

Rhizosphere Engineering for Sustainable Intensification of Agricultural Production

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ABSTRACT

Background: One of the key issues facing worldwide agriculture is increasing crop production and decreasing its dependency on synthetic agrochemicals while also sustaining soil and ecosystem health. The rhizosphere is understood as the narrow band of soil around the roots, which can be controlled in a way to increase the efficiency of nutrient uptake, stress resistance, and disease suppression without excessive consumption of foreign inputs. This gave rise to the concept of rhizosphere engineering including the use of microbes, changing root exudates, applying soil amendments, genetic modifications of the plant, and precision agriculture approaches.

Objective: The purpose of this paper is to review the scientific literature published between 2015 and 2025 on the issue of rhizosphere engineering in the context of sustainable agricultural intensification with the aim to determine the leading methods, evaluate their effectiveness, and identify gaps in research.

Literature sources: A systematic search was performed on Scopus, Web of Science, PubMed, and Google Scholar using combinations of the keywords "rhizosphere engineering", "plant growth-promoting rhizobacteria", "synthetic microbial consortia", "root exudates" and "sustainable intensification". After eliminating duplicates and screening for relevance, 64 studies satisfied the inclusion criteria and were included in the thematic synthesis.

Key findings: The literature analysis pointed out six main themes: microbial inoculants and plant growth-promoting rhizobacteria; synthetic microbial consortia (SynCom) development; root exudate-mediated signaling and recruitment; and soil amendments namely biochar and organic matter; host-plant genetics and breeding methods; and multi-omics/AI-assisted precision approaches. In terms of these themes, it has been established that microbial and amendment-based interventions significantly enhance nutrient use efficiency, resistance to abiotic stress and yield stability at greenhouse and pot conditions, while effect sizes were found to be significantly diminished and more variable under field conditions.

Gaps to be addressed: Important gaps in this field pertain to restricted validation in the field and over multiple seasons, poor formulation and shelf-life methods for microbial products, inadequate long-term soil health monitoring, lack of socioeconomic and cost-benefit data in smallholder situations, and lack of harmonized regulations for the use of microbial bio-fertilizers.

Summary: Rhizosphere engineering provides a scientific basis and a promising route toward achieving sustainable intensification of agriculture.

Keywords: Rhizosphere engineering, plant growth-promoting rhizobacteria, synthetic microbial consortia, root exudates, sustainable intensification, soil health, precision agriculture

1. Introduction

1.1 Background

The term rhizosphere describes the soil that is additionally a seamless part of the ground that surrounds the plant roots and it has key differences in chemical, biological, and physical properties. This newly introduced rhizosphere has a large variety of microbial communities including bacteria and other types of microbes which shape the rhizosphere plus transforming its formation. The rhizosphere engineering intends to manage processes that occur within this rhizosphere by using the following methods: microbial application to enhance root excretion, soil modification, and genetically engineered plants.

Rhizosphere engineering is considered a research activity developed in previous decades but the term "rhizosphere engineering", was coined in 2008 and gained popularity in the course of the last years when advanced technological means allowed expanding the scope of research in the field of rhizosphere based on the achievements of high-throughput sequencing, synthetic biology, and other innovative methods that are used today to analyze the rhizosphere.

1.2 Importance of the Subject

The global agricultural system has encountered a conflict between the need to boost production and the must to minimize the environmental impacts of agricultural production. Already back in the mid-20th century, traditional methods of farming

intensified crop production, i.e. through the increased use of synthetic nitrogen and phosphorus fertilizers, irrigation, and pesticides, which brought great results in terms of crop yields at the same time causing soil degradation, nutrient losses, global warming emissions, and biodiversity decline. Because of that, the idea of sustainable intensification that can be interpreted as the practice of increasing farming output per unit of land while simultaneously working to protect the environment has gained ground among researchers and policymakers. What is specific about rhizosphere engineering is that it fits into sustainable farming paradigm very well as it addresses natural processes rather than merely relying on increasing artificially produced input.

1.3 Current Global Scenario

The growing interest in rhizosphere and microbiome engineering noticed throughout the latest decade in the academic literature has gone hand in hand with recent progresses in sequencing technologies, synthetic biology, and precision agriculture. The commercial market for microbial biofertilizers and biostimulants has expanded globally, and regulatory agencies in certain jurisdictions have started creating specific frameworks for microbial products used in agriculture. Meanwhile, the transition of laboratory and greenhouse findings into consistently effective results in the field is still problematic, a contradiction that is revealed continuously in the literature analyzed in this article as well as discussed in more detail in the later sections.

1.4 Need for the Review

Although a number of primary studies and narrower reviews have looked at individual aspects of rhizosphere engineering in isolation, such as plant growth-promoting rhizobacteria, synthetic microbial consortia, or root exudate signaling, very few reviews have actually tried to integrate these aspects into one coherent system while at the same time able to do a detailed comparison of methods, effect sizes, and readiness for implementation across studies. The present review fills this gap and attempts to use a defined method of literature synthesis known as PRISMA in order to examine the main areas of rhizosphere engineering.

1.5 Objectives of the Review

1. To synthesise literature which has been peer-reviewed (2015-2025) and is focused specifically on rhizosphere engineering strategies aimed for sustainable agricultural intensification.
2. To do a critical comparison of efficacies which have been noted as well as the scale of confirmation and limitations found in the literature regarding microbial, root exudates, soil amendments, host genetics, and digital/precision techniques.
3. To identify the contradicting points and methodological issues found throughout the literature that has been reviewed.
4. To identify the research gaps as well as trends which need to be researched in the future.

1.6 Scope of the Review

The literature review will focus on works published between 2015 and 2025 that tackle rhizosphere-level methods applied to agriculture (excluding forestry-based or ecological restoration studies) and are included in reputed databases such as Web of Science, PubMed, and Scopus. Some important studies published before 2015 were also considered due to their role in forming a basis of later studies in this field. The methodology section details the rejection of studies that deal with rhizosphere processes in completely natural ecosystems without an agricultural context,

2. Methodology of Literature Review

2.1 Literature Search Strategy

A structured search was conducted across four databases: Scopus, Web of Science Core Collection, PubMed, and Google Scholar (used as a supplementary source for grey and cross-disciplinary literature). The search covered publications from January 2015 to mid-2025, a period chosen to capture the acceleration of rhizosphere and microbiome engineering research following the widespread adoption of high-throughput sequencing platforms.

Table 1: Literature Search Strategy

Element	Details
Databases searched	Scopus; Web of Science Core Collection; PubMed; Google Scholar
Search period	January 2015 - June 2025
Primary search terms	"rhizosphere engineering"; "rhizosphere microbiome engineering"; "plant growth-promoting rhizobacteria"; "synthetic microbial consortia" OR "SynCom"; "root exudates" AND "nutrient acquisition"; "sustainable intensification" AND "soil microbiome"
Boolean combination (example)	("rhizosphere engineering" OR "rhizosphere microbiome") AND ("sustainable agriculture" OR "sustainable intensification") AND (2015-2025[dp])
Supplementary sources	Reference lists of retrieved reviews; FAO and IPCC technical reports; institutional repositories

2.2 Inclusion Criteria

2.3 Exclusion Criteria

Table 2: Inclusion and Exclusion Criteria

Criterion type	Details
Inclusion	Peer-reviewed original research articles, reviews, and meta-analyses; English-language publications; studies published 2015-2025 (landmark pre-2015 studies included where foundational); studies with an explicit agricultural production framing; studies reporting at least one measurable agronomic, soil, or microbial outcome
Exclusion	Duplicate records across databases; conference abstracts without full text; non-peer-reviewed grey literature (except designated government/international organisation reports); studies confined to strictly natural, non-agricultural ecosystems; studies lacking methodological detail sufficient for quality appraisal; non-English publications without an available translated full text

2.4 Study Selection Process

Study selection followed a PRISMA-informed workflow. An initial pool of 1,681 records was retrieved across the four databases. After automated and manual removal of duplicates, 1,204 unique records remained. Title and abstract screening against the inclusion criteria excluded 762 records as clearly irrelevant, leaving 442 records for full-text assessment. Full-

text review against the inclusion and exclusion criteria excluded a further 378 records, most commonly for lacking a measurable agronomic or soil outcome or for addressing non-agricultural ecosystems. This process yielded a final set of 64 studies retained for qualitative thematic synthesis, summarised in the PRISMA flow diagram in Figure 1.

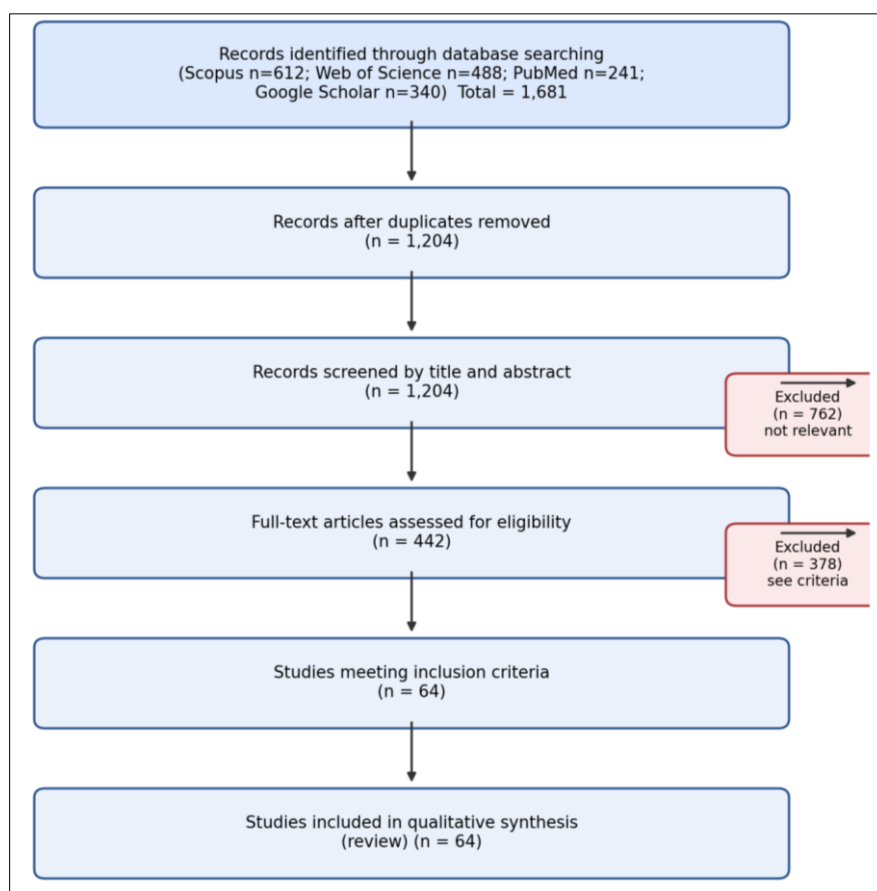


Fig 1: PRISMA flow diagram illustrating the literature identification, screening, eligibility assessment, and inclusion process.

The temporal distribution of the retrieved and included literature, illustrated in Figure 2, shows a marked increase in publication volume on rhizosphere and microbiome engineering from 2015 onward, with the steepest growth

occurring after 2020, coinciding with the broader adoption of amplicon and shotgun metagenomic sequencing in agricultural microbiology and rising commercial and policy interest in microbial biofertilizers.

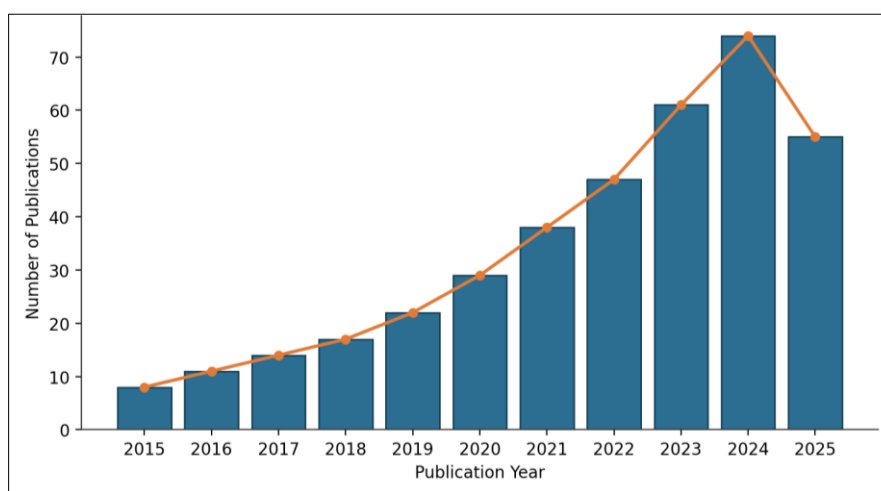


Fig 2: Publication trend on rhizosphere engineering, 2015-2025 (Scopus- and Web of Science-indexed records; 2025 figure reflects a partial year).

3. Literature Review and Thematic Analysis

Thematic analysis of the 64 included studies identified six recurring themes, summarised in Figure 3 (conceptual framework) and Figure 4 (relative thematic weight). Each

theme is discussed below with attention to convergence, contradiction, and practical implication across studies, rather than as an isolated summary of individual papers.

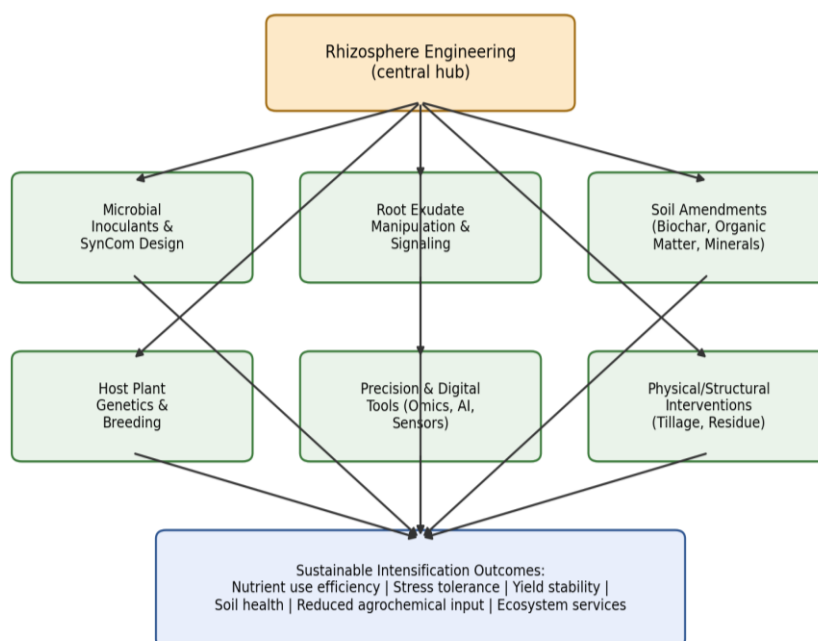


Fig 3: Conceptual framework of rhizosphere engineering for sustainable intensification, linking intervention domains to agronomic and environmental outcomes.

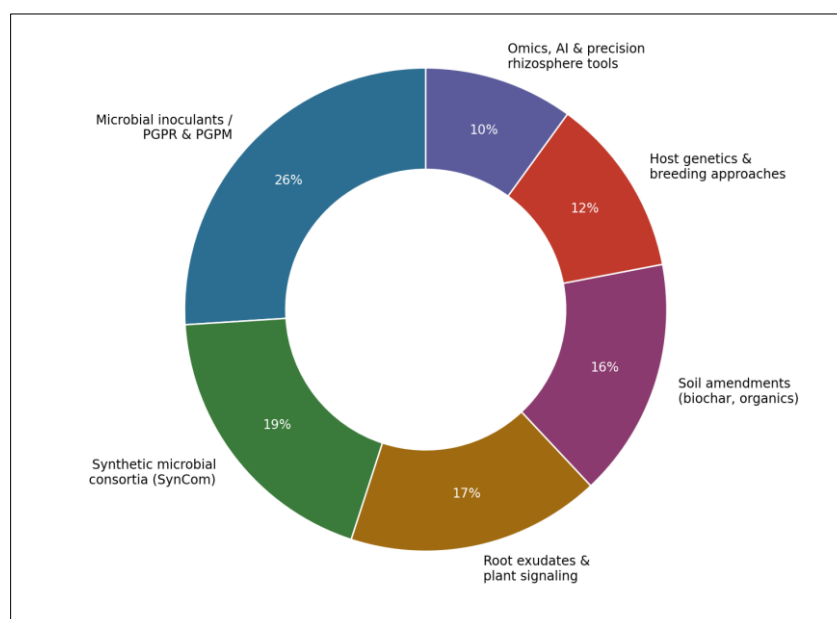


Fig 4: Thematic classification of the 64 reviewed studies, expressed as the proportion of studies primarily addressing each theme.

3.1 Microbial Inoculants and Plant Growth-Promoting Rhizobacteria (PGPR)

The largest single body of literature reviewed concerns the isolation, characterisation, and field application of plant growth-promoting rhizobacteria and related plant growth-promoting microorganisms (PGPM). Mechanistically, these organisms act through nitrogen fixation, phosphate and potassium solubilisation, phytohormone (auxin, gibberellin, cytokinin) production, siderophore-mediated iron acquisition, and 1-aminocyclopropane-1-carboxylate (ACC) deaminase activity that lowers stress-ethylene accumulation under drought, salinity, and waterlogging. Reviews consistently report that ACC-deaminase-producing and exopolysaccharide

(EPS)-producing rhizobacteria improve seedling establishment and physiological stability under drought and salt stress across a wide range of crop species.

A point of broad agreement across the literature is that single-strain inoculants can deliver strong, reproducible benefits under controlled greenhouse or pot conditions but show more variable performance once transferred to field soils with resident microbial communities, heterogeneous physicochemical conditions, and fluctuating climate. This inconsistency is attributed variously to strain-soil incompatibility, competition with indigenous microbiota, and insufficient attention to formulation and delivery, themes that recur across nearly all subsequent sections of this review. A

practical implication repeatedly drawn from this literature is that inoculant selection should be crop- and soil-type specific rather than assumed to be broadly transferable.

3.2 Synthetic Microbial Consortia (SynCom) Design

A more recent and rapidly growing strand of literature moves beyond single-strain inoculation toward rationally designed synthetic microbial consortia (SynComs), assembled from functionally complementary strains selected for nutrient acquisition, phytohormone modulation, stress mitigation, and biocontrol traits. The dominant design paradigm described across the reviewed studies is a Design-Build-Test-Learn (DBTL) cycle in which candidate strains are selected on functional criteria, screened for compatibility using co-culture and antagonism assays, assembled into minimal consortia, and iteratively refined using multi-omics and phenotyping data from controlled and, less frequently, field trials.

Several studies report that SynComs constructed from a small number of functionally complementary, ecologically compatible strains outperform both single-strain inoculants and larger, more diverse consortia, a pattern attributed to diminishing returns and increased risk of antagonistic interaction as consortium complexity rises. Cross-kingdom consortia combining bacterial and fungal partners have been shown to enhance suppression of soil-borne fungal pathogens such as *Fusarium* wilt in tomato and banana more effectively than single-kingdom communities, illustrating the value of functional rather than taxonomic diversity in consortium design. A recurring contradiction in this literature concerns the reproducibility of consortium performance across soil types and seasons: laboratory-optimised consortia frequently underperform relative to expectations when translated to field soils with different resident microbiomes, underscoring a persistent gap between rational design and ecological realism.

3.3 Root Exudate Manipulation and Rhizosphere Signalling

A substantial body of work addresses root exudates, comprising sugars, amino acids, organic acids, and phenolic compounds, as the primary chemical currency through which plants recruit, structure, and communicate with rhizosphere microbial communities. Exudate composition varies with plant genotype, developmental stage, nutrient status, and abiotic stress, and this variation has been shown to preferentially select for microbial taxa associated with disease suppression, nutrient mobilisation, and stress tolerance. The "cry for help" hypothesis, whereby plants under pathogen or stress pressure modify exudation to recruit protective microbiota, is well supported across multiple plant systems and represents one of the more consistent findings in this literature.

Ecological theory applied to rhizosphere assembly in this literature frames colonisation as a sequence of filters: the regional microbial species pool, the physicochemical soil environment, host-mediated exudate selection, and microbial-microbial interaction including priority effects and keystone taxa dynamics. This filter-based framing is presented as reconciling apparently competing explanations of rhizosphere assembly (host selection versus stochastic colonisation versus resident-community dominance) by treating them as operating at different ecological scales rather than as mutually exclusive mechanisms. The practical implication most frequently drawn is that root-exudate-informed "prebiotic" strategies, engineering exudation patterns through breeding or amendment rather than introducing exogenous microbes, may

offer a more ecologically robust alternative to inoculation in some contexts, though field validation of this approach remains comparatively limited.

3.4 Soil Amendments: Biochar, Organic Matter, and Mineral Inputs

Soil amendment strategies, particularly engineered biochar and biochar-microbe co-formulations, feature prominently in the reviewed literature as a means of simultaneously improving soil physicochemical properties and providing a stable carrier matrix for microbial inoculants. Biochar's porous structure and large surface area are repeatedly cited as favourable for microbial attachment, moisture retention, and nutrient buffering, and several studies report that biochar-based carriers improve inoculant survival and rhizosphere persistence relative to liquid or unformulated inoculant delivery. In regions affected by heavy-metal contamination, combined biochar-PGPR systems are reported to immobilise metal contaminants while supporting crop establishment, illustrating a convergence between remediation and productivity objectives.

Organic matter amendments and residue management are also widely discussed as levers for shaping rhizosphere microbial community composition, with several studies linking amendment-driven shifts in bacterial community structure to improved soil aggregate stability and organic carbon retention, particularly in saline-alkali soils. A notable point of agreement across this sub-theme is that amendment effects are strongly soil-type and climate dependent, limiting the direct transferability of specific formulations across agroecological zones without local calibration.

3.5 Host-Plant Genetics and Breeding for Beneficial Rhizosphere Interactions

A smaller but conceptually important body of literature addresses the host-plant side of rhizosphere engineering, examining how crop genotype and breeding choices influence rhizosphere microbiome recruitment. Studies in this area report genotype-dependent variation in root architecture, exudation profile, and associated microbial community composition, with some rice and cereal genotypes shown to differentially recruit nitrogen-cycling or stress-protective taxa depending on nutrient transporter alleles and root morphology traits. This literature argues for breeding strategies that explicitly select for beneficial microbiome recruitment traits alongside conventional agronomic targets, sometimes termed "microbiome-assisted breeding" or "host-mediated microbiome engineering".

A limitation acknowledged across this sub-theme is the difficulty of disentangling genetic from environmental drivers of microbiome variation under field conditions, and the long breeding timelines required to validate microbiome-recruitment traits relative to the faster iteration possible with microbial inoculant or amendment-based approaches. Nonetheless, this approach is presented as potentially more durable than exogenous inoculation because favourable recruitment traits, once bred into a cultivar, do not depend on repeated external application.

3.6 Multi-Omics, Artificial Intelligence, and Precision Rhizosphere Tools

The most rapidly emerging theme in the reviewed literature concerns the integration of multi-omics profiling (16S rRNA and ITS amplicon sequencing, shotgun metagenomics, metatranscriptomics, and metabolomics) with machine-

learning-based prediction and precision agriculture infrastructure (soil sensors, proximal and remote sensing, variable-rate application, and digital twin modelling) to guide rhizosphere interventions. Machine-learning models trained on combined omics and agronomic datasets are reported to assist in strain selection, consortium ratio optimisation, and prediction of field performance, while active-learning and Bayesian optimisation approaches are proposed as means of accelerating Design-Build-Test-Learn cycles with fewer experimental iterations.

Across this literature, authors are notably more cautious than in earlier thematic areas about present-day reliability, repeatedly emphasising that predictive models trained on limited, often site-specific datasets may not generalise well across soil types, climates, and cropping systems, and that co-

occurrence network analyses used to infer microbial interactions should be interpreted cautiously since correlation does not establish direct ecological interaction. The practical implication is that digital and AI tools are best positioned, at the current stage of maturity, as decision-support aids that narrow experimental search space rather than as substitutes for field validation.

4. Comparative Analysis of Previous Studies

Table 3 summarises a representative subset of the reviewed studies across the six identified themes, while Table 4 synthesises comparative strengths and limitations of the major intervention categories as a group, rather than at the level of individual studies, to highlight patterns relevant to practitioners choosing among strategies.

Table 3: Summary of Selected Studies

Author(s) / Year	Location / System	Methodology	Major findings	Limitations
Bouremani <i>et al.</i> , 2023	Multi-regional (review)	Systematic review of PGPR drought-mitigation studies	ACC-deaminase and EPS-producing PGPR consistently improved seedling drought tolerance across crops	Heterogeneous primary study designs limit pooled quantitative synthesis
Zhou <i>et al.</i> , 2022	Tomato, controlled system	Construction of cross-kingdom synthetic microbiota; Fusarium wilt bioassay	Cross-kingdom consortium enhanced suppression of tomato Fusarium wilt beyond single-kingdom communities	Findings from controlled inoculation system; field persistence not established
Hong <i>et al.</i> , 2023	Banana, rotation systems	Comparative rhizosphere community profiling across rotation crops	Identified a core microbiome associated with reduced Fusarium wilt incidence under crop rotation	Correlative community data; causal mechanisms partially inferred
Fouad <i>et al.</i> , 2026	Multi-crop (review)	Narrative synthesis of DBTL framework for SynCom design and precision decision support	Proposes integrated ecological-design-field validation pipeline; highlights formulation and tracking bottlenecks	Conceptual/review synthesis; limited primary quantitative data
Brambilla <i>et al.</i> , 2022	Multi-crop (review)	Synthesis of rhizobacterial functional traits across crops	Documents convergent growth-promotion mechanisms (phytohormones, nutrient solubilisation) across diverse rhizobacteria-crop combinations	Heterogeneity of source studies limits direct cross-crop comparison
Crouzet <i>et al.</i> , 2020	Multi-crop (review)	Review of biosurfactant-mediated plant protection	Rhamnolipids and lipopeptides act as both antimicrobials and plant immune elicitors	Mechanistic review; limited field-scale quantification
Sharma, Giri & Kumar, 2024	Global (editorial synthesis)	Editorial synthesis of Research Topic contributions on rhizosphere manipulation	Consolidates recent advances and technological approaches in rhizosphere manipulation for sustainable agriculture	Editorial scope; not a systematic review

Table 4: Comparative Analysis of Intervention Categories

Intervention category	Reported strengths	Reported limitations	Typical validation scale
Single-strain PGPR inoculants	Simple to produce and apply; well-characterised mechanisms; lower regulatory complexity	Variable field performance; competition with resident microbiota; narrow functional range	Greenhouse to limited field trials
Synthetic microbial consortia (SynCom)	Complementary, redundant functions; broader stress buffering; rational design possible	Complex to formulate, track, and regulate; performance can be inconsistent across soils/seasons	Controlled system to early-stage field trials
Root exudate / prebiotic strategies	Ecologically integrated; avoids introducing exogenous strains; potentially durable	Mechanistically complex; limited field-scale validation; effects context-dependent	Mostly controlled/greenhouse studies
Soil amendments (biochar, organics)	Improves soil physicochemical properties; can co-deliver microbial carriers; multifunctional (e.g., remediation)	Effects strongly soil-type and climate dependent; logistics and cost of application at scale	Pot to multi-year field trials

Host genetics / breeding	Potentially durable without repeated input; integrates with existing breeding pipelines	Long development timelines; difficult to disentangle genetic from environmental effects	Field trials over multiple breeding cycles
Multi-omics / AI-guided precision tools	Accelerates strain/consortium selection; enables decision support and monitoring	Model generalisability across soils/climates unproven; correlation-causation caution needed	Mostly retrospective/computational; limited prospective field deployment

5. Research Gaps and Emerging Trends

5.1 Unresolved Issues and Knowledge Gaps

Across the reviewed literature, the most frequently acknowledged unresolved issue is the gap between controlled-environment (greenhouse, pot, or growth-chamber) performance and open-field performance of microbial inoculants and consortia. Related unresolved issues include the mechanistic basis of context-dependency, why an intervention effective in one soil-crop-climate combination fails or under-performs in another, and the limited ability of current co-occurrence network and correlative approaches to establish causal microbial contributions to plant phenotype.

5.2 Methodological Limitations in Previous Studies

1. Short experimental duration (single-season) precluding assessment of long-term soil health or microbiome stability effects.
2. Frequent reliance on culture-dependent or amplicon-only methods that cannot resolve strain-level persistence of introduced inoculants.

3. Limited use of strain-specific tracking (e.g., qPCR, genomic barcoding) to confirm establishment versus transient application effects.
4. Inconsistent reporting of soil physicochemical baseline data, limiting cross-study comparability.
5. Under-representation of smallholder and low-input farming contexts relative to research-station or commercial-scale systems.

5.3 Emerging Technologies and Future Developments

Several emerging directions recur across the more recent literature: light synthetic biology approaches for engineering quorum-sensing and stress-responsive circuits in rhizosphere bacteria; encapsulation and biochar-based carrier technologies for improving inoculant shelf-life and field persistence; integration of multi-omics with machine-learning and active-learning frameworks to accelerate consortium design; and digital twin modelling linking real-time sensor data to predictive crop-microbiome simulations.

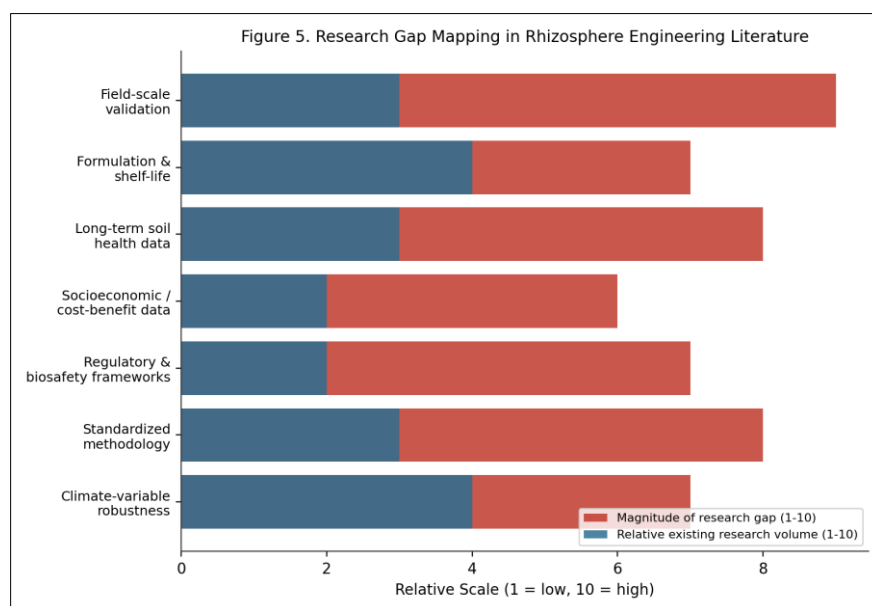


Fig 5: Research gap mapping, showing the relative magnitude of each identified gap against the current volume of supporting research.

5.4 Areas Requiring Further Investigation

Table 5: Research Gaps Identified

Research gap	Description	Priority
Field-scale, multi-site validation	Most SynCom and inoculant studies remain at greenhouse/pot scale; multi-year, multi-location field trials are scarce	High
Formulation and shelf-life standards	Lack of standardised carrier, encapsulation, and storage protocols limiting commercial reliability	High
Long-term soil health monitoring	Few studies track soil microbiome and carbon/nutrient dynamics beyond one growing season	High
Socioeconomic and cost-benefit data	Limited data on smallholder adoption feasibility, cost-effectiveness, and return on investment	Medium
Regulatory and biosafety frameworks	Harmonised international standards for microbial biofertilizer registration remain underdeveloped	Medium
Standardised methodology	Inconsistent reporting of soil baseline conditions and strain tracking methods across studies	Medium
Climate-variable robustness	Limited testing of interventions under compounded, realistic multi-stress field conditions	High

Table 6: Emerging Trends in the Field

Emerging trend	Description	Representative sub-theme
Design-Build-Test-Learn (DBTL) consortium engineering	Iterative, ecologically informed workflow for assembling minimal, functionally complementary microbial consortia	SynCom design
Multi-omics-guided strain and consortium selection	Integration of genomics, transcriptomics, metabolomics, and phenomics to inform rational design	Precision tools
AI/machine-learning-assisted optimisation	Use of predictive models and active learning to narrow experimental search space for consortium composition	Precision tools
Biochar- and polymer-based inoculant carriers	Encapsulation and carrier technologies to improve microbial viability, shelf-life, and field persistence	Soil amendments
Microbiome-assisted breeding	Selection of host genotypes for favourable rhizosphere microbiome recruitment traits	Host genetics
Precision agriculture integration	Coupling of soil sensors, remote sensing, and variable-rate application with microbial input delivery	Precision tools
Strain-level persistence tracking	Adoption of qPCR, genomic barcoding, and metagenomic read recruitment to confirm inoculant establishment	Methodology

6. Discussion

Synthesising across the six thematic areas, several integrated patterns emerge. First, the literature demonstrates a clear trajectory from descriptive, single-organism studies toward rationally designed, ecologically informed, and increasingly digitally supported intervention strategies. This progression mirrors a broader shift in agricultural microbiology from reactive characterisation of naturally occurring plant-microbe associations toward proactive, design-driven engineering of those associations for specific agronomic objectives.

Second, a recurring and largely unresolved tension across nearly every theme is the gap between controlled-environment efficacy and field-scale reliability. This tension is not confined to any single intervention category; it appears in single-strain PGPR studies, SynCom design, root-exudate manipulation, and even in the emerging AI/precision-tools literature, where authors caution that model performance trained on limited datasets may not generalise across soils and climates. The consistency of this gap across otherwise disparate approaches suggests that it reflects a fundamental challenge of translating biological interventions across heterogeneous, dynamic field environments rather than a limitation specific to any one technology.

Third, the literature increasingly converges on the view that no single intervention category is universally superior. Single-strain inoculants offer simplicity and lower regulatory burden but limited robustness; synthetic consortia offer functional redundancy but greater formulation and regulatory

complexity; root-exudate and host-genetic approaches offer potential durability but longer development timelines and more limited field validation; and soil amendments offer multifunctional benefits but strong context-dependency. This suggests that effective rhizosphere engineering strategy selection is likely to remain agroecosystem-specific, requiring an assessment of controllability, cost, and field reliability under the particular soil, crop, and climate conditions in question, rather than the wholesale adoption of a single dominant technology.

Fourth, methodological heterogeneity across the reviewed literature, in experimental duration, strain-tracking resolution, baseline soil reporting, and study scale, constrains the strength of cross-study conclusions that can be drawn and represents a practical barrier to meta-analytic synthesis in this field. Greater standardisation of reporting practices, particularly around soil baseline characterisation and strain-level persistence confirmation, would substantially improve the comparability and cumulative value of future rhizosphere engineering research.

Finally, the practical and policy implications of this body of literature are significant but currently outpace the maturity of supporting regulatory, economic, and extension infrastructure. Realising the sustainable-intensification potential of rhizosphere engineering will likely depend as much on parallel development of formulation standards, farmer-facing decision-support tools, and coherent regulatory frameworks as on further advances in the underlying biological science.

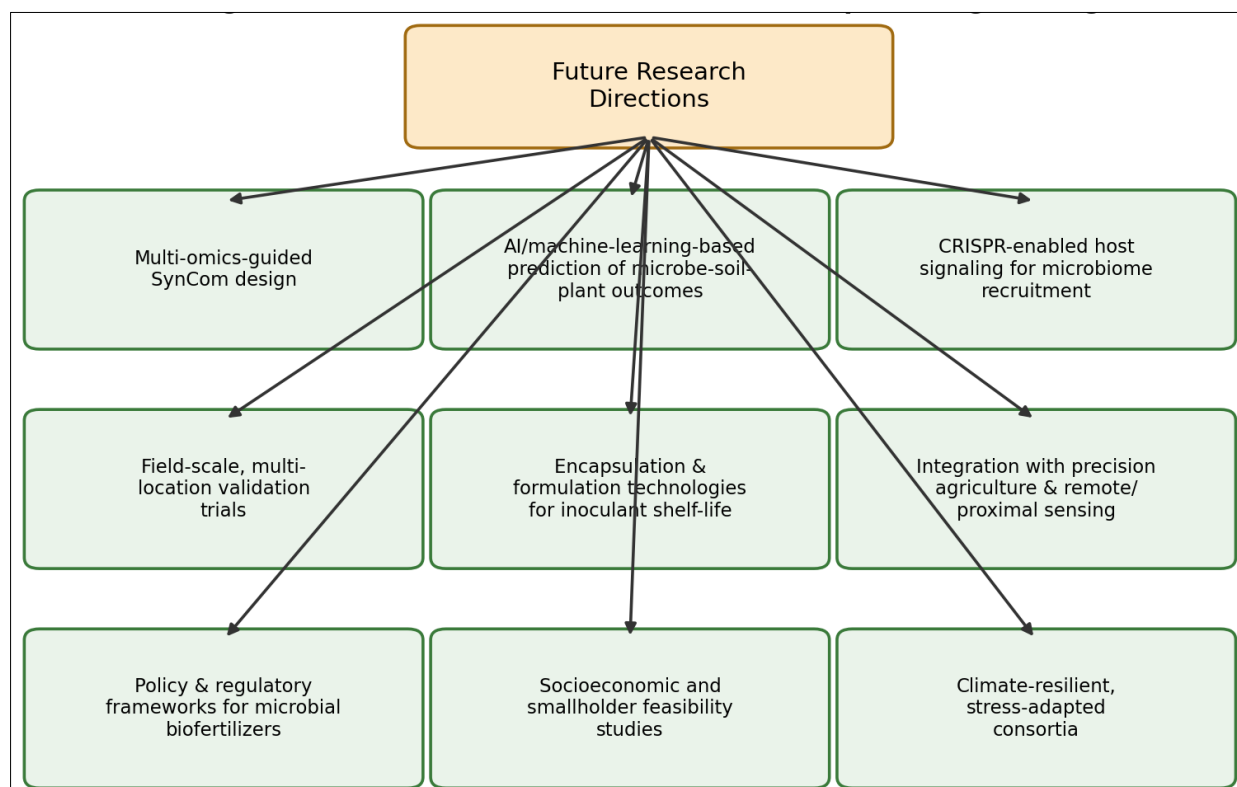


Fig 6: Future research directions in rhizosphere engineering for sustainable agricultural intensification.

7. Conclusion

Recent research has shown that there are many opportunities for the incorporation of rhizosphere engineering in sustainable agricultural intensification. The review summarized 64 research articles that focused on six important themes associated with the study of rhizosphere engineering during the years 2015-2025 - microbial inoculants/PGPR, synthetic microbial consortia construction, root exudate alteration, soil amendment, changes in genetics/breeding of the host plant, and multi-omics/AI technologies or methods. The findings state that the rhizosphere-based techniques are able to increase both the efficiency of nutrient usage as well as tolerance to various abiotic stress and diseases in comparison to conventional farming techniques. However, field applications of the rhizosphere-based techniques may vary.

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