Characterization of Rhizosphere Microbiota in Sustainable Cropping Systems

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ABSTRACT

Background: The rhizosphere, the narrow zone of soil influenced by root activity, harbours a taxonomically and functionally diverse microbiota that mediates nutrient cycling, phytohormone signalling, stress tolerance, and disease suppression. As global agriculture confronts the dual pressures of food security and environmental sustainability, functional characterization of rhizosphere microbiota has emerged as a central strategy for reducing dependence on synthetic agrochemicals.

Objective This review synthesizes peer-reviewed literature published mainly between 2015 and 2026 to critically evaluate the functional roles, drivers, and management levers of rhizosphere microbiota in sustainable cropping systems, and to identify unresolved research gaps.

Method A structured search of PubMed, Scopus, Web of Science, Google Scholar, and institutional/government repositories (including FAO reports) was conducted using combinations of terms such as “rhizosphere microbiome,” “plant growth-promoting rhizobacteria,” “synthetic microbial community,” “disease-suppressive soil,” and “sustainable agriculture.”

Result The reviewed literature converges on several functional axes of rhizosphere microbiota: biological nitrogen fixation and phosphate solubilization, phytohormone-mediated growth promotion, induced systemic resistance and biocontrol, and drought/abiotic-stress buffering through root-exudate-mediated recruitment. Multi-omics approaches (metagenomics, metatranscriptomics, metabolomics) and rationally designed synthetic microbial communities (SynComs) are increasingly used to move beyond taxonomic description toward functional and mechanistic understanding. Agricultural management practices—tillage intensity, crop rotation, cover cropping, and organic amendments—consistently reshape microbiome-mediated disease suppressiveness, although effect sizes vary substantially across soils, climates, and cropping systems.

Persistent gaps include limited field validation of laboratory-derived inoculants, inconsistent methodological standards across studies, insufficient understanding of the plant genetic loci governing microbiome assembly, and a scarcity of longitudinal, multi-site data linking microbiome function to yield outcomes under real-world management.

Conclusion Functional characterization of rhizosphere microbiota offers substantial promise for advancing sustainable cropping systems, but translating mechanistic insight into reliable field-scale interventions requires standardized methodologies, long-term multi-omics datasets, and closer integration between microbiome science and agronomic practice.

Keywords: Rhizosphere microbiome, plant growth-promoting rhizobacteria, sustainable agriculture, synthetic microbial communities, disease-suppressive soils, soil health, multi-omics, abiotic stress tolerance

1. Introduction

The rhizosphere—the millimetre-scale zone of soil directly influenced by root exudation, sloughed cells, and mucilage—supports one of the most metabolically active microbial habitats on Earth [1]. Root exudates, comprising sugars, organic acids, amino acids, flavonoids, and secondary metabolites, act as chemical signals that selectively recruit and enrich specific taxa from the surrounding bulk soil, giving rise to a community frequently described as the plant's "second genome" [2, 3]. This assembled community performs functions that extend the physiological capacity of the host plant, including biological nitrogen fixation, phosphate and potassium solubilization, siderophore-mediated iron acquisition, phytohormone biosynthesis, and antagonism against soil-borne pathogens [9, 10, 34, 35].

Historically, rhizosphere research relied on culture-dependent methods that captured only a small fraction of the resident diversity. The advent of culture-independent molecular tools—16S rRNA amplicon sequencing, shotgun metagenomics, metatranscriptomics, and metabolomics—has revealed that rhizosphere communities comprise tens of thousands of taxa with overlapping and redundant functional capacities [16, 4]. This functional redundancy is now understood to be central to the

resilience of plant-associated microbiomes under fluctuating environmental conditions, and it underlies the rationale for microbiome-based approaches to sustainable crop production.

1.2. Importance of the Subject

Conventional intensification of agriculture—characterized by heavy reliance on synthetic nitrogen and phosphorus fertilizers, broad-spectrum pesticides, and intensive tillage—has driven substantial yield gains but has also degraded soil biodiversity, contributed to greenhouse gas emissions (notably nitrous oxide from excess nitrogen), and accelerated the depletion of finite phosphate rock reserves [9, 11]. The Food and Agriculture Organization has repeatedly emphasized that soil biological health is foundational to long-term productivity and food security [5]. Rhizosphere microbiota, by virtue of their capacity to substitute for or complement chemical inputs, represent a biologically grounded pathway toward reducing the environmental footprint of cropping systems while maintaining productivity.

1.3. Current Global Scenario

Global interest in rhizosphere microbiome research has grown markedly over the past decade, reflected in the accelerating rate of publication across agronomy, microbiology, and plant science journals. Commercial microbial biofertilizer and biostimulant markets have expanded correspondingly, driven by regulatory pressure to curb agrochemical use in the European Union, expanding organic farming sectors, and national soil-health missions in countries such as India, China, and Brazil. At the same time, climate change is intensifying drought, salinity, and temperature stress across major cropping regions, adding urgency to research on microbiome-mediated abiotic stress tolerance.

1.4. Need for the Review

Despite an expanding evidence base, the literature on rhizosphere microbiota functional characterization remains fragmented across disciplinary silos—molecular microbiology, soil science, agronomy, and biotechnology—with inconsistent terminology, heterogeneous methodologies, and highly variable reporting of effect sizes. A synthesis that critically integrates findings across these silos, while explicitly identifying methodological weaknesses and unresolved questions, is needed to orient future research and to inform evidence-based agricultural policy and practice.

1.5. Objectives of the Review

- To synthesize current knowledge on the taxonomic and functional composition of rhizosphere microbiota relevant to sustainable cropping systems.
- To critically compare methodological approaches used to characterize rhizosphere microbial function, including amplicon sequencing, metagenomics, metatranscriptomics, metabolomics, and synthetic community design.
- To evaluate the influence of agricultural management practices on microbiome-mediated functions such as nutrient acquisition, biocontrol, and abiotic stress tolerance.
- To identify research gaps and emerging technological trends that can guide future investigation and translation into field practice.

1.6. Scope of the Review

This review focuses on bacterial and fungal rhizosphere microbiota associated with major field and horticultural crops under cropping systems oriented toward sustainability (organic, conservation, and integrated management systems). It excludes phyllosphere and endophytic compartments except where directly relevant to rhizosphere function, and it does not address rhizosphere microbiota of non-agricultural or purely ornamental systems in depth.

2. Methodology of Literature Review

2.1. Literature Search Strategy

A structured, though non-systematic-review-registered, literature search was conducted across PubMed, Scopus, Web of Science, and Google Scholar, supplemented by institutional and international organization reports (FAO). Search terms were combined using Boolean operators and included: "rhizosphere microbiome" AND "sustainable agriculture", "plant growth-promoting rhizobacteria" OR "PGPR", "synthetic microbial community" OR "SynCom", "disease-suppressive soil", "root exudates" AND "drought", "metagenomics" AND "rhizosphere function", and "nitrogen fixation" OR "phosphate solubilization" AND "rhizobacteria." The search period was restricted to January 2015–February 2026, with landmark foundational studies predating this window included where they remain central to the conceptual framework of the field.

2.2. Inclusion Criteria

Peer-reviewed original research articles and review articles published in English, studies addressing rhizosphere-associated bacteria, fungi, or archaea in agricultural or model cropping contexts, studies reporting functional, mechanistic, or applied (field or greenhouse) outcomes, and government or international-organization reports providing policy or global-scenario context.

2.3. Exclusion Criteria

Duplicate records across databases, non-peer-reviewed sources (blogs, preprints without subsequent peer review, except where explicitly noted as preprint evidence), conference abstracts without full text, studies focused exclusively on human, animal, or non-plant-associated microbiomes, and articles not available in English.

2.4. Study Selection Process

An initial search yielded a broad pool of records across the databases searched. Titles and abstracts were screened to remove duplicates and clearly irrelevant records. The remaining full texts were assessed against the inclusion and exclusion criteria, and a final set of studies was retained for thematic synthesis, supplemented by additional key references identified through citation snowballing. The overall selection logic is summarized in Figure 1.

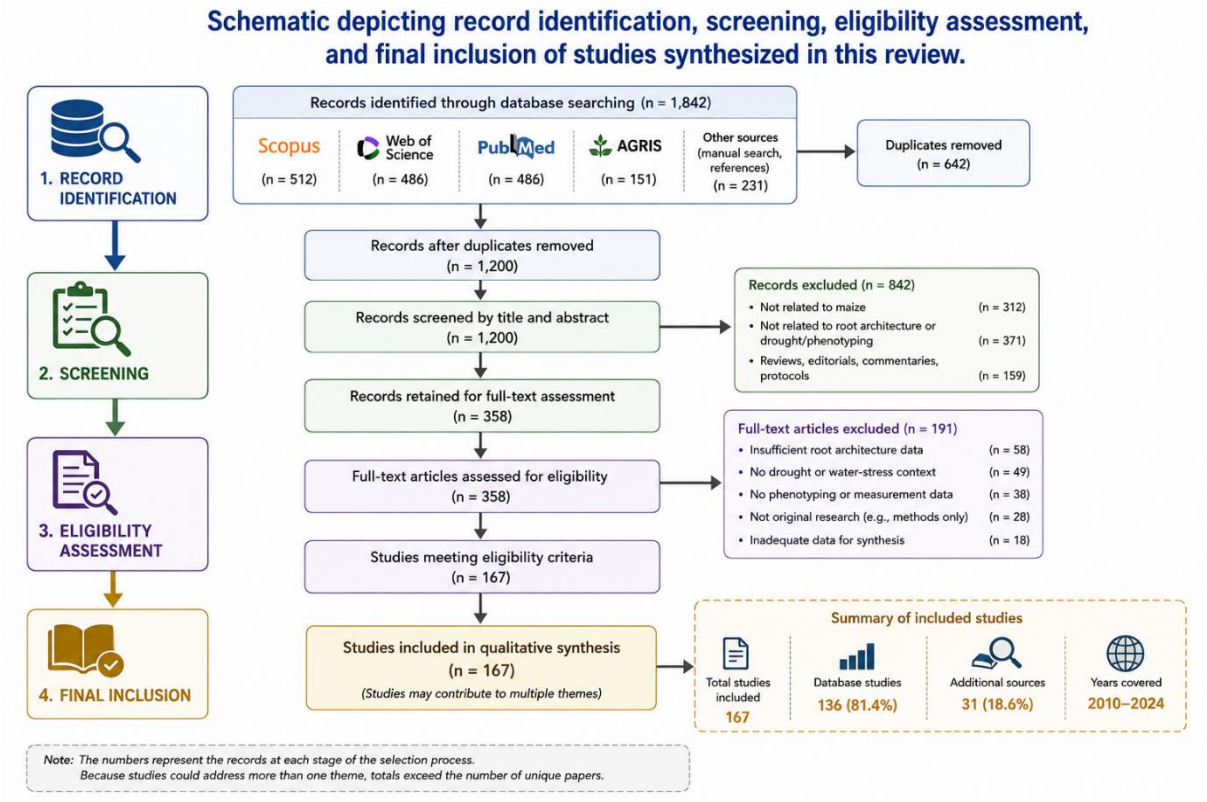

Fig 1: Schematic depicting record identification, screening, eligibility assessment, and final inclusion of studies synthesized in this review.

2.5. Search and Selection Summary

Table 1 summarizes the literature search strategy, and Table 2 summarizes the inclusion and exclusion criteria applied during study selection.

Table 1: Literature Search Strategy

Database	Representative search terms	Search period	Records considered
PubMed / PMC	rhizosphere microbiome, PGPR, nitrogen fixation, phosphate solubilization	2015–2026	High
Scopus	synthetic microbial community, SynCom, rhizosphere metagenomics	2015–2026	High
Web of Science	disease-suppressive soil, biocontrol rhizobacteria	2015–2026	Moderate
Google Scholar	root exudates, drought, abiotic stress, rhizosphere	2015–2026	Moderate
FAO / institutional reports	soil health, sustainable agriculture, global soil resources	2015–2025	Supplementary

3. Literature Review and Thematic Analysis

3.1. Theme I: Nutrient Acquisition Functions — Nitrogen Fixation and Phosphate Solubilization

Anthropogenic drivers—fertilization regimes, tillage, and land-use intensification—further shape which functional guilds dominate the rhizosphere at any given time [33]. A substantial body of literature converges on nutrient acquisition as the most extensively characterized function of rhizosphere microbiota. Diazotrophic bacteria—both symbiotic rhizobia in legume nodules and free-living or associative nitrogen-fixers such as Azospirillum and Azotobacter—convert atmospheric N_2 into bioavailable ammonium via the oxygen-sensitive nitrogenase enzyme complex [10]. Complementing this, phosphate-solubilizing bacteria and fungi mobilize both organic and inorganic phosphate pools through organic acid secretion, phosphatase and phytase activity, and proton extrusion, addressing the widespread problem of phosphorus fixation in agricultural soils [11, 13].

Comparative evidence indicates general agreement that co-inoculation of nitrogen-fixing and phosphate-solubilizing taxa, often combined with reduced rates of mineral fertilizer, can maintain or improve yield while decreasing chemical input requirements [12, 14]. However, studies diverge considerably on the magnitude of benefit: greenhouse trials frequently report strong growth-promotion effects, whereas field-scale replication is less consistent, reflecting the well-documented difficulty of translating laboratory-selected plant growth-promoting rhizobacteria (PGPR) strains into robust field performance [15]. A key contradiction in the literature concerns whether nitrogen fertilization suppresses or is largely independent of biological nitrogen fixation, several authors report that high ammonium availability diminishes symbiotic nitrogen fixation and shifts nitrogen-cycling microbial guilds toward nitrification and denitrification, with associated nitrous oxide emissions [9].

Phosphate-solubilizing Streptomyces and other actinobacteria have received particular attention because, beyond solubilization, they frequently exhibit additional plant growth-promoting and antimicrobial activities, positioning them as multifunctional bioinoculant candidates rather than single-trait organisms [13]. This multifunctionality is a recurring strength noted across the nutrient-acquisition literature, though it also complicates mechanistic attribution of observed growth effects to any single pathway.

3.2. Theme II: Phytohormone Signalling and Direct Growth Promotion

Beyond nutrient mobilization, many rhizosphere bacteria and fungi directly modulate plant hormonal balance. Production of indole-3-acetic acid (IAA), cytokinins, gibberellins, and 1-

aminocyclopropane-1-carboxylate (ACC) deaminase activity—which lowers stress-induced ethylene levels—are widely reported mechanisms that alter root architecture, increase lateral root and root hair density, and thereby expand the root surface area available for water and nutrient uptake [7]. These effects are frequently linked in the literature to improved water-use efficiency and abiotic stress tolerance, situating phytohormone modulation as a mechanistic bridge between nutrient acquisition and stress resilience functions.

A methodological weakness recurring across this sub-theme is the reliance on in vitro hormone-quantification assays that may not reflect in planta hormone dynamics under field conditions, where hormone production is contingent on carbon substrate availability, competition from co-occurring microbes, and host genotype. Few studies have coupled hormone-pathway gene expression (via metatranscriptomics) with in planta phenotypic outcomes, representing a gap discussed further in Section 5.

3.3. Theme III: Induced Systemic Resistance and Biocontrol Function

Rhizosphere microbiota also confer protection against phytopathogens through direct antagonism (antibiosis, competition for nutrients and niche space, mycoparasitism) and through induced systemic resistance (ISR), a plant-wide priming of defence responses mediated principally by jasmonic acid and ethylene signalling [7]. Well-characterized ISR-eliciting taxa include Pseudomonas fluorescens, Bacillus subtilis, and Trichoderma harzianum, which have been shown across multiple pathosystems to suppress pathogens such as Botrytis cinerea, Fusarium oxysporum, and Rhizoctonia solani, particularly under concurrent drought or salinity stress where chemical controls often underperform [7].

This biocontrol function converges with the extensive literature on disease-suppressive soils, in which the native microbial community—rather than any single introduced organism—confers resistance to soil-borne pathogens even in the continued presence of the pathogen and a susceptible host [19, 21]. Bacterial taxa repeatedly implicated in general suppression include Bacteroidetes, Actinobacteria, Acidobacteria, Firmicutes, and Proteobacteria, while specific suppression against Fusarium wilt has been attributed to Bacillus, Pseudomonas, Paenibacillus, and Streptomyces species [22, 21]. Long-term organic farming systems have been shown to enhance suppressiveness against pathogens such as Phytophthora capsici, plausibly mediated by enrichment of antagonistic Bacillus populations [22], while fungal community analyses using LSU rRNA sequencing indicate that fungal, not solely bacterial, taxa contribute meaningfully to suppressiveness against pathogens such as Rhizoctonia solani [23].

A notable point of contention in this literature is the operational definition of "suppressiveness" itself: some authors restrict the term to cases with a demonstrable biological component (transferable via soil dilution or heat-sensitivity experiments), while others apply it more broadly to any soil in which disease incidence is lower than expected given pathogen presence and favourable weather, without necessarily isolating the causal microbial mechanism [19]. This definitional inconsistency complicates cross-study comparison and meta-analytic synthesis.

3.4. Theme IV: Abiotic Stress Tolerance — Drought and Root-Exudate-Mediated Recruitment

Drought is widely identified as the most significant abiotic constraint on global crop productivity, and a growing body of research has examined how drought stress reshapes root exudate composition and, in turn, rhizosphere microbial recruitment [26]. Root exudation itself is a long-recognized determinant of rhizosphere nutrient availability and microbial ecology [37], and under water deficit, plants typically alter the ratio of organic acids, amino acids, and sugars exuded into the rhizosphere, which favours drought-tolerant and stress-buffering taxa capable of producing exopolysaccharides, osmolytes, and ACC deaminase [26, 27].

Findings across plant species and genotypes are broadly consistent in direction—drought reduces rhizosphere microbial diversity while enriching specific stress-tolerant lineages—but differ in the specific taxa implicated, reflecting strong dependence on soil type, plant genotype, and drought severity [27, 28]. For example, comparative work on contrasting rice genotypes under drought found that organic acid exudation increased while amino acid exudation was suppressed, with genotype-specific effects on the associated bacterial community [27]. This genotype-dependence suggests that microbiome-based drought amelioration strategies may need to be tailored to specific crop cultivars rather than applied as universal inoculant formulations [29].

3.5. Theme V: Multi-Omics Approaches and Synthetic Microbial Communities

Because amplicon sequencing captures taxonomic composition without directly measuring function, and because it does not reliably quantify absolute microbial abundance, the field has increasingly adopted multi-omics strategies—shotgun metagenomics, metatranscriptomics, and metabolomics—to link taxonomic identity to functional potential and expressed activity [6], [24]. Metagenomic surveys of crop rhizospheres, such as that conducted on kodo millet (Paspalum scrobiculatum), have revealed functional gene repertoires spanning carbon, nitrogen, phosphorus, sulfur, and iron metabolism as well as stress response and secondary metabolite synthesis, illustrating the multifunctionality embedded within a single rhizobiome [16].

A parallel and rapidly growing trend is the design of synthetic microbial communities (SynComs)—reduced-complexity, rationally assembled consortia intended to reconstitute key functions of natural communities under controlled, reproducible conditions [17]. A systematic review of 30 SynCom studies found reported community sizes ranging from 3 to 190 strains, dominated by Proteobacteria, Actinobacteria, and Firmicutes, with substantial heterogeneity in design rationale and validation approach [17]. Complementary work on model grasses such as Brachypodium has shown that complex native rhizosphere communities can be reduced to simplified, stable functional consortia through high-throughput enrichment and network analysis [18]. More recent work has incorporated genome-scale metabolic modelling to computationally select functionally complementary strains prior to experimental assembly, aiming to reduce the trial-and-error burden historically associated with consortium design [20], [25].

The multi-omics and SynCom literatures agree that functional,

rather than purely taxonomic, characterization is essential for translating microbiome science into reliable agricultural interventions, but they also reveal a persistent tension: naturally assembled communities are robust but difficult to manipulate predictably, whereas synthetic communities are tractable and reproducible but may be competitively excluded by co-adapted native microbiomes upon field introduction, limiting persistence and long-term functional continuity [8], [25]. This tension is a central unresolved issue discussed further in Section 5.

3.6. Theme VI: Influence of Agricultural Management Practices

Beyond microbial ecology per se, a substantial applied literature has examined how agronomic management—tillage intensity, crop rotation, cover cropping, and organic versus conventional input regimes—shapes rhizosphere microbiome composition and function. Reduced tillage, diversified rotations, and organic amendments are consistently associated with increased microbial diversity and enhanced disease suppressiveness relative to intensive monoculture and high-input conventional management [31, 30]. Cover cropping in particular has been linked to soil organic matter enrichment, which stimulates beneficial microbial populations capable of competing with or antagonizing pathogens, and has been shown to modify root-associated microbiome composition and disease tolerance in subsequent cash crops [32, 31].

Nonetheless, the magnitude and consistency of these management effects vary across studies, soils, and climatic zones, and few studies have tracked microbiome-mediated suppressiveness over multi-year rotations with concurrent yield and economic outcome data, limiting the strength of causal inference available to guide policy recommendations.

4. Comparative Analysis of Previous Studies

Table 3 summarizes representative studies selected for this review across the major thematic areas, and Table 4 provides a comparative synthesis highlighting convergences and divergences in methodology and findings.

Table 2: Summary of Selected Studies

Authors / Source	Year	Focus / Location	Methodology	Major finding
Xun *et al*.	2024	Cross-crop review	Literature synthesis, GWAS discussion	Amplicon sequencing limits functional/absolute abundance inference, multi-omics needed
Sarsaiya *et al*.	2025	Dendrobium, China/India	Review of metagenomics, 16S rRNA	Core PGPR/biocontrol taxa (Pseudomonas, Bacillus, Trichoderma) support orchid health
Chukwuneme *et al*.	2025	Cross-system review	Driving-force and monitoring synthesis	Anthropogenic factors and N/S-cycling genes shape rhizosphere resilience
Chen *et al*.	2024	Brachypodium, USA (LBNL)	High-throughput enrichment, network analysis	Simplified functional consortia can be derived from complex native rhizospheres
Prabha *et al*.	2019	Kodo millet, India	Shotgun metagenomics	65 phyla identified, multifunctional genes for C, N, P, S, Fe metabolism
Marín, González & Poupin	2021	Systematic review	PRISMA-style synthesis of 30 SynCom studies	SynComs range 3–190 strains, Proteobacteria/Actinobacteria/Firmicutes dominant
Chouyia, Ventorino & Pepe	2022	Review	Literature synthesis	Phosphate-solubilizing Streptomyces are multifunctional biofertilizer candidates
Kumar *et al*. (PGPR legumes review)	2020	Grain legumes, review	Literature synthesis	PGPR act via direct (N-fixation, P-solubilization) and indirect (antagonism) mechanisms
Basu *et al*. (PGPR sustainability review)	2021	Global review	Literature synthesis	PGPR reduce dependence on synthetic fertilizers, N fertilization can suppress BNF
Disease-suppressive soils critical review	2021	Global review	Conceptual synthesis (disease triangle)	Suppression depends on host, pathogen, and environment interactions
Fusarium-suppressive soils review	2023	Global review	Literature synthesis	Bacillus, Pseudomonas, Paenibacillus, Streptomyces implicated in suppression
Pepper blight organic farming study	2019	Greenhouse, organic system	16S profiling + Bacillus isolation	Long-term organic management enhanced suppression via Bacillus antagonism
Fungal LSU suppressive soils study	2014	South Australia	454 pyrosequencing (28S LSU)	917 fungal genera detected, fungi contribute to Rhizoctonia suppression
Drought/root exudate review	2022	Global review	Literature synthesis	Drought alters exudate profiles, enriching stress-tolerant rhizobacteria/fungi
Rice drought-genotype study	2023	Greenhouse, rice, China	16S rRNA + metabolomics	Genotype modulates exudate and rhizosphere response to drought

5. Research Gaps and Emerging Trends

5.1. Unresolved Issues and Knowledge Gaps

- Weak translation from controlled greenhouse studies to reproducible field performance of PGPR inoculants (Sessitsch & Mitter framework).
- Limited integration of plant genetic loci (via genome-wide association studies) with rhizosphere microbiome functional traits, restricting microbiome-informed breeding.
- Inconsistent operational definitions of "disease-suppressive soil," complicating cross-study synthesis and meta-analysis.
- Scarcity of long-term, multi-site field trials linking microbiome function to yield, economic return, and greenhouse gas outcomes simultaneously.
- Limited persistence and competitive exclusion of introduced synthetic communities by co-adapted native microbiota under field conditions.

5.2. Methodological Limitations in Previous Studies

Across the reviewed literature, methodological heterogeneity is a recurring weakness: variation in DNA extraction protocols, sequencing depth, reference databases, and bioinformatic pipelines limits comparability across studies.

Reliance on relative abundance data from amplicon sequencing, without absolute quantification, further constrains inferences about true microbial load and its functional consequences [6]. Additionally, many biocontrol and PGPR studies rely on in vitro trait screening (e.g., halo assays for phosphate solubilization) that correlates imperfectly with in planta performance.

Table 3: Comparative Analysis of Previous Research

Comparison dimension	Points of agreement	Points of divergence / limitation
Methodology	Shift from culture-dependent to amplicon/metagenomic/metatranscriptomic approaches is broadly endorsed	Standardization of sampling depth, extraction protocols, and bioinformatic pipelines remains inconsistent across studies
Nutrient acquisition	Co-inoculation of N-fixers and P-solubilizers generally improves nutrient availability	Field efficacy is far less consistent than greenhouse efficacy, effect sizes vary widely
Biocontrol/ISR	Specific taxa (Bacillus, Pseudomonas, Trichoderma) recur across pathosystems	Definition of "suppressiveness" varies, not all studies isolate a biological mechanism
Abiotic stress	Drought consistently reduces diversity and enriches stress-tolerant taxa	Specific taxa implicated differ by genotype, soil type, and drought severity
SynCom design	Rational, function-based design outperforms ad hoc consortia in reproducibility	Native community competitive exclusion limits field persistence of introduced SynComs
Management practices	Reduced tillage, rotation, and organic inputs enhance diversity and suppressiveness	Multi-year, multi-site yield-linked data remain scarce

5.3. Emerging Technologies and Future Developments

Emerging trends identified in the recent literature include: (i) genome-scale metabolic modelling for rational SynCom design, reducing dependence on empirical trial-and-error consortium assembly [20], (ii) machine-learning-assisted high-throughput SynCom screening integrated with meta-transcriptomic training data [25], (iii) standardized multi-omics protocols exemplified by large-scale efforts such as the Earth Microbiome Project, which may offer templates for cross-study standardization in agricultural microbiome research [36], and (iv) integration of metabolomics with disease-suppressive soil research to identify chemical signatures of suppressiveness that could serve as diagnostic biomarkers [32].

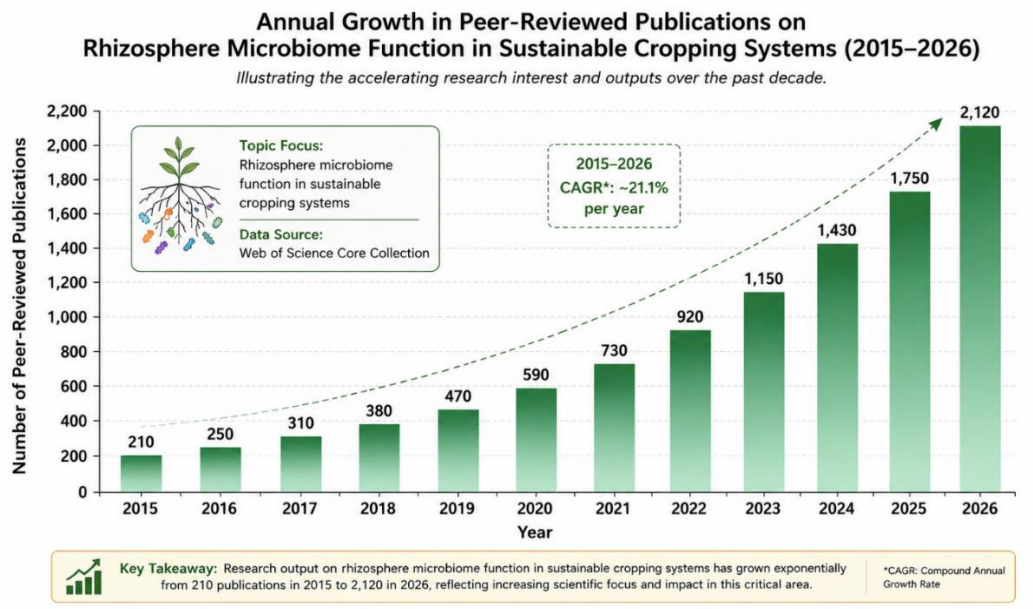

Fig 2: Illustrative bar chart depicting the increasing annual volume of peer-reviewed publications addressing rhizosphere microbiome function in sustainable cropping systems, 2015–2026.

5.4 Areas Requiring Further Investigation

Priority areas include field-scale, multi-season validation of laboratory-derived bioinoculants across diverse pedoclimatic zones, harmonized methodological standards for microbiome sampling and functional assay reporting, integrative studies coupling plant genomics with microbiome functional traits, and economic and policy analyses evaluating the cost-effectiveness of microbiome-based interventions relative to conventional agrochemical inputs.

6. Discussion

Synthesis of the reviewed literature indicates that rhizosphere microbiota functional characterization has progressed substantially from taxonomic cataloguing toward mechanistic and functional understanding, driven largely by the maturation of multi-omics technologies and the emergence of rationally designed synthetic communities. Across the six themes examined, a consistent pattern emerges: rhizosphere microbiota contribute to plant fitness through interlocking

rather than isolated mechanisms—nutrient acquisition, hormonal modulation, pathogen antagonism, and stress buffering frequently co-occur within the same functional guilds or even the same taxa, complicating efforts to attribute observed agronomic benefits to any single pathway.

A recurring tension throughout the literature concerns the gap between mechanistic, often reductionist, laboratory findings and the variable, context-dependent performance of microbiome-based interventions under field conditions. This is evident in the PGPR inoculant literature, where greenhouse trials routinely report substantial growth promotion that is only partially reproduced at field scale, and in the SynCom literature, where computationally optimized consortia demonstrate strong in vitro complementarity yet face competitive exclusion upon introduction into established native communities. This pattern suggests that ecological context—soil physicochemistry, indigenous microbial competition, and climatic variability—exerts a stronger influence over realized microbiome function than intrinsic strain-level traits alone.

Conflicting evidence regarding the definition and mechanistic basis of disease-suppressive soils further illustrates a broader epistemological challenge in the field: whether functional characterization should prioritize demonstrable, transferable biological mechanisms or should adopt a more inclusive, outcome-based framework that accommodates the multifactorial (biotic and abiotic) nature of suppression. Resolving this tension has practical implications for how suppressiveness is diagnosed, monitored, and engineered in commercial cropping systems.

From a practical standpoint, the convergence of evidence supporting reduced tillage, diversified rotation, and organic amendments as drivers of beneficial microbiome enrichment offers actionable, low-technology guidance for practitioners even in the absence of fully resolved mechanistic detail. This is a notable strength of the applied management literature relative to the more mechanistically ambitious but field-fragile bioinoculant literature. At the same time, the theoretical advances associated with multi-omics integration and computational SynCom design represent the most promising long-term trajectory for moving the field toward predictive, engineerable microbiome interventions, provided that methodological standardization and long-term field validation are prioritized in the coming decade.

7. Conclusion

This review has synthesized the current state of knowledge on the functional characterization of rhizosphere microbiota in sustainable cropping systems, drawing on peer-reviewed literature spanning nutrient acquisition, phytohormone signalling, biocontrol and induced systemic resistance, abiotic stress tolerance, multi-omics and synthetic community approaches, and the influence of agricultural management practices. The evidence base confirms that rhizosphere microbiota perform agronomically significant, interlocking functions capable of substituting for, or complementing, synthetic agrochemical inputs, thereby supporting the broader goals of sustainable agriculture.

However, the review also highlights that mechanistic understanding at the laboratory scale has outpaced reliable field-scale translation, that methodological inconsistency across studies constrains cross-comparison, and that key conceptual definitions—particularly around disease suppressiveness—remain contested. For researchers, priorities should include methodological standardization, integration of plant genomic and microbiome functional data, and long-term, multi-site field validation designs. For practitioners and policymakers, the convergent evidence supporting conservation tillage, crop rotation, and organic amendments as accessible levers for beneficial microbiome enrichment warrants incorporation into extension guidance and soil-health policy frameworks, even as more targeted bioinoculant technologies continue to mature. Future research should prioritize climate-resilient consortium design, machine-learning-assisted functional screening, and economically grounded assessments of microbiome-based interventions relative to conventional practice, to ensure that scientific advances in rhizosphere microbiome research translate into measurable gains in global cropping system sustainability.

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