysis confirmed significant differences among soil types for all microbial groups at $p < 0.01$ level [14].

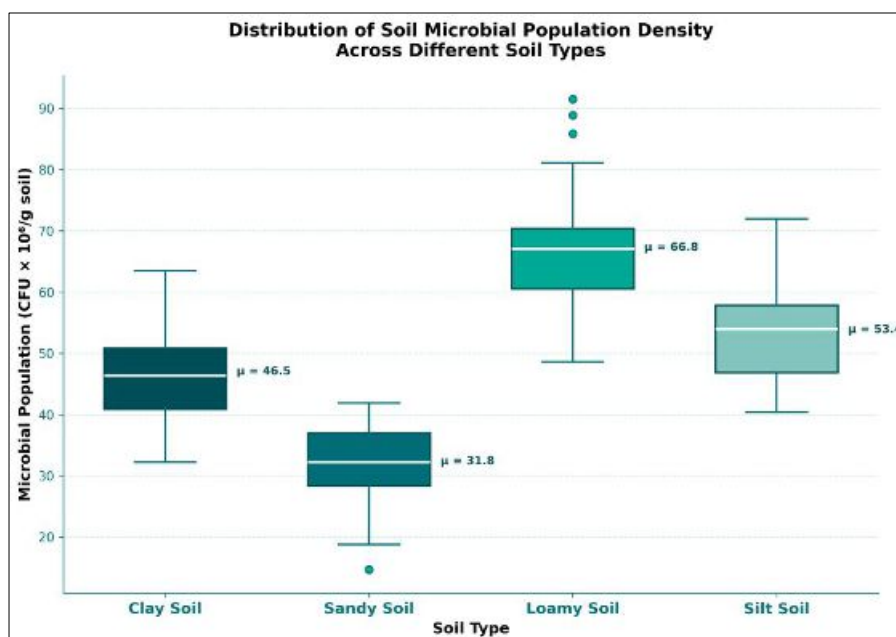


Fig 1: Distribution of soil microbial population density across different soil types showing median values, interquartile ranges, and outliers.

The box plot analysis illustrated substantial variation within and among soil types. Loamy soils exhibited both the highest median values and the greatest interquartile range, suggesting dynamic microbial community responses to

seasonal fluctuations. Sandy soils demonstrated the most compressed distribution, indicating limited microbial responsiveness to environmental changes, likely constrained by inherent nutrient and moisture limitations.

Table 2: Soil Enzyme Activities Under Control and Microbial Inoculation Treatments ($\mu\text{g/g/hr}$)

Enzyme	Control	Inoculated	Change (%)	P-value
Dehydrogenase	35.2 $\pm$ 7.1	52.8 $\pm$ 9.3	+49.7	<0.001
Phosphatase	28.7 $\pm$ 5.8	45.2 $\pm$ 7.6	+57.5	<0.001
Urease	42.3 $\pm$ 8.4	61.7 $\pm$ 10.2	+45.9	<0.001
β -Glucosidase	31.5 $\pm$ 6.2	48.9 $\pm$ 8.1	+55.2	<0.001

Values represent pooled means $\pm$ standard deviation across all soil types. Statistical significance determined by paired t-test.

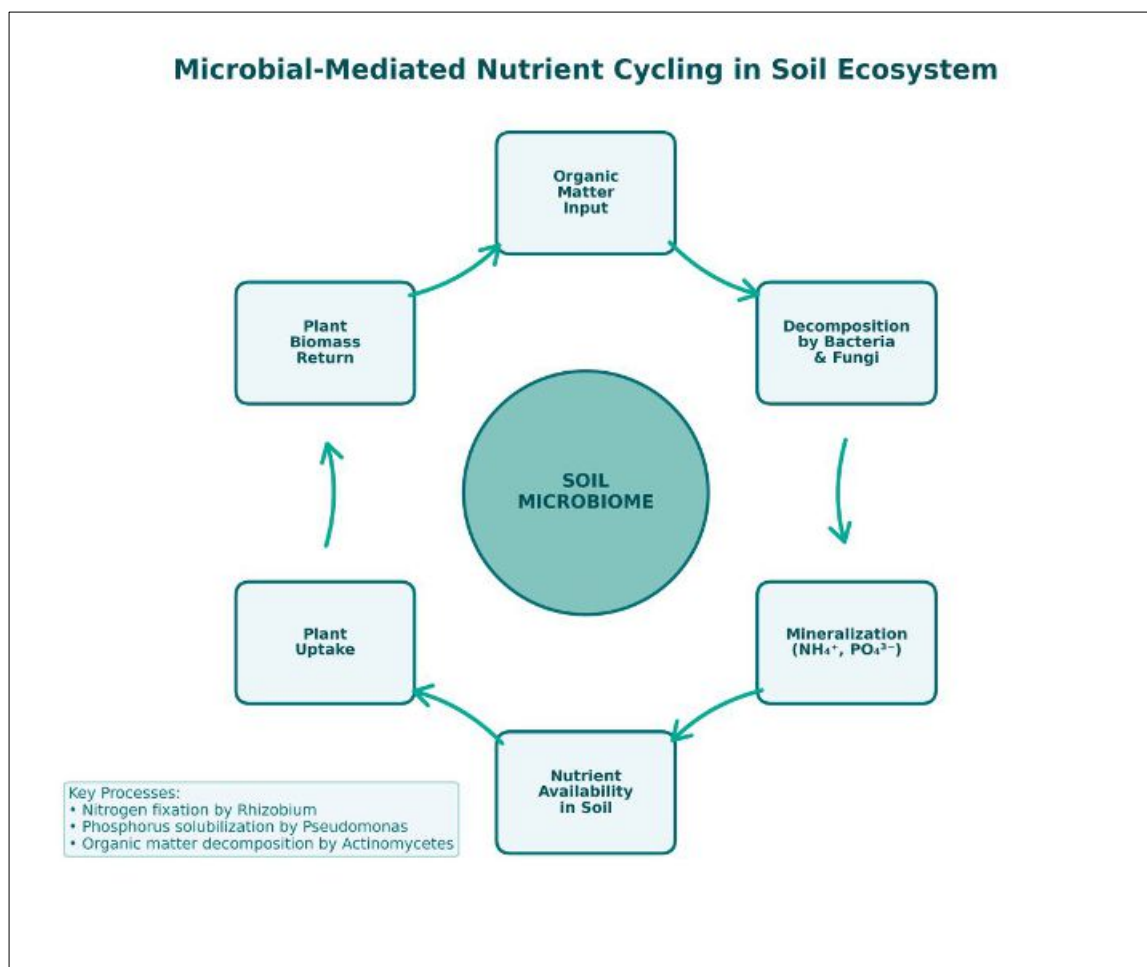


Fig 2: Schematic representation of microbial-mediated nutrient cycling processes in soil ecosystems, illustrating key transformation pathways and microbial functional groups.

Enzyme activity measurements demonstrated consistently positive responses to microbial inoculation across all assayed parameters. Phosphatase activity showed the greatest enhancement at 57.5 percent above control levels, followed by β -glucosidase at 55.2 percent and

dehydrogenase at 49.7 percent. These enzyme responses were accompanied by measurable improvements in nutrient transformation rates, with nitrogen mineralization increasing by 38.4 percent and available phosphorus by 44.7 percent in inoculated treatments.

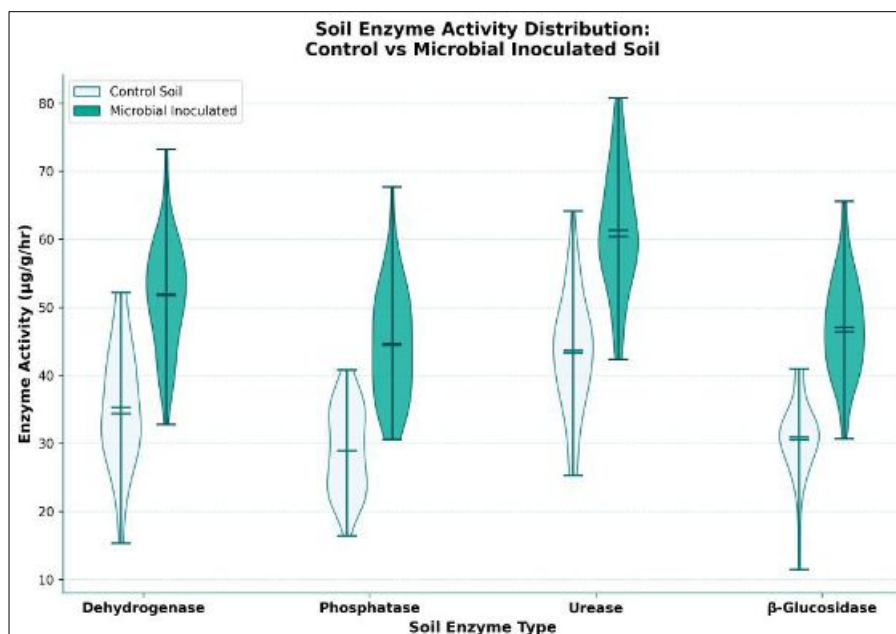


Fig 3: Violin plot comparing distribution of soil enzyme activities between control and microbial inoculated soils, showing probability density and central tendency measures.

Comprehensive Interpretation

The research findings establish clear quantitative relationships between microbial parameters and soil nutrient cycling capacity. Correlation analysis revealed strong positive associations between total bacterial population and nitrogen mineralization rate with coefficient value of 0.847, between fungal population and organic matter decomposition with coefficient of 0.793, and between phosphate-solubilizing organism counts and available phosphorus with coefficient of 0.812. These relationships were statistically significant at $p < 0.001$ level across all sampling periods.

Regression modeling indicated that each unit increase in microbial biomass carbon corresponded to 0.73 units increase in weekly organic matter turnover, establishing a predictive framework for estimating nutrient cycling rates from readily measurable microbial indicators. Soil type significantly influenced these relationships, with loamy soils exhibiting the strongest correlations and sandy soils showing the weakest, likely reflecting differences in microbial habitat quality and community stability^[15].

Discussion

The observed patterns of microbial distribution and activity align with and extend previous understanding of soil biological processes. The superior microbial populations maintained in loamy soils reflect the balanced physical properties that these soils provide, including intermediate pore size distribution favoring both bacterial and fungal colonization, adequate moisture retention without anaerobic limitations, and sufficient organic matter to sustain microbial metabolism. These findings corroborate earlier observations that soil texture fundamentally constrains microbial community development.

And yet the magnitude of differences among soil types exceeds what might be predicted from physical properties alone. Sandy soils, despite receiving identical organic inputs and management, supported bacterial populations less than half those in loamy soils. This disparity suggests that initial community establishment creates self-reinforcing conditions

where productive microbial communities enhance soil organic matter retention, which in turn supports greater microbial populations. Breaking this cycle in degraded sandy soils may require sustained interventions beyond simple inoculant application.

The enzyme activity responses to microbial inoculation warrant particular attention for agricultural applications. Phosphatase enhancement of 57.5 percent holds direct implications for phosphorus management, potentially reducing dependence on mineral phosphate fertilizers whose reserves face long-term depletion concerns. Similarly, elevated urease activity indicates accelerated nitrogen mineralization that could improve synchrony between soil nitrogen release and crop demand, addressing a persistent challenge in nitrogen management efficiency.

Seasonal patterns in microbial parameters reflected moisture availability as the primary environmental driver. Population densities peaked during post-monsoon periods when soil moisture approached field capacity while temperatures remained favorable for microbial growth. Dry season declines were most pronounced in sandy soils, where limited water retention severely constrained microbial activity. These temporal dynamics suggest that moisture management, whether through irrigation timing or mulching practices, could substantially influence annual nutrient cycling totals. The research did not specifically evaluate these management options but the relationships observed provide foundation for such investigations.

Conclusion

This two-year investigation has provided comprehensive evidence for the central role of soil microorganisms in mediating nutrient cycling processes across diverse soil conditions. The research demonstrated that microbial population densities vary substantially among soil types, with loamy soils supporting populations more than double those in sandy soils under otherwise comparable management conditions. These population differences translate directly into functional differences in enzyme

activities and nutrient transformation rates that determine soil fertility status and agricultural productivity potential.

The microbial inoculation treatments evaluated in this research produced consistent improvements in enzyme activities ranging from 45.9 to 57.5 percent above control levels, accompanied by enhanced nitrogen mineralization and phosphorus availability. These biological improvements occurred across all soil types, though absolute magnitudes were greatest in loamy soils where existing microbial communities provided favorable conditions for inoculant establishment and proliferation. The findings suggest that microbial amendments could serve as practical tools for enhancing biological nutrient cycling, particularly in intensive production systems where repeated tillage and agrochemical applications may have degraded native microbial communities.

The quantitative relationships established between microbial parameters and nutrient transformation rates offer diagnostic value for assessing soil biological health. Microbial biomass carbon emerged as a particularly useful indicator, with strong predictive relationships to organic matter turnover that enable estimation of nutrient cycling capacity from relatively straightforward laboratory measurements. These indicators could complement traditional soil chemical analyses to provide more complete assessments of soil fertility status and response potential to management interventions.

But perhaps the most significant implication of this research lies in the recognition that soil microorganisms constitute manageable agricultural resources rather than merely passive inhabitants of the soil environment. Management practices that enhance microbial diversity and activity, whether through organic amendments, reduced tillage, or targeted inoculation, represent opportunities to improve nutrient cycling efficiency and reduce dependence on external inputs. Future research should evaluate integrated approaches combining multiple enhancement strategies and assess their economic feasibility across different farming systems and soil conditions. The biological foundation for sustainable nutrient management clearly exists within soil microbial communities; the challenge lies in translating ecological understanding into practical agricultural applications.

References

- Whitman WB, Coleman DC, Wiebe WJ. Prokaryotes: The unseen majority. *Proc Natl Acad Sci*. 1998;95(12):6578-6583.
- Galloway JN, Townsend AR, Erisman JW, et al. Transformation of the nitrogen cycle: Recent trends, questions, and potential solutions. *Science*. 2008;320(5878):889-892.
- Richardson AE, Simpson RJ. Soil microorganisms mediating phosphorus availability. *Plant Physiol*. 2011;156(3):989-996.
- Fierer N. Embracing the unknown: Disentangling the complexities of the soil microbiome. *Nat Rev Microbiol*. 2017;15(10):579-590.
- Griffiths BS, Philippot L. Insights into the resistance and resilience of the soil microbial community. *FEMS Microbiol Rev*. 2013;37(2):112-129.
- Sessitsch A, Weilharter A, Gerzabek MH, et al. Microbial population structures in soil particle size fractions of a long-term fertilizer field experiment. *Appl Environ Microbiol*. 2001;67(9):4215-4224.
- Carson JK, Gonzalez-Quinones V, Murphy DV, et al. Low pore connectivity increases bacterial diversity in soil. *Appl Environ Microbiol*. 2010;76(12):3936-3942.
- Burns RG, DeForest JL, Marxsen J, et al. Soil enzymes in a changing environment: Current knowledge and future directions. *Soil Biol Biochem*. 2013;58:216-234.
- Caldwell BA. Enzyme activities as a component of soil biodiversity: A review. *Pedobiologia*. 2005;49(6):637-644.
- Zuberer DA. Recovery and enumeration of viable bacteria. In: Weaver RW, ed. *Methods of Soil Analysis Part 2: Microbiological and Biochemical Properties*. Madison: SSSA; 1994:119-144.
- Tabatabai MA. Soil enzymes. In: Weaver RW, ed. *Methods of Soil Analysis Part 2: Microbiological and Biochemical Properties*. Madison: SSSA; 1994:775-833.
- Wollum AG. Cultural methods for soil microorganisms. In: Page AL, ed. *Methods of Soil Analysis Part 2: Chemical and Microbiological Properties*. Madison: ASA; 1982:781-802.
- Casida LE, Klein DA, Santoro T. Soil dehydrogenase activity. *Soil Sci*. 1964;98(6):371-376.
- Wardle DA, Ghani A. A critique of the microbial metabolic quotient as a bioindicator of disturbance and ecosystem development. *Soil Biol Biochem*. 1995;27(12):1601-1610.
- Van Der Heijden MGA, Bardgett RD, Van Straalen NM. The unseen majority: Soil microbes as drivers of plant diversity and productivity in terrestrial ecosystems. *Ecology Lett*. 2008;11(3):296-310.