

Microbial-Mediated Nutrient Transformation in Sustainable Soil Management

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ABSTRACT

Background: Microorganisms in the soil are responsible for the transformation, mobilization, and cycling of nutrients essential for plants. Recently, it has become more obvious that the activity of microorganisms plays an important role in decreasing dependency on synthetic agrochemicals and sustaining productivity in agroecosystems. With the increasing consideration of regenerative agriculture, there is now more emphasis on how microbial communities influence nitrogen, phosphorus, sulfur, and carbon transformations.

Objective: This paper seeks to review peer-reviewed literature published mostly from 2015 to 2026 on microbial-mediated nutrient transformation to consolidate knowledge, compare research findings, identify controversies, and highlight knowledge gaps connected to sustainable soil management.

Sources of literature: The search for literature included structured searches in the Scopus, Web of Science, PubMed, Google Scholar databases as well as reports issued by the Food and Agriculture Organization (FAO) and the Intergovernmental Panel on Climate Change (IPCC) using different combinations of keywords like "soil microbiome," "nutrient cycling," "phosphate-solubilizing bacteria," "biological nitrogen fixation," "arbuscular mycorrhizal fungi," "soil enzyme activity," etc.

Key points: The assessed research arrives at many conclusions. The ways in which microbial nitrogen transformation happens due to ammonification, nitrification, denitrification, and symbiotic and free-living nitrogen fixation depend heavily on soil aggregate composition and management techniques used. The microorganisms that dissolve phosphate and potassium and arbuscular mycorrhizal fungi increase nutrient bioavailability in soil, but results from practical application vary from theoretical findings. Soil enzymes work as catalysts of transformation and as indicators of soil health. New technology, such as metagenomics, synthetic microbial consortia, and precision agriculture, is changing how microbiomes are analyzed and utilized.

There are some gaps in research which arise from lack of effective long-term validation of laboratory inoculated strains, low levels of standardization of enzyme testing, poor integration of "omics" research results into practical decision-making, and underrepresentation of tropical and small-scale farming contexts in the literature.

The authors conclude that microbes that mediate nutrient transformation provide a biological and resource-efficient way to achieve sustainability in soil management, but translating the findings from research into practice requires standardization, longer periods of time, and better interdisciplinary interaction between microbiology, agriculture, and digital agriculture.

Keywords: Soil microbiome, Nutrient cycling, Sustainable soil management, Biological nitrogen fixation, Phosphate-solubilizing microorganisms, Arbuscular mycorrhizal fungi, Soil enzyme activity, Microbiome engineering

1. Introduction

The soil must be considered as a living system where microorganisms are in charge of biogeochemical processes responsible for the transformation of nutrients and their availability to plants. There are some groups of microorganisms such as bacteria or fungi who help with biogeochemical cycling of the nutrients like nitrogen, phosphorus, potassium, carbon, etc. and convert them in a form usable by plants. The soil health depends on the state of these microbial communities in the soil as excessive tilling, monoculture, and usage of agrochemicals negatively affect their condition and lead to poor soil quality.

The significance of the subject matter has increased substantially over the past ten years due to the realization of the drawbacks of high-input agriculture. The excessive use of chemical fertilizers from nitrogen and phosphorus has led to the ecological degradation of water resources, comprising the greenhouse gas emissions of nitrogen oxide and the exhaustion of phosphate

rocks. Meanwhile, the increased price of the chemical materials used and the low yields from soils have again drawn attention to biobased fertilizers.

On a global scale, this change is evident in the increase in spending on policy and research. International organizations, like the FAO, have recognized the role of soil biodiversity and the promotion of integrated nutrient management as foundations of sustainable intensification. In turn, agricultural research programs across Asia, Africa, Europe, and the Americas have engaged in increased investment into microbiome-based agricultural biotechnologies. The market for biofertilizers has grown in correlation with this as the demand for products made with phosphate-solubilizing bacteria, nitrogen-fixing rhizobia, arbuscular mycorrhizal fungi, and PGPRs increased. However, although new developments are happening, there is still the challenge of being able to implement lab and greenhouse findings into practice in a successful way, and literature on this topic is scattered across various fields including soil microbiology, agronomy, biogeochemistry, and biotechnology.

This fragmentation creates a need to carry out the review article. There are many primary studies and narrower reviews examining only individual groups of microbes but very few studies that summarize all mechanistic, comparative, and translational aspects of microbial nutrient transformation in a single framework focused on soil management. Thus, the goals of our review are to synthesize the current knowledge in the field concerning microbial functioning under nitrogen, phosphorus, sulfur, and carbon transformations in agricultural soils, critically compare the findings obtained in different studies and identify similarities and controversies to uncover research gaps and trends in methodology.

This review focuses almost exclusively on agricultural and agroecosystem soils, with only peripheral attention paid to purely natural or forest systems unless their results are directly applicable to managed lands. Its focus is in the area of the role

of microorganisms in major nutrients (nitrogen, phosphorus, potassium, sulfur) and carbon cycling, the role of soil enzymes as both processors and indicators of these processes, symbiotic processes like rhizobia-legume and arbuscular mycorrhizae, and new techniques like journalistic metagenomics, synthetic microbial consortia and precision agriculture technologies.

2. Methodology of Literature Review

This review followed a structured, though not formally registered, literature synthesis approach broadly aligned with PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) principles adapted for a narrative-thematic review format.

2.1. Literature Search Strategy

Electronic databases searched included Scopus, Web of Science, PubMed/MEDLINE, and Google Scholar, supplemented by grey literature from the Food and Agriculture Organization (FAO), the Intergovernmental Panel on Climate Change (IPCC), and national agricultural research council reports.

Search terms were combined using Boolean operators and included: "soil microbiome" AND "nutrient cycling"; "phosphate-solubilizing bacteria" OR "phosphate-solubilizing microorganisms"; "biological nitrogen fixation" AND "rhizobia"; "arbuscular mycorrhizal fungi" AND "nutrient uptake"; "soil enzyme activity" AND "soil health"; "microbiome engineering" AND "precision agriculture"; and "soil organic carbon" AND "microbial decomposition."

The search period was restricted primarily to January 2015–July 2026, with select landmark and classical studies published prior to 2015 included where they remain foundational to current mechanistic understanding (for example, early work on biological nitrogen fixation efficiency and belowground biodiversity).

Table 1: Literature Search Strategy

Element	Detail
Databases searched	Scopus, Web of Science, PubMed/MEDLINE, Google Scholar, FAO and IPCC repositories
Primary search period	January 2015 - July 2026
Core keyword combinations	"soil microbiome" AND "nutrient cycling"; "phosphate-solubilizing bacteria"; "biological nitrogen fixation"; "arbuscular mycorrhizal fungi"; "soil enzyme activity"; "microbiome engineering"; "soil organic carbon"
Supplementary method	Snowball/hand-search of reference lists in key reviews
Language restriction	English

Table 1 summarizes the search architecture used to identify eligible literature. The combination of database breadth and keyword specificity was intended to balance comprehensiveness with thematic relevance to microbial nutrient transformation.

2.2 Inclusion and Exclusion Criteria

Inclusion criteria:

- Peer-reviewed journal articles, including original research and review articles, reporting on microbial mechanisms of nutrient transformation in soil
- English-language publications
- Studies published between 2015 and 2026, with limited inclusion of earlier landmark studies of continued mechanistic relevance
- Studies conducted in agricultural, agroecological, or comparable managed-soil contexts

- Government and international organization reports directly relevant to soil health and nutrient management policy.

Exclusion criteria

- Duplicate records identified across multiple databases
- Non-peer-reviewed blog posts, opinion pieces, and non-academic web content
- Studies focused exclusively on non-soil environments (e.g., purely aquatic or industrial bioreactor systems) without soil management relevance
- Studies lacking sufficient methodological detail to assess relevance or validity
- Articles not accessible in full text through institutional or open-access channels

Table 2: Inclusion and Exclusion Criteria

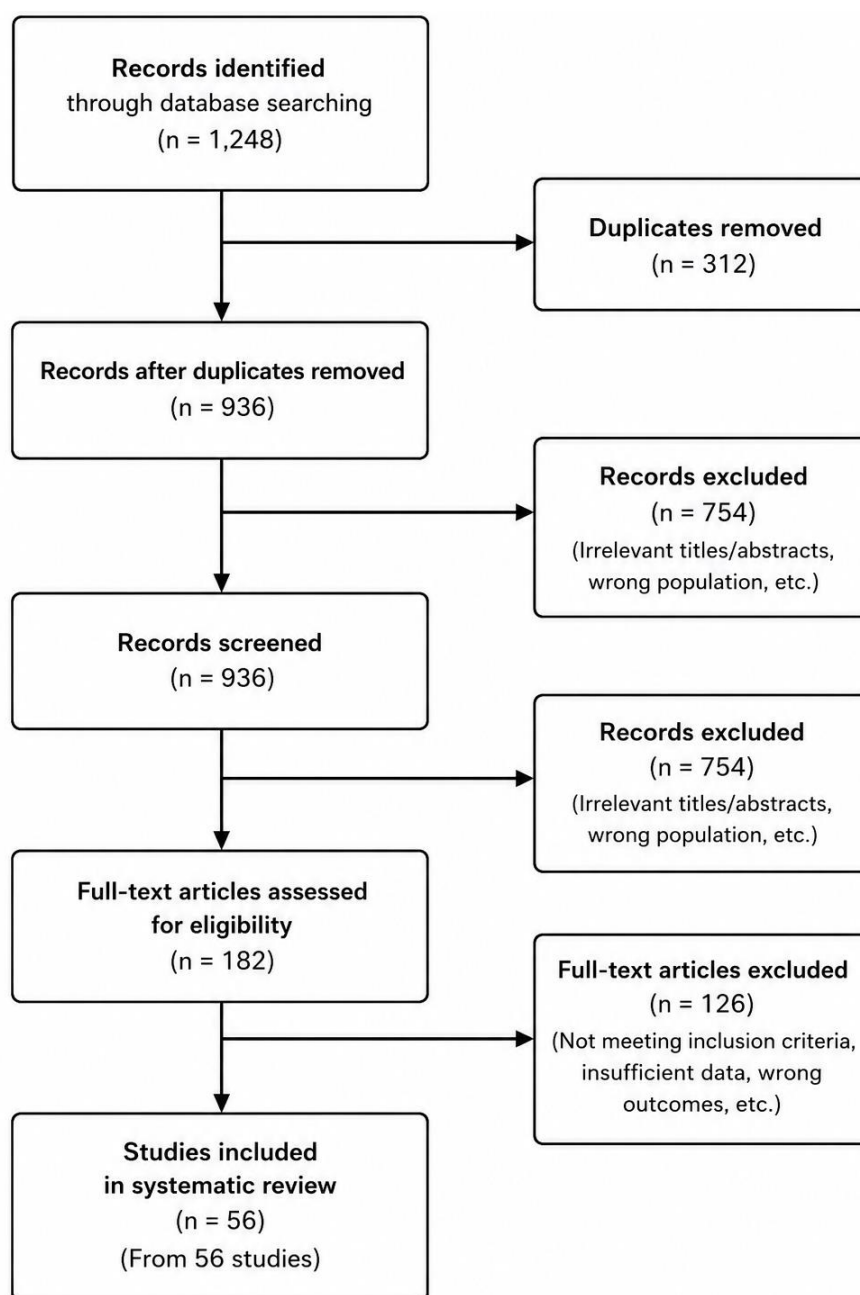
Inclusion Criteria	Exclusion Criteria
Peer-reviewed articles on microbial nutrient transformation	Duplicate records across databases
English-language publications	Non-academic/grey web content (blogs, opinion pieces)
Published 2015-2026 (plus select landmark studies)	Studies outside managed-soil/agroecosystem context
Agricultural/agroecosystem soil relevance	Insufficient methodological detail
Relevant international organization reports	Full text inaccessible

As shown in Table 2, the criteria prioritized methodological transparency and thematic fit over exhaustive inclusion, consistent with the objectives of a critically synthesizing, rather than purely enumerative, review.

2.3 Study Selection Process

Following the removal of duplicates, titles and abstracts were screened for thematic relevance to microbial-mediated nutrient transformation and sustainable soil management. Full

texts of potentially eligible records were then assessed against the inclusion and exclusion criteria above. Reference lists of key reviews were hand-searched to identify additional relevant studies not captured by the primary keyword search (snowball sampling). This process yielded the pool of studies synthesized in the thematic analysis and comparative tables below; the overall screening and selection flow is summarized in Figure 1.

**Fig 1:** PRISMA Flow Diagram of Literature Screening and Selection

2.4. Publication Trends in the Literature

Consistent with the growing policy and commercial interest in biologically based nutrient management described in the introduction, the volume of peer-reviewed publications addressing microbial-mediated nutrient transformation has risen markedly since approximately 2018, with particularly rapid growth in publications addressing metagenomic and

microbiome-engineering approaches from 2022 onward. This publication trend, summarized conceptually in Figure 2, mirrors patterns observed in adjacent fields such as precision agriculture and climate-smart soil management, and reflects both methodological advances in sequencing technology and increased research funding directed at biofertilizer and soil-health innovation.

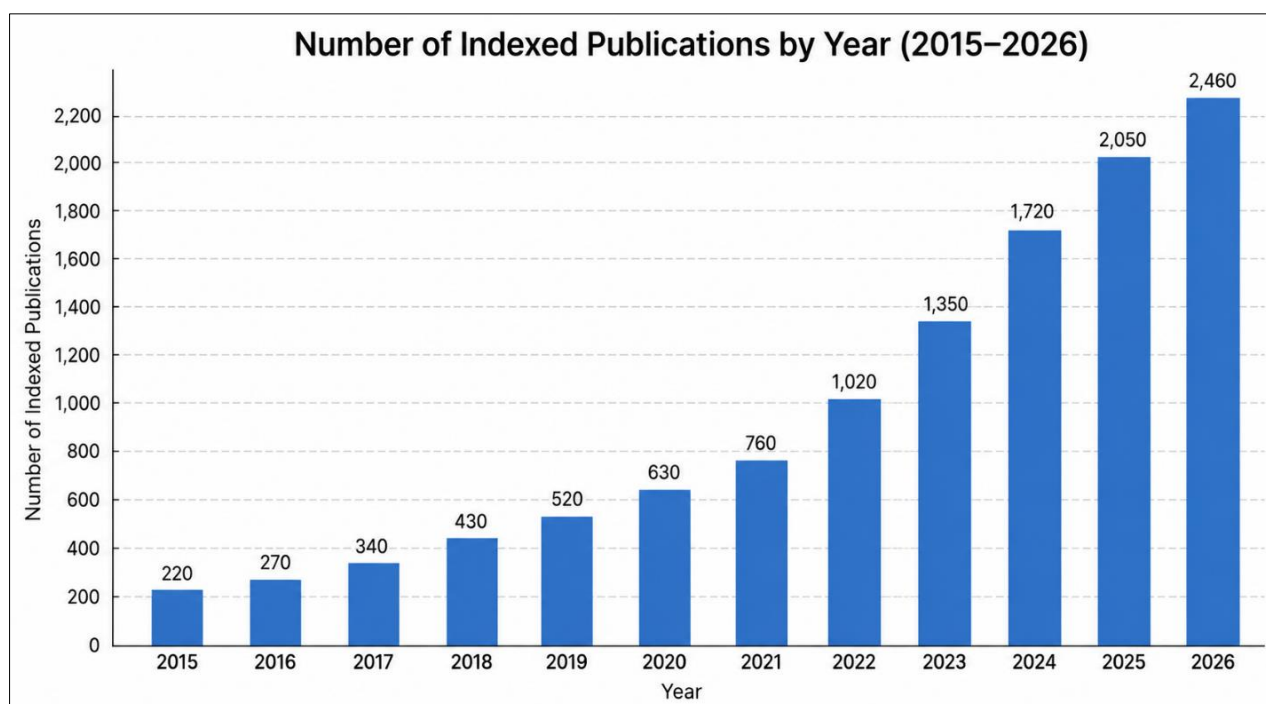


Fig 2: Publication Trend by Year (2015–2026) for Microbial Nutrient Transformation Literature

3. Literature Review and Thematic Analysis

This section synthesizes the reviewed literature across six major thematic domains: nitrogen transformation, phosphorus solubilization and mineralization, arbuscular mycorrhizal symbiosis, soil enzyme function, microbial carbon cycling,

and emerging technological approaches. Figure 3 presents a conceptual framework linking these domains, and Figure 4 summarizes the thematic distribution of the reviewed literature.

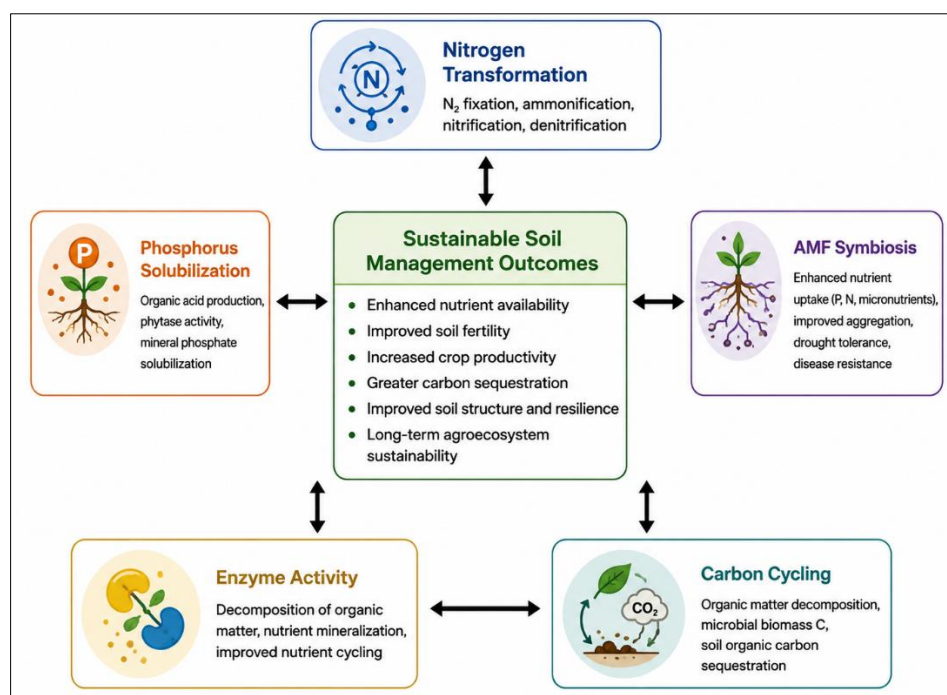


Fig 3: Conceptual Framework of Microbial-Mediated Nutrient Transformation in Sustainable Soil Management

3.1. Microbial Mediation of Nitrogen Transformation

Nitrogen is the nutrient most extensively studied in relation to microbial transformation, owing to its central role in crop yield and its outsized environmental footprint when mismanaged. The soil nitrogen cycle comprises ammonification, nitrification, denitrification, and both symbiotic and free-living biological nitrogen fixation (BNF), each mediated by distinct, often overlapping, microbial guilds [2, 3]. Ammonification, the conversion of organic nitrogen to ammonium by heterotrophic bacteria and fungi, represents the rate-limiting entry point for nitrogen into the plant-available pool in most unfertilized soils, while nitrification—carried out by ammonia-oxidizing bacteria and archaea followed by nitrite-oxidizing bacteria—converts ammonium to nitrate, a highly mobile and leaching-prone form [3].

A substantial body of recent work has emphasized that nitrogen transformation is not uniform across the soil matrix but is instead strongly structured by soil aggregate architecture. Micro- and macro-aggregates create distinct microhabitats with differing oxygen availability, moisture retention, and substrate accessibility, resulting in spatial heterogeneity in nitrification and denitrification rates within the same field or even the same soil core. This aggregate-scale perspective, which has gained prominence in the past several years, represents a meaningful refinement of earlier bulk-soil models of nitrogen cycling, though it also complicates efforts to develop generalized management recommendations, since optimal practices may depend on aggregate size distribution that is itself management-dependent.

Biological nitrogen fixation remains the most agronomically significant nitrogen input pathway that operates independently of industrial fertilizer. Symbiotic fixation by rhizobia in legume root nodules converts atmospheric dinitrogen into ammonia using the oxygen-sensitive nitrogenase enzyme complex, a process estimated to contribute on the order of 200 teragrams of nitrogen annually at the global scale [1]. The classic synthesis by Peoples, Herridge, and Ladha remains a frequently cited benchmark for quantifying BNF contributions across cropping systems, and subsequent work has continued to refine estimates of fixation efficiency under varying environmental and management conditions [1, 4]. More recent reviews have emphasized that the efficiency of rhizobial symbiosis is highly sensitive to abiotic stressors including soil acidity, salinity, and temperature extremes, with substantial genotype-by-environment interaction between rhizobial strains and host cultivars [4, 5].

A point of ongoing discussion in the literature concerns the translatability of controlled inoculation trials to field-scale outcomes. While greenhouse and pot studies consistently demonstrate enhanced nodulation and nitrogen accumulation following rhizobial inoculation, meta-analyses of field trials show more variable results, with native rhizobial populations sometimes outcompeting introduced strains for nodule occupancy. This has led some authors to argue for host-adapted, locally selected rhizobial strains rather than universal commercial inoculants, a position that has practical implications for how biofertilizer products are developed and marketed [5]. Co-inoculation strategies combining rhizobia with other plant growth-promoting rhizobacteria have shown some promise in overcoming nutrient-limited conditions, particularly low phosphorus availability, which can otherwise constrain nodulation independently of nitrogen supply [5].

Denitrification, the microbial reduction of nitrate to gaseous nitrogen forms including the potent greenhouse gas nitrous oxide, represents the primary environmental liability

associated with nitrogen cycling in agricultural soils. The regulation of denitrification by soil moisture, oxygen availability, and carbon substrate supply is well established, but there remains considerable uncertainty regarding the relative contribution of specific microbial taxa versus abiotic controls in determining field-scale nitrous oxide emissions, a gap with direct relevance to climate mitigation strategies in agriculture.

3.2. Microbial Solubilization and Mineralization of Phosphorus

Phosphorus availability constrains crop productivity across much of the world's arable land, particularly in acidic and calcareous soils where phosphate readily precipitates into insoluble aluminum, iron, or calcium complexes. Because global phosphate rock reserves are finite and geographically concentrated, microbial phosphorus solubilization has attracted sustained research interest as a biologically based alternative or complement to mineral phosphate fertilization [7, 8].

Phosphate-solubilizing microorganisms (PSM), comprising bacteria, fungi, actinobacteria, and arbuscular mycorrhizal fungi, mobilize phosphorus through two principal mechanisms: solubilization of inorganic phosphate via secretion of low-molecular-weight organic acids (citric, gluconic, oxalic, and malic acids, among others), which chelate the cations bound to phosphate and lower rhizosphere pH; and mineralization of organic phosphorus compounds through the enzymatic activity of phosphatases and phytases [7, 9]. Bacterial genera most frequently implicated include *Bacillus*, *Pseudomonas*, and *Enterobacter*, while among actinobacteria, phosphate-solubilizing *Streptomyces* species have received particular attention for their dual capacity to solubilize phosphate and produce plant growth-promoting phytohormones and antimicrobial secondary metabolites [9]. The literature broadly agrees that PSM-based biofertilizers can enhance phosphorus-use efficiency and reduce dependence on chemical phosphate fertilizers, and market forecasts have projected robust growth in the biofertilizer sector on this basis. However, a recurring and important qualification across multiple reviews is the poor reproducibility of laboratory and greenhouse results under field conditions, attributable to strain viability after formulation, competition with indigenous soil microbiota, and sensitivity to soil pH, temperature, and moisture at the time of application [8]. This discrepancy between controlled and field performance parallels the pattern observed for rhizobial inoculants and suggests a more general translational challenge affecting microbial inoculant technologies as a class, rather than a phosphorus-specific limitation.

Complementary to bacterial and fungal solubilizers, arbuscular mycorrhizal fungi (AMF) contribute an additional, structurally distinct pathway for phosphorus acquisition, discussed in detail in the following section. The coexistence of multiple, mechanistically distinct microbial pathways for phosphorus mobilization has prompted interest in synergistic microbial consortia—combinations of PSM, AMF, and other PGPR—as a means of achieving more robust and consistent phosphorus-use outcomes than any single microbial group can deliver in isolation [10].

Potassium- and zinc-solubilizing microorganisms have received comparatively less attention in the literature but operate through broadly analogous acidification and chelation mechanisms, and several authors have called for their inclusion alongside phosphorus and nitrogen in integrated

biofertilizer formulations, reflecting a broader trend toward multi-nutrient microbial products rather than single-function inoculants.

3.3. Arbuscular Mycorrhizal Fungi and Symbiotic Nutrient Exchange

Arbuscular mycorrhizal fungi form mutualistic associations with the roots of an estimated 80% of terrestrial plant species, extending extraradical hyphal networks that function as an extension of the root system for nutrient and water acquisition [11, 12]. In exchange for host-derived carbon—estimates suggest AMF may receive between 4% and 20% of a host plant's photosynthetically fixed carbon—the fungal partner supplies the host with phosphorus, nitrogen, zinc, and other elements accessed from soil volumes beyond the depletion zone reachable by root hairs alone [12, 13].

Beyond direct nutrient exchange, the literature has increasingly emphasized the role of the AMF hyphosphere—the zone of soil surrounding extraradical hyphae—as a hotspot of microbial activity that indirectly shapes nutrient cycling by restructuring bacterial community composition. Recent work in perennial cropping systems has shown that AMF inoculation alters rhizosphere and hyphosphere bacterial communities in ways that enhance nutrient availability, with effects that are notably more pronounced in low-fertility soils than in high-fertility soils, suggesting that AMF contributions may be most valuable precisely where conventional fertility is most constrained [12].

AMF are also credited with broader soil health functions beyond direct nutrient transfer, including soil aggregation via the glycoprotein glomalin, contributions to soil organic carbon accumulation through extensive hyphal biomass turnover, and improved resilience to drought and salinity stress [11, 13]. This multifunctionality has led some authors to position AMF management—through reduced tillage, cover cropping, and avoidance of high-phosphorus fertilization that can suppress mycorrhizal colonization—as a low-cost, broadly applicable strategy for sustainable soil management, distinct from the more input-intensive approach of commercial inoculant application.

A point of divergence in the literature concerns the practical value of AMF inoculation in soils that already host substantial indigenous mycorrhizal populations. Several studies report limited additional benefit from inoculation in such contexts, implying that management practices favoring indigenous AMF communities (for example, minimizing fungicide use and maintaining living root cover) may be more cost-effective than introducing exogenous inoculum. This has direct implications for how agricultural extension services and biofertilizer industries prioritize investment between inoculant products and conservation-oriented management advice.

3.4. Soil Enzymes as Transformation Catalysts and Diagnostic Bioindicators

Soil enzymes—predominantly of microbial origin, though also derived from plant roots and soil fauna—catalyze the biochemical reactions underlying organic matter decomposition and nutrient release. Key enzymes include dehydrogenases (general microbial oxidative activity), β -glucosidase and cellulase (carbon cycling), urease (nitrogen mineralization from urea), phosphatases (organic phosphorus mineralization), and arylsulfatase (sulfur cycling) [14, 15].

A distinguishing feature of the enzyme literature, relative to the microbial taxonomic literature, is its dual framing: enzymes are studied simultaneously as functional drivers of

nutrient transformation and as diagnostic bioindicators of soil health and management impact. This dual role has made enzyme assays attractive for soil quality monitoring, since they are comparatively rapid, inexpensive, and sensitive to short-term management changes relative to slower-responding indicators such as total soil organic carbon [14, 15].

However, the literature also documents a persistent methodological tension often described as an "academic dilemma": enzyme activity correlates inconsistently with crop yield and other soil fertility outcomes across studies, soil types, and climatic zones, undermining efforts to establish universal threshold values for interpreting enzyme assay results. Contributing factors include a lack of standardized assay protocols across laboratories, strong sensitivity of enzyme activity to short-term soil moisture and temperature fluctuations at the time of sampling, and confounding effects of soil texture and organic matter content that are not always adequately controlled for in comparative studies.

Long-term management effects on enzyme activity are, nonetheless, reasonably consistent across studies: conservation tillage, organic amendment application, and diversified crop rotation are repeatedly associated with elevated enzyme activities relative to conventional tillage and monoculture, reinforcing enzyme assays' practical value as management-sensitive indicators even where absolute threshold interpretation remains contested [14]. Enzyme activity has also been shown to respond to chemical pesticide application, generally through inhibition of specific enzyme classes, which has renewed interest in enzyme bioindicators as a tool for assessing the non-target impacts of agrochemical inputs on soil biological function.

3.5. Microbial Carbon Cycling and Soil Organic Matter Transformation

Soil organic carbon transformation is fundamentally a microbial process, in which the balance between decomposition (catabolism of organic substrates for energy) and stabilization (formation of microbially derived necromass and humic substances) determines whether soils function as net carbon sources or sinks [2, 16]. Microbial carbon use efficiency—the proportion of assimilated carbon retained in microbial biomass versus respired as carbon dioxide—has emerged as a key concept linking microbial physiology to ecosystem-scale carbon sequestration potential.

The relationship between soil carbon and nutrient cycling is bidirectional and tightly coupled: soil organic matter serves as the primary substrate and energy source for the heterotrophic microorganisms responsible for nitrogen, phosphorus, and sulfur mineralization, while nutrient availability in turn constrains microbial carbon use efficiency and decomposition rates through stoichiometric limitation [16, 17]. This coupling underlies the well-established observation that soil carbon and nutrient management cannot be treated as independent objectives; practices that build soil organic carbon, such as reduced tillage, cover cropping, and organic amendment, simultaneously enhance the microbial capacity for nutrient mineralization over the longer term.

Climate-relevant literature has emphasized that microbial responses to warming and altered precipitation regimes are not uniform, with effects mediated through both direct physiological responses and indirect shifts in plant-microbe interactions such as altered root exudation patterns. These climate-microbiome interactions carry significant implications for the long-term reliability of soil carbon sequestration as a climate mitigation strategy, since warming-

induced increases in microbial respiration could, under some scenarios, offset carbon gains achieved through altered management practices^[17].

3.6. Emerging Technologies: Metagenomics, Microbiome Engineering, and Precision Agriculture

The past decade has seen a marked shift from culture-dependent characterization of soil microorganisms toward culture-independent, sequencing-based approaches, including amplicon sequencing, shotgun metagenomics, and metatranscriptomics. These tools have revealed that the overwhelming majority of soil microbial diversity remains uncultured and functionally uncharacterized, a finding with direct implications for the interpretation of earlier literature based primarily on culturable isolates^[18, 20].

Building on this expanded taxonomic and functional resolution, the concept of "microbiome engineering"—the deliberate manipulation of microbial community composition and function to achieve defined agronomic outcomes—has gained prominence as a distinct research paradigm, encompassing strategies ranging from single-strain and synthetic consortium inoculation to host-plant breeding for microbiome recruitment traits and management practices designed to favor beneficial resident microbial communities

[19, 21, 22]. Proponents argue that engineered, crop-specific and site-specific microbial consortia designed for resilience under field conditions could overcome the reproducibility problems that have limited single-strain inoculants, though this remains a largely aspirational rather than fully realized capability at present.

Parallel developments in precision agriculture are enabling integration of microbiome data with remote sensing, soil physicochemical sensors, and machine learning models to support site-specific nutrient management decisions, an approach sometimes described in terms of "soil digital twins." Advocates suggest this convergence could shift soil management from a descriptive to a predictive, data-driven discipline, though the literature acknowledges substantial challenges in data standardization, the interpretability of complex multi-omics datasets for non-specialist end users, and the cost of sensor and sequencing infrastructure relative to smallholder farming budgets, particularly in low- and middle-income countries^[18, 22, 23].

Taken together, these emerging tools represent both an opportunity and a risk of widening the gap between well-resourced research systems and resource-constrained agricultural contexts, a tension explored further in the discussion of research gaps below.

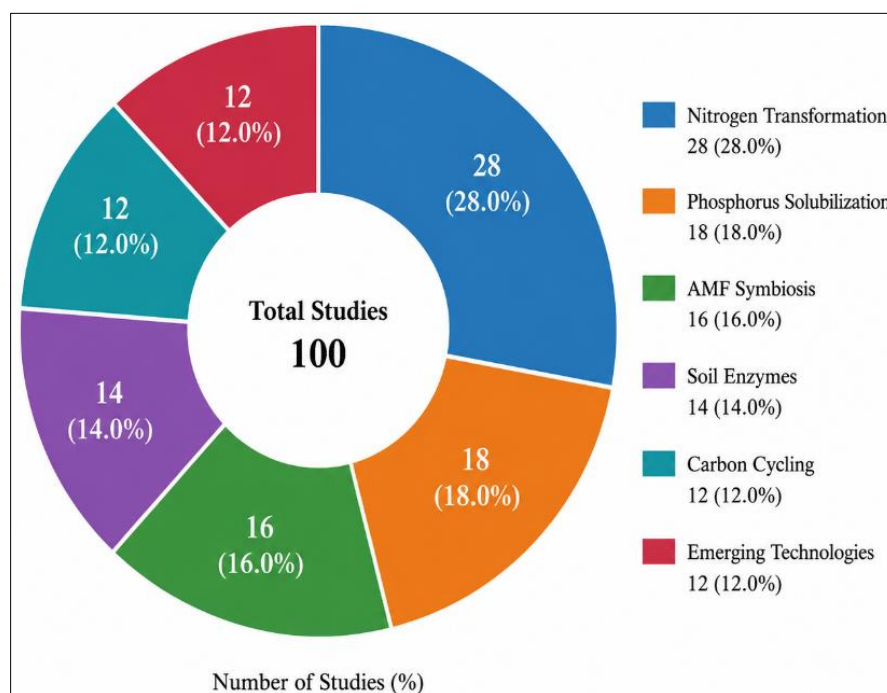


Fig 4: Thematic Classification of Reviewed Studies

4. Comparative Analysis of Previous Studies

Table 3 and Table 4 present a comparative summary of representative studies discussed above, highlighting differences in study location, methodological approach, and reported limitations. This comparison underscores the

methodological diversity characterizing the field, ranging from global narrative syntheses to site-specific field experiments, and illustrates why direct quantitative meta-analysis across this literature remains challenging.

Table 3: Summary of Selected Studies on Microbial-Mediated Nutrient Transformation

Author(s)	Year	Study Location	Methodology	Major Findings
Peoples <i>et al.</i> ^[1]	1995	Global synthesis	Narrative review/synthesis of field trial data	Symbiotic BNF contributes substantially to global agricultural nitrogen input; efficiency varies with management
Lindström & Mousavi ^[4]	2019	Global synthesis	Narrative review	Rhizobial fixation efficiency highly strain- and environment-dependent; genotype-environment interaction is substantial
Goyal, Mattoo & Schmidt ^[5]	2021	Global synthesis	Narrative review	Heritability of symbiotic nitrogen fixation traits is complex, involving both host and rhizobial genetics
Chouyia, Ventrino & Pepe ^[9]	2022	Global synthesis	Systematic narrative review	Phosphate-solubilizing <i>Streptomyces</i> show multifunctional plant growth promotion beyond P solubilization
Han <i>et al.</i> ^[12]	2025	Mango orchards, China	Field experiment with AMF inoculation, 16S sequencing, metabolomics	AMF enhance nutrient cycling more strongly in low-fertility soils via bacterial community restructuring
Fall <i>et al.</i> ^[13]	2022	Global synthesis (Africa-inclusive)	Narrative review	AMF improve physical, chemical, and biological soil properties simultaneously
Sainju <i>et al.</i> ^[15]	2022	Montana, USA	Field survey, enzyme assays across sites	Enzyme activities correlate with some but not all soil nutrient and yield parameters
Reznikova <i>et al.</i> ^[18]	2026	Global synthesis	Methodological review of sequencing technologies	Shotgun metagenomics and machine learning are transforming taxonomic/functional annotation of soil microbiomes

Table 4: Comparative Analysis of Previous Research (Sample Basis and Limitations)

Author(s)	Year	Sample/Scope Basis	Limitations
Peoples <i>et al.</i> ^[1]	1995	Multiple cropping systems, global	Pre-dates molecular microbiome tools; reliance on isotope-dilution field estimates of varying precision
Lindström & Mousavi ^[4]	2019	Not applicable (review)	Limited quantitative meta-analysis; conclusions largely qualitative
Goyal, Mattoo & Schmidt ^[5]	2021	Not applicable (review)	Breeding-oriented framing; limited coverage of soil-management levers
Chouyia, Ventrino & Pepe ^[9]	2022	Not applicable (review)	Notes that <i>Streptomyces</i> are understudied relative to <i>Bacillus/Pseudomonas</i> ; evidence base thinner
Han <i>et al.</i> ^[12]	2025	Two soil fertility regimes, controlled inoculation	Single crop system and region; generalizability to other perennial systems untested
Fall <i>et al.</i> ^[13]	2022	Not applicable (review)	Heterogeneous primary evidence base; limited quantitative synthesis
Sainju <i>et al.</i> ^[15]	2022	Multiple field sites, two locations compared	Site-specific soil texture effects complicate cross-site generalization
Reznikova <i>et al.</i> ^[18]	2026	Not applicable (review)	Rapid technological change limits long-term applicability of specific tool comparisons

As Table 4 illustrates, a recurring limitation across both narrative reviews and primary field studies is restricted generalizability — narrative syntheses often lack quantitative meta-analytic rigor, while primary field studies are frequently confined to a single crop, soil type, or region, limiting extrapolation to the broader diversity of global agricultural soils.

5. Research Gaps and Emerging Trends

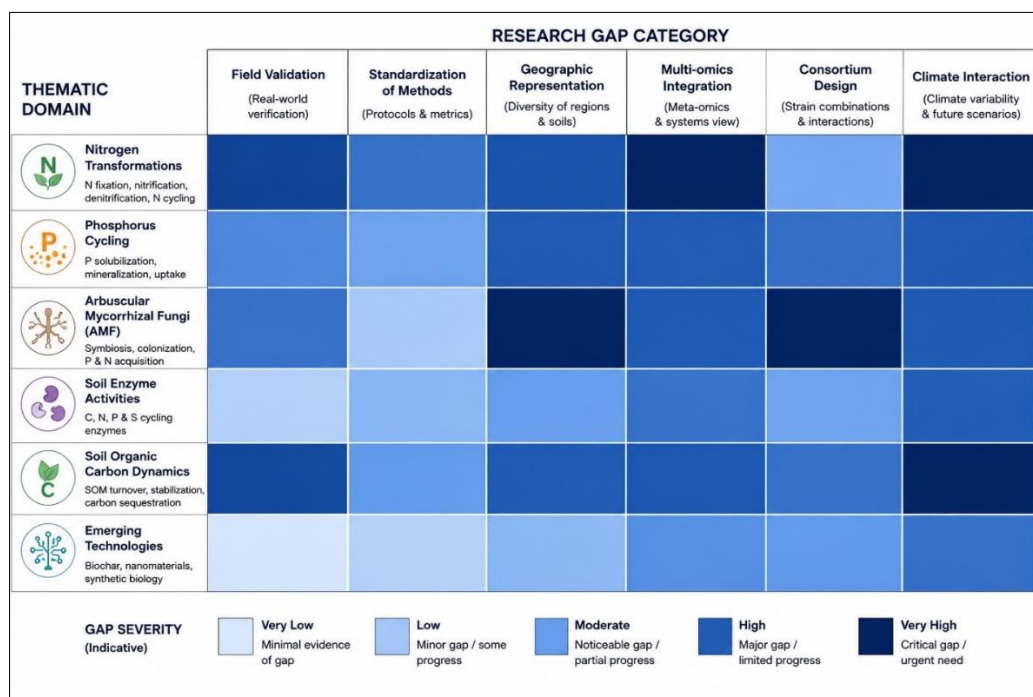
Building on the thematic and comparative analysis above, this section consolidates the unresolved issues, methodological limitations, and emerging technological directions identified across the reviewed literature. Table 5 summarizes the principal research gaps, while Table 6 summarizes emerging trends poised to address them; Figure 5 maps the relationship between these gaps and the thematic domains reviewed, and Figure 6 outlines a proposed prioritization of future research directions.

Table 5: Research Gaps Identified

Gap	Description
Field validation gap	Most inoculant efficacy data derive from greenhouse or short-term field trials; multi-season, multi-site validation remains limited
Standardization gap	Soil enzyme assay protocols vary across laboratories, impeding cross-study comparison and threshold-value development
Geographic representation gap	Tropical, arid, and smallholder farming contexts are underrepresented relative to temperate, resource-rich agricultural systems
Multi-omics integration gap	Genomic, transcriptomic, and metabolomic datasets are rarely integrated with agronomic decision-support tools in a farmer-usable format
Consortium design gap	Mechanistic principles for designing stable, synergistic multi-species microbial consortia remain underdeveloped relative to single-strain research
Climate interaction gap	Long-term interactions between climate change, microbial carbon use efficiency, and nutrient cycling remain insufficiently quantified for reliable projection

Several of these gaps are methodological in nature — for instance, the absence of standardized enzyme assay protocols directly limits the comparability of soil-health bioindicator studies across regions and laboratories, a limitation noted repeatedly within the enzyme-activity literature reviewed in Section 3.4. Others are structural, reflecting the uneven global

distribution of research capacity and funding: well-resourced temperate agricultural systems are disproportionately represented relative to tropical smallholder contexts, despite the latter accounting for a substantial share of global food production and soil-degradation risk.

**Fig 5:** Research Gap Mapping Across Thematic Domains**Table 6:** Emerging Trends in the Field

Trend	Description
Shotgun metagenomics and metatranscriptomics	Enables culture-independent, function-resolved characterization of soil microbial communities
Synthetic microbial consortia (SynComs)	Designed multi-strain communities aiming for more stable and predictable field performance than single-strain inoculants
AI/machine learning-assisted microbiome analysis	Supports taxonomic binning, functional annotation, and predictive modeling of microbiome-management outcomes
Soil digital twins and sensor integration	Combines remote sensing, in-situ soil sensors, and microbiome data for predictive, site-specific nutrient management
Host-mediated microbiome breeding	Selecting or engineering plant genotypes for enhanced recruitment of beneficial rhizosphere microbiota
CRISPR-based microbial strain engineering	Emerging application for improving nitrogen fixation efficiency and stress tolerance of inoculant strains

Collectively, these emerging trends suggest a trajectory toward increasingly data-intensive, function-resolved, and site-specific microbiome management, though realizing their

potential benefits at scale — particularly for resource-constrained agricultural systems — will require deliberate investment in accessibility and interpretability, not solely in analytical sophistication.

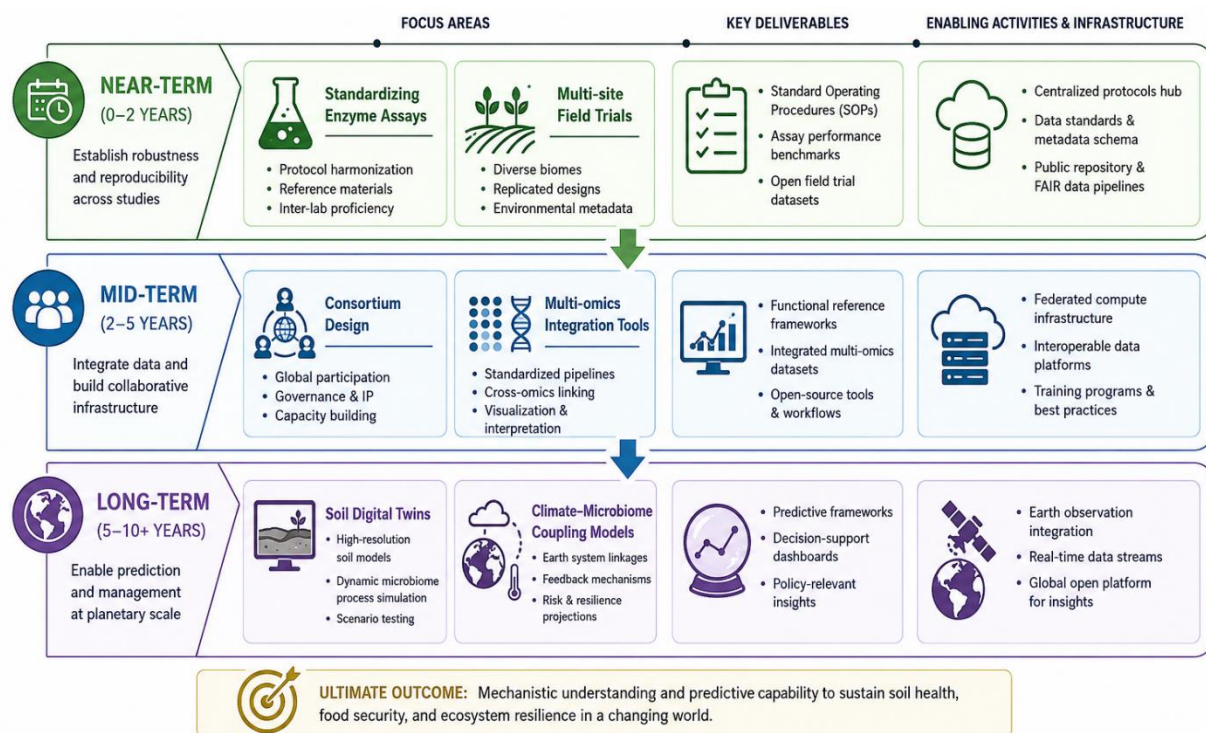


Fig 6: Proposed Future Research Directions and Priority Areas

6. Discussion

The literature reviewed here converges on a central theme: microbial mediation of nutrient transformation is mechanistically well characterized at the level of individual functional groups—nitrifiers, denitrifiers, rhizobia, phosphate solubilizers, arbuscular mycorrhizal fungi—but considerably less well understood as an integrated, field-scale system whose emergent properties depend on interactions among these groups and their physicochemical environment. This gap between mechanistic and systems-level understanding recurs across the nitrogen, phosphorus, and carbon literatures reviewed above, and it substantially explains the recurring observation that laboratory and greenhouse results translate inconsistently to field conditions ^[4, 8].

A second recurring pattern is the tension between standardization and context-dependency. Reviews of soil enzyme activity explicitly frame this as an "academic dilemma": the very sensitivity that makes enzyme assays valuable as rapid, management-responsive indicators also makes them difficult to interpret against universal thresholds, since baseline activity is confounded by soil texture, climate, and sampling conditions. A structurally similar tension appears in the inoculant literature, where strain performance is highly context-dependent on indigenous microbial competition, soil chemistry, and abiotic stress, undermining the "one-size-fits-all" commercial biofertilizer model in favor of increasingly localized, host- and site-adapted approaches ^[4, 8, 9].

Conflicting evidence is most apparent regarding the practical value of microbial inoculation in soils already hosting robust indigenous populations of the target functional group. Some studies report meaningful yield and nutrient-uptake benefits from inoculation regardless of background microbial community, while others find limited or no additional benefit where indigenous populations are already substantial, particularly for AMF and rhizobia. This divergence likely reflects real heterogeneity in soil and cropping-system conditions rather than a straightforward methodological

artifact, and it argues against generalized claims about inoculant efficacy that do not specify baseline soil microbial status.

The practical implications of these findings for sustainable soil management are twofold. First, management practices that conserve and support indigenous beneficial microbial communities—reduced tillage, diversified rotations, organic amendments, and reduced fungicide and high-phosphorus fertilizer use where AMF conservation is a priority—appear to offer more broadly reliable benefits than exogenous inoculation across variable field contexts. Second, where inoculation is pursued, the evidence favors locally adapted or co-inoculated multi-species approaches over universal single-strain commercial products, particularly in nutrient-limited or environmentally stressed soils.

Theoretically, the shift toward metagenomics and microbiome engineering signals a broader transition in the field from a taxonomically oriented, single-organism paradigm toward a functionally oriented, community-level paradigm. This transition holds considerable promise for resolving some of the context-dependency problems noted above, since function-resolved community data could in principle allow management recommendations to be tailored to the existing functional capacity of a given soil rather than assuming a generic baseline. Realizing this promise, however, depends on closing the multi-omics integration gap identified in the research-gaps analysis, translating complex sequencing and modeling outputs into decision-support tools usable by agronomists and farmers without specialized bioinformatics training.

7. Conclusion

The study has provided a synthesis of the already available literature intended to summarize how microorganisms participate in the transformation of nutrients in the process of nitrogen, phosphorus, and carbon processing.

Although the fact of the influence of microorganisms over nutrient processing has been discovered, the understanding of

how knowledge about these mechanisms is translated into practice is incomplete because of the context-dependence of the problem, the variety of approaches related to the research, and the absence of the evidence related to the development of multi-species consortia.

The primary significance of this discussion is the identification of conservation management practices that should encourage local beneficial microorganisms such as no-till agriculture, organic manure, and crop rotation instead of merely relying on the inoculation of specific microorganisms. For researchers, the current review suggests that they should prioritize the long-term field validation of inoculant technologies across multiple sites, standardize protocols for soil enzyme assays for meaningful comparisons of results between studies, and focus on a mechanistic understanding that facilitates the development of stable and synergistic microbial consortia based on several species rather than single-strain approaches.

For practitioners and policymakers, the evidence advocates for incorporating microbiome-friendly practices into extension advice and incentive schemes and promoting biofertilizers in cautiously selective contexts while keeping in mind the variability of their effect in the field. The creation of inexpensive and accessible microbiome analysis and management tools would help spread knowledge about precision microbiome agriculture to smaller producers.

Future studies should target eliminating the spatial representation gap by means of broader research on tropical smallholder farming systems, enhancing multi-omics data integration into user-friendly systems for farmers and assessing long-run interactions between climate change, microbial carbon use efficiency, and nutrient cycling in order to develop the means of climate-resilient soil management. Closing these gaps is crucial in tapping into the beneficial role of microbial-mediated nutrient transformation in sustainable soil management.

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