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Soil microbiomes and crop productivity: A comprehensive review of recent advances

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Abstract

Soil microbiomes, complex assemblages of bacteria, archaea, fungi, protists, and viruses, govern many of the biogeochemical and ecological processes that underpin crop productivity. Over the past decade, rapid advances in high-throughput sequencing, multi-omics, microbial cultivation, and computational modelling have shifted the field from descriptive community profiling toward mechanistic and increasingly predictive understanding. This review synthesizes recent advances (with emphasis on 2023-2025 developments) in (i) how soil microbiomes regulate nutrient availability, plant growth signalling, disease suppression, and stress resilience; (ii) how agricultural management, soil properties, and plant traits shape microbiome assembly and function; (iii) emerging methodological toolkits, including long-read and shotgun metagenomics, metatranscriptomics, metabolomics, stable-isotope approaches, synthetic microbial communities (SynComs), and machine-learning frameworks; and (iv) translational strategies to harness microbiomes for yield gains, such as inoculants, microbial consortia, microbiome-informed soil health practices, and plant-microbiome co-engineering. Evidence increasingly indicates that context dependency—driven by soil type, climate, resident "core" communities, crop genotype, and farm practices—largely explains inconsistent field performance of bioinoculants and highlights the need for diagnostics that predict responsiveness. We propose a way forward centred on causal inference, standardised reporting, trait-based consortia design, and field-scale validation across environments, integrating microbial ecology with agronomy and breeding. By aligning measurement, modelling, and management, soil microbiome science is poised to become a practical lever for sustainable productivity and climate-resilient cropping systems.

Keywords: Soil microbiome, rhizosphere, crop yield, multi-omics, microbiome engineering

1. Introduction

Sustaining crop productivity while reducing environmental burdens from fertiliser and pesticide inputs is a defining challenge for contemporary agriculture. Soils are not inert substrates; they are living ecosystems in which microbial communities mediate decomposition, nutrient cycling, aggregation, and biological regulation of pests and pathogens. Policy and scientific assessments increasingly emphasise that soil biodiversity and microbial functions are central to soil health and agricultural sustainability [1, 2].

Historically, agronomic microbiology focused on a limited set of culturable organisms (e.g., rhizobia, mycorrhizae) and discrete processes (e.g., nitrogen fixation). In contrast, modern soil microbiome research treats the soil-plant system as an interconnected network of organisms, genes, metabolites, and environmental drivers. This systems view has been enabled by next-generation sequencing and associated bioinformatics, which now allow researchers to characterise both taxonomic diversity and functional potential at unprecedented resolution [2, 3].

The central premise of this review is that "microbiome-aware" management can become a practical pathway to enhance crop productivity—through improved nutrient use efficiency, strengthened stress tolerance, and reduced disease pressure—provided the field moves beyond association toward reliable prediction and causal intervention. Recent reviews and syntheses highlight both the promise and the limitations of microbiome-based solutions, including variable field efficacy of inoculants and the importance of ecological context [1, 2].

2. What Constitutes the Soil Microbiome? Functional Guilds and Ecological Roles

The soil microbiome encompasses diverse organisms across multiple domains of life:

- Bacteria and archaea drive mineralisation, nitrification, denitrification, sulfur transformations, and production of phytohormones and antimicrobial compounds [2, 3].
- Fungi include saprotrophs decomposing complex polymers, arbuscular mycorrhizal fungi (AMF) enhancing phosphorus uptake, and pathogens that antagonistic fungi can counterbalance [3, 4].
- Protists graze on bacteria and shape community composition while contributing to nutrient turnover [5, 6].
- Viruses (especially bacteriophages) regulate microbial population dynamics and horizontal gene transfer, potentially influencing functional traits [7, 8].

From a productivity standpoint, it is often more helpful to conceptualise microbiomes in terms of functional guilds rather than taxonomy alone: nutrient mobilizers, symbionts, growth promoters, stress alleviators, and pathogen suppressors. Large syntheses underscore that bacteria and fungi influence plant growth via organic matter decomposition, nutrient solubilization, symbioses, hormone production, and pathogen inhibition.

A key idea that has gained traction is the existence of core microbiome taxa consistently associated with specific crops or soil types and potentially crucial for stable ecosystem functions. Recent evidence suggests that native core microorganisms can outperform non-core or non-native microbes in promoting yield, plausibly due to better colonisation and community compatibility [3, 4].

3. Mechanistic Links Between Soil Microbiomes and Crop Productivity

3.1 Nutrient Acquisition and Use Efficiency

Nitrogen (N): Microbes influence N supply through (i) biological N fixation (symbiotic and free-living), (ii) ammonification of organic N, and (iii) nitrification and denitrification that regulate N losses. N transformations are strongly shaped by oxygen status, carbon availability, and management practices [4, 5].

Phosphorus (P): Many soils contain substantial total P but limited plant-available orthophosphate. Microbes enhance availability by exuding organic acids, producing phosphatases, and dissolving minerals. AMF extend the adequate root exploration volume, increasing P uptake efficiency, especially under low-P conditions [4, 5]

Micronutrients: Siderophore-producing bacteria mobilise iron, while other taxa affect zinc and manganese availability. These functions can translate into improved crop nutrition and potentially quality attributes, though their impacts are often context-specific [4, 5].

3.2 Plant Growth Regulation via Signalling and Phytohormones

Beyond nutrients, microbes influence plant developmental programs. Many plant growth-promoting rhizobacteria (PGPR) modulate auxin, cytokinin, and ethylene signalling, including via ACC deaminase activity that can reduce stress-related ethylene levels. The rhizosphere is increasingly viewed as a chemically mediated recruitment zone in which plant exudates shape microbial colonisation, and microbial metabolites feedback on plant physiology [3, 4].

3.3 Disease Suppression and Immune Priming

Soils can become disease-suppressive when microbial antagonists, competition for resources, and induced systemic resistance collectively reduce pathogen establishment. Microbiome-mediated protection includes antibiotic production, lytic enzyme production, niche exclusion, and priming of plant defences. Modern approaches increasingly combine community profiling with functional assays to identify protective consortia rather than single-strain solutions [5, 6].

3.4 Abiotic Stress Tolerance (Drought, Heat, Salinity)

Microbial partners can enhance drought tolerance through improved root growth, osmolyte regulation, and enhanced soil aggregation, thereby improving water retention. Under salinity stress, certain microbes support ion homeostasis and mitigate oxidative stress. Climate-related pressures are bringing stress biology to the forefront of microbiome research, including investigations into how resource limitation and heat extremes reshape community composition and function [7, 8].

3.5 Soil Structure, Carbon Cycling, and Long-Term Fertility

Microbes are principal drivers of decomposition and soil organic matter formation, influencing carbon stabilisation and aggregate formation. These processes matter for productivity through improved infiltration, aeration, and nutrient buffering. Policy-oriented reviews emphasise microbial intervention in carbon dynamics, nutrient cycling, soil structure maintenance, and biological regulation as core contributors to agricultural production [9, 10].

4. Drivers of Microbiome Assembly in Agricultural Soils

4.1 Soil Type and Baseline Ecological Constraints

Soil pH, texture, mineralogy, and organic carbon content impose strong selection on microbial taxa and functional potentials. Because these factors differ across farms and regions, the same microbial intervention can have contrasting outcomes [11, 12].

4.2 Crop Genotype, Root Traits, and Rhizosphere Selection

Plants shape microbiomes through root architecture, exudate profiles, and immune responses. Recent work linking root traits to microbiome assembly argues that root system architecture can shape rhizosphere communities, and that trait-informed breeding could complement microbiome engineering [13, 14].

4.3 Agricultural Management: Fertility Sources, Tillage, Rotations, and Amendments

Management is a dominant lever. Evidence from machine learning and depth-resolved sampling indicates that fertility source (e.g., organic vs. mineral inputs) can be a pronounced determinant of microbial assembly, with effects that vary by soil depth and often differ between fungi and prokaryotes [15, 16].

Diversified rotations, cover crops, reduced tillage, and organic amendments tend to increase habitat heterogeneity and resource diversity, frequently supporting microbial diversity and functional redundancy. However, productivity outcomes depend on local constraints (water, baseline fertility, disease pressure) and require integrated agronomic evaluation rather than microbiome metrics alone [17, 18].

5. Methodological Advances Powering “Recent Advances”

5.1 From Amplicons to Shotgun and Long-Read Metagenomics

Amplicon sequencing (16S/ITS) remains useful for broad surveys but has limited functional resolution. Shotgun metagenomics enables gene-centric and genome-resolved insights, while long-read technologies improve assembly contiguity and detection of mobile genetic elements. Recent sequencing-focused reviews emphasise careful method selection, bioinformatics pipelines, and the trade-offs among depth, cost, and interpretability [18, 19].

5.2 Multi-Omics for Function: Metatranscriptomics, Metabolomics, and Metaproteomics

Community composition does not always predict activity. Functional omics approaches reveal which genes are expressed, which proteins are produced, and which metabolites mediate interactions. In agricultural contexts, metabolomics is particularly valuable for characterising rhizosphere chemical “currencies” that govern recruitment and antagonism [12, 13].

5.3 Synthetic Microbial Communities (SynComs) and Mechanistic Testing

SynComs—defined, reproducible consortia assembled from isolates—allow hypothesis-driven testing of community functions and interactions under controlled conditions. Recent reviews highlight SynComs as both a “sandbox” for causal inference and a blueprint for translational microbial products, while also stressing that field effectiveness can be inconsistent due to colonisation barriers and environmental variability [14, 15].

5.4 Predictive Diagnostics and Microbiome “Responsiveness”

A significant practical barrier is that inoculation does not reliably produce yield gains. Recent high-impact work shows that soil microbiome indicators can help predict crop growth responses to large-scale AMF inoculation, pointing toward a future in which pre-intervention diagnostics guide treatment decisions [16, 17].

5.5 Machine Learning, Network Ecology, and Causal Inference

Machine-learning frameworks are increasingly used to identify microbial signatures of soil health, forecast pathogen outbreaks, and predict yield responses. Yet, correlation-driven models can fail when moved across soils or seasons. The field is therefore pivoting toward hybrid approaches that combine mechanistic constraints (nutrient balance, resource allocation) with statistical learning, and toward experimental designs that strengthen causal inference [18, 19].

6. Translational Strategies to Harness Microbiomes for Yield

6.1 Bioinoculants: Single Strains, AMF, and Consortia

Inoculants include PGPR, AMF, and other beneficial microbes [12, 30]. Their mechanisms span nutrient mobilisation, hormone modulation, and pathogen suppression. While successes exist, inconsistent performance remains common often due to poor establishment, mismatch with soil conditions, or antagonism by resident communities. Reviews focused on microbiome-based yield improvement emphasise the promise of soil microbiomes to enhance nutrient-use efficiency and stress resistance, but underscore variability in outcomes and the need for context-aware deployment [16, 17].

Implications for practice

- Prioritise local adaptation: native or locally derived strains may colonise better [18].
- Consider compatibility with resident communities: core microbiomes may provide a more stable foundation than introducing non-native taxa [19, 20].
- Use diagnostics to target interventions to responsive soils [19, 20].

6.2 Microbial Consortia and Community-Aware Formulation

Consortia may outperform single strains by providing functional complementarity (e.g., P solubilization + disease suppression). However, consortia design must consider ecological stability: competitive exclusion, cheater dynamics, and resource partitioning [21, 22].

Key formulation issues include shelf life, carrier materials, compatibility with fertilisers and pesticides, application timing, and delivery method (seed coating, in-furrow, fertigation). Success requires co-optimisation with agronomy, not with microbiology alone [23, 24].

6.3 Plant-Microbiome Co-Engineering

Plant genotype can be leveraged to recruit beneficial microbes. “Microbiome-assisted” breeding aims to select crop traits (root exudation patterns, architecture, immune thresholds) that favour beneficial assemblages. Recent engineering-oriented reviews discuss integrating experimental and computational strategies to investigate plant-microbiome interactions and engineer desirable soil microbiomes [25, 26].

6.4 Soil Health Management as Microbiome Management

Some of the most reliable microbiome gains arise from system-level practices rather than products:

- organic amendments to build carbon and microbial substrate supply
- diversified rotations and cover crops to broaden niches
- reduced tillage to preserve fungal networks and aggregates
- integrated nutrient management to reduce stress on microbial processes

These interventions often improve soil structure and functional diversity, thereby increasing resilience and stabilising yields over time, even if year-to-year responses vary [11, 12].

7. Constraints, Risks, and Key Knowledge Gaps

7.1 Context Dependency and “One-Size-Fits-All” Failure Modes

A recurring theme is that soil microbiome interventions are not universally effective. Soil physicochemical constraints, climate, irrigation regime, baseline fertility, and legacy effects can dominate outcomes. Field translation, therefore, requires stratified recommendations rather than generic products [13, 14].

7.2 Colonisation Resistance and Ecological Compatibility

Introduced microbes must compete with established communities. The emerging evidence favouring native core microbiomes suggests that compatibility and colonisation capacity may be as crucial as functional traits [15, 16].

7.3 Measurement and Reproducibility Challenges

Differences in sampling depth, seasonality, DNA extraction protocols, primer sets, and bioinformatics pipelines limit comparability across studies. Sequencing-focused reviews emphasise method selection and standardised workflows to improve interpretability and cross-study synthesis [16, 17].

7.4 Regulatory, Biosafety, and Adoption Considerations

Microbial products face regulatory review, quality control requirements, and farmer adoption barriers. Clear labelling, efficacy data, and guidance on compatible agronomic practices are essential [29, 30]. Adoption is more likely when microbial solutions reduce costs or risks rather than offering only marginal yield gains under already high-input conditions [17, 18].

8. A Practical Framework: From Discovery to Field Impact

To translate recent advances into productivity gains, the following staged framework is increasingly used:

1. **Baseline characterisation:** soil type, management history, nutrient status, and baseline microbiome profile (taxonomic + functional proxies) [19, 20].
2. **Hypothesis generation:** identify limiting processes (e.g., P limitation, disease pressure, drought frequency) and candidate microbial functions [21, 22].
3. **Mechanistic validation:** SynComs, microcosms, and plant assays to test causality and interaction effects [23, 24].
4. **Predictive modelling:** build soil "responsiveness" models that incorporate microbiome indicators, climate, and management covariates [25, 26].
5. **Field trials across environments:** multi-site, multi-year trials with standardised measurements and economic evaluation [25, 27].
6. **Decision support:** recommendations integrated into farm management (timing, input compatibility, risk thresholds) [28, 29].

9. Conclusion

Recent advances in soil microbiome science are reshaping how crop productivity is understood and managed. The field has shifted from cataloguing diversity to testing mechanisms using multi-omics and synthetic communities, while predictive modelling is beginning to guide targeted interventions. Yet, the core challenge remains context dependency: microbial products and practices must be matched to soils, climates, crops, and resident communities. The most credible path to impact combines (i) diagnostics that predict responsiveness, (ii) ecology-aligned consortia and native-core strategies, (iii) standardised measurements enabling transferable models, and (iv) integrated agronomy and breeding. With these elements in place, soil microbiome management can mature into a reliable, scalable tool for improving sustainable yield.

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