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Research Article

Role of Soil Microbiome in Suppressing Soil-Borne Pathogens

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Abstract

The soil microbiome constitutes a vast and complex community of bacteria, fungi, archaea, protists, and viruses that play pivotal roles in maintaining soil health and agricultural productivity. Among its numerous ecological functions, the suppression of soil-borne plant pathogens stands out as one of the most agriculturally significant. Soil-borne pathogens, including *Fusarium, Pythium, Rhizoctonia and Phytophthora* species, are responsible for enormous economic losses in global agriculture annually. The inherent capacity of certain soils to suppress these pathogens—termed disease-suppressive soils—has been linked directly to the richness, diversity, and functional activity of the resident microbial communities. This review comprehensively examines the mechanisms through which the soil microbiome suppresses soil-borne pathogens, including antibiosis, competition for nutrients and space, induced systemic resistance, mycoparasitism and volatile compound production. It further explores the ecological and agronomic factors that shape microbial community structure and suppressive capacity, including soil pH, organic matter content, crop rotation, and the application of biological control agents. Understanding the intricate interactions within the rhizosphere and bulk soil microbiome offers transformative opportunities for the development of sustainable, microbiome-mediated disease management strategies, reducing dependence on chemical fungicides while maintaining high crop yields. Despite these advances, a critical knowledge gap persists in translating mechanistic insights into consistent, field-applicable biocontrol outcomes, particularly under variable soil conditions and diverse agricultural systems. Future research should prioritize the development of predictive microbiome-based models, the standardization of synthetic community formulations, and the integration of multi-omics approaches to unlock the full suppressive potential of soil microbial ecosystems for next-generation, sustainable crop protection.

More Information

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Introduction

Soil represents one of the most biologically diverse habitats on Earth, harboring billions of microorganisms per gram of soil, encompassing thousands of bacterial and fungal species, along with archaea, nematodes, protozoa, and viruses [1]. This community of microorganisms—collectively termed the soil microbiome—is now recognized as a central determinant of soil health, plant productivity, and ecosystem resilience. Among the many services rendered by the soil microbiome, its capacity to protect plants against soil-borne diseases has attracted significant scientific and agricultural interest [2].

Soil-borne plant pathogens cause devastating losses across virtually all major crops worldwide. Species of *Fusarium*, *Rhizoctonia*, *Pythium*, *Phytophthora*, *Sclerotinia*, and *Verticillium* infect roots and crowns, leading to damping-off, root rot, crown rot, and vascular wilts that collectively account for multi-billion-dollar losses annually [3]. Chemical fungicides, while effective, raise concerns about environmental contamination, development of resistance, and disruption of beneficial microbial communities [4]. This has prompted growing interest in harnessing the natural suppressive potential of soil microbial communities.

The concept of disease-suppressive soils—soils in which pathogens cannot establish or cause disease despite their presence—has been known for decades but is now being elucidated at the mechanistic and genomic levels [5]. Landmark studies have demonstrated that transferring small amounts of suppressive soil to conducive soil can transfer disease suppression, confirming its microbial basis [6]. Highthroughput sequencing technologies, metagenomics, and metabolomics have revolutionized our ability to characterize these communities and understand their functional roles [7].

This review synthesizes current knowledge on how the soil microbiome suppresses soil-borne pathogens, covering the principal mechanisms of suppression, the ecological drivers shaping suppressive communities, and the practical implications for developing next-generation biological disease management strategies. The manuscript draws on established literature to present a mechanistic framework for understanding and exploiting the suppressive potential of soil microbial communities.

Soil microbiome: composition and diversity

The soil microbiome is extraordinarily diverse. A single gram of fertile agricultural soil may contain up to 10^9 bacterial cells representing tens of thousands of species, hundreds of fungal taxa, diverse archaea, and a complex virome [8]. Dominant bacterial phyla in most soils include Proteobacteria, Actinobacteria, Firmicutes, Bacteroidetes, and Acidobacteria, though community composition varies considerably with soil type, land use, climate, and plant species [1].

Fungi, despite lower abundance than bacteria by cell count, often dominate soil biomass and play essential roles in nutrient cycling and plant protection [9]. Key fungal genera with biocontrol relevance include *Trichoderma, Gliocladium, Coniothyrium* and various mycorrhizal fungi. Archaea, particularly ammonia-oxidizing archaea, contribute significantly to nitrogen cycling, while bacteriophages and mycoviruses influence the population dynamics of both bacteria and fungi [10].

Community structure within the soil is not homogeneous but varies along spatial gradients. The rhizosphere—the narrow zone of soil immediately surrounding and influenced by plant roots—harbors microbial densities 10 to 100 times greater than bulk soil and is particularly enriched in plant-growth-promoting and biocontrol microorganisms [11]. Root exudates containing sugars, amino acids, organic acids, and secondary metabolites selectively recruit specific microbial taxa to the rhizosphere, a process described as the 'cry for help' hypothesis, in which pathogen attack amplifies rhizosphere recruitment of protective microbes [12].

Mechanisms of pathogen suppression by soil microbiome

Antibiosis

Antibiosis—the production of antibiotics and secondary metabolites toxic to pathogens—is among the most extensively documented mechanisms of microbial biocontrol. *Pseudomonas fluorescens* strains produce 2,4-diacetylphloroglucinol (2,4-DAPG), phenazines, pyoluteorin, and pyrrolnitrin, which are directly toxic to *Fusarium oxysporum*, *Pythium ultimum*, and *Gaeumannomyces graminis* var. *tritici*, the causal agent of take-all disease in wheat [13]. The importance of 2,4-DAPG in suppressive soils was definitively established by demonstrating that its production in the rhizosphere correlated with suppression of take-all disease, and that 2,4-DAPG-deficient mutants lost biocontrol efficacy [14].

Bacillus species produce a remarkable array of lipopeptides and polyketides including iturin, fengycin, surfactin, and bacillomycin, which disrupt fungal cell membranes and inhibit spore germination [15]. *Streptomyces* species, abundant in the actinobacterial community, produce volatile antifungal compounds and enzymes including chitinases and glucanases that degrade fungal cell walls [16]. The diversity of antibiotic producers and compounds ensures redundancy in suppressive capacity, so that no single mechanism dominates.

Competition for nutrients and ecological niches

Competition for limiting resources—particularly iron, carbon, and colonization sites on root surfaces—constitutes a powerful mechanism of pathogen suppression. Iron is essential for microbial growth but is often limiting in aerobic soils. Many biocontrol bacteria produce high-affinity iron-chelating compounds called siderophores, which sequester iron and deprive pathogens of this essential nutrient [17]. Fluorescent pseudomonads are particularly renowned for siderophore-mediated competition; their pseudobactin siderophores have higher iron affinity than those of most soil-borne pathogens, giving them a competitive advantage.

Competition for carbon substrates in the rhizosphere is equally important. By rapidly colonizing roots and rhizosphere soil, biocontrol bacteria outcompete pathogens for resources and block their establishment. [18]. This is facilitated by the ability of biocontrol bacteria to utilize root exudate compounds more efficiently than pathogens. The application of organic amendments and compost promotes these competitive interactions by stimulating the overall metabolic activity of native suppressive microorganisms [19]. A particularly illustrative example of carbon-based competitive exclusion involves certain *Pseudomonas* species that preferentially and rapidly metabolize specific root exudate compounds—including malic acid, citric acid, and succinic acid—that are abundant in the rhizosphere. *Pseudomonas putida* and *P. fluorescens*, possessing efficient organic acid uptake systems encoded by the *gac* regulatory system and specialized chemotaxis receptors, colonize root surfaces more rapidly and establish higher population densities than soil-borne pathogens such as *Fusarium oxysporum*, which relies predominantly on passive diffusion for nutrient acquisition [20,21]. This metabolic prioritization effectively starves the pathogen of the carbon substrates required for germination and infection, demonstrating how differential resource utilization efficiency directly translates into competitive exclusion and pathogen suppression.

Induced Systemic Resistance (ISR)

Beneficial soil microorganisms can prime the plant immune system to respond more rapidly and robustly to pathogen attack—a phenomenon termed induced systemic resistance (ISR). Unlike pathogen-triggered systemic acquired resistance (SAR), which is dependent on salicylic acid, ISR is typically mediated through jasmonic acid and ethylene signaling pathways and does not involve prior activation of defenses [22]. Certain strains of *Pseudomonas*, *Bacillus* and *Trichoderma* are potent ISR elicitors; their cell surface components including lipopolysaccharides, flagellins, and volatile organic compounds are recognized by plant pattern recognition receptors, activating broad-spectrum resistance [23].

Mycorrhizal fungi, which colonize the roots of most land plants, also contribute to ISR. Arbuscular mycorrhizal fungi (AMF) alter root exudate chemistry and prime plant defenses, resulting in reduced severity of diseases caused by *Fusarium*, *Phytophthora* and *Pythium* [24]. The spatial separation of AMF hyphal networks from soil-borne pathogens enables signaling without direct competition, making AMF-mediated protection particularly valuable in field conditions.

Mycoparasitism

Mycoparasitism—the direct parasitism of one fungus by another—is a well-established mechanism deployed by *Trichoderma* species against soil-borne fungal pathogens. *Trichoderma harzianum, T. virens* and *T. asperellum* attach to and penetrate the hyphae of *Rhizoctonia solani, Botrytis cinerea, Sclerotinia sclerotiorum* and *Pythium* species, secreting cell wall-degrading enzymes including chitinases, glucanases, and proteases that dissolve the pathogen's cell wall [25]. Mycoparasitism by *Trichoderma* is specific and involves chemotropic hyphal growth guided by signals from the target pathogen.

Beyond *Trichoderma*, *Coniothyrium minitans* is an obligate mycoparasite of *Sclerotinia sclerotiorum* sclerotia, reducing sclerotial viability in soil and diminishing primary inoculum levels. *Pythium oligandrum* is a mycoparasite of several oomycete pathogens and also produces secondary metabolites that induce plant defenses [26]. The layered deployment of mycoparasitism alongside antibiosis and ISR provides comprehensive protection against a broad spectrum of pathogens.

Production of Volatile Organic Compounds (VOCs)

Soil bacteria and fungi produce diverse volatile organic compounds (VOCs) that diffuse through soil pore spaces and inhibit pathogen growth at a distance without requiring physical contact. Bacillus subtilis produces 2,3-butanediol and acetoin, which not only suppress *Botrytis cinerea* and *Erwinia carotovora* but also elicit ISR in Arabidopsis and other plants [27]. *Trichoderma* species emit 6-pentyl-α-pyrone, isobutyl alcohol, and other volatiles that are toxic to *Fusarium oxysporum* and *Phytophthora infestans* [28]. The capacity of VOCs to act at a distance through soil makes them particularly relevant in the context of whole-soil suppressive capacity.

Hyperparasitism of pathogen structures

Several microorganisms in the soil are capable of directly attacking the dormant propagules of soil-borne pathogens, including sclerotia, chlamydospores, and oospores. Bacteria of the genus *Lysobacter* and *Myxococcus* produce lytic enzymes and antibiotic compounds that degrade fungal cell walls and destroy resting structures [29]. This direct attack on persistent inoculum structures is particularly valuable because these structures are the primary source of initial infection in subsequent growing seasons. The enrichment of hyper-parasitic microorganisms in suppressive soils represents a natural and sustainable mechanism of long-term disease management.

A conceptual diagram illustrating the six primary mechanisms by which the soil microbiome suppresses soil-borne pathogens. The central panel depicts a plant root surrounded by the rhizosphere. Six radiating pathways illustrate: (1) Antibiosis — beneficial bacteria (Pseudomonas, Bacillus, Streptomyces) secreting antibiotics (2,4-DAPG, iturin, phenazines) directly toxic to pathogen hyphae; (2) Competition — siderophore-producing pseudomonads sequestering iron, and rapid root colonizers outcompeting pathogens for carbon substrates; (3) Induced Systemic Resistance (ISR) — root-colonizing microbes triggering jasmonic acid/ethylene signaling cascades leading to systemic plant immunity; (4) Mycoparasitism — Trichoderma hyphae coiling around and penetrating pathogen hyphae (Rhizoctonia, Botrytis, Sclerotinia) via chitinase and glucanase secretion; (5) Volatile Organic Compounds (VOCs) — diffusion of 2,3-butanediol and 6-pentyl-alpha-pyrone through soil pore spaces inhibiting pathogen spore germination at a distance; (6) Hyperparasitism — Lysobacter and Myxococcus attacking sclerotia and chlamydospores, degrading persistent inoculum structures. Arrows indicate signal or compound flow; inhibitory interactions shown with blunted-end lines] (Table 1).

Ecological and agronomic factors shaping suppressive microbiome

The suppressive capacity of the soil microbiome is not static but is profoundly influenced by a range of ecological and agronomic factors. Soil pH is a master variable that determines microbial community composition: bacterial diversity generally peaks at near-neutral pH, while fungi tolerate a wider range [30]. Soil organic matter content fuels microbial activity; soils rich in organic carbon support greater microbial biomass and diversity, which correlates with enhanced suppressiveness [19].

Table 1: Summary of major biocontrol organisms and their mechanisms of pathogen suppression

Biocontrol organism	Mechanism(s) of action	Target pathogens	Key reference(s)
Pseudomonas fluorescens	Antibiosis (2,4-DAPG, phenazines, pyoluteorin); siderophore-mediated competition; ISR elicitation	*Fusarium oxysporum, Pythium ultimum, Gaeumannomyces graminis*	[13,14]
Bacillus subtilis	Antibiosis (iturin, fengycin, surfactin); VOC production (2,3-butanediol, acetoin); ISR elicitation	*Botrytis cinerea, Fusarium spp., Rhizoctonia solani*	[15,27]
Trichoderma harzianum / T. asperellum	Mycoparasitism (chitinases, glucanases, proteases); VOC production; ISR elicitation	*Rhizoctonia solani, Botrytis cinerea, Sclerotinia sclerotiorum, Pythium spp.*	[25,28]
Streptomyces spp.	Antibiosis (volatile antifungals); cell wall-degrading enzymes (chitinases, glucanases)	*Fusarium spp., Pythium spp., Rhizoctonia solani*	[16]
Coniothyrium minitans	Mycoparasitism of sclerotia; reduction of primary inoculum	*Sclerotinia sclerotiorum*	[26]
Pythium oligandrum	Mycoparasitism of oomycetes; secondary metabolite-mediated ISR	*Pythium ultimum, Phytophthora spp.*	[26]
Lysobacter / Myxococcus spp.	Hyperparasitism; lytic enzyme production; antibiotic-mediated destruction of sclerotia and chlamydospores	*Fungal pathogens with persistent propagules (Fusarium, Sclerotinia)*	[29]
Arbuscular Mycorrhizal Fungi (AMF)	ISR via root exudate modification; priming of plant immune defenses; physical exclusion via hyphal networks	*Fusarium spp., Phytophthora spp., Pythium spp.*	[24]

Crop rotation profoundly shapes the rhizosphere microbiome. Monoculture cropping leads to the buildup of specific pathogens and depletion of suppressive microorganisms, while diverse rotations sustain higher microbial diversity and functional redundancy [31]. The inclusion of legumes in rotations enriches nitrogen-fixing bacteria and modifies rhizosphere chemistry in ways that recruit biocontrol microorganisms. Cover cropping with species such as *Brassica* introduces glucosinolate-derived isothiocyanates through bio-fumigation, further suppressing soilborne pathogens [32].

Tillage practices also significantly impact soil microbiome structure and function. Conservation tillage and no-till systems preserve soil aggregate structure, fungal hyphal networks, and microbial spatial organization, supporting communities associated with greater suppressiveness compared to conventionally tilled soils [33]. The application of biological control agents as inoculants can augment native suppressive populations, though the success of inoculants in the field is often variable due to competitive displacement by native microbiota [4].

Disease-suppressive soils: natural models of microbiome function

Disease-suppressive soils represent natural laboratories for understanding microbiome-mediated pathogen suppression. The most intensively studied suppressive soils include the take-all decline soils of wheat fields in the Pacific Northwest of the United States, Dutch soils suppressive to Fusarium wilt of radish, and Avocado-growing soils in California suppressive to *Phytophthora* root rot [5,6]. In each case, suppression is associated with specific microbial communities rather than physicochemical soil properties alone.

Metagenomics and amplicon sequencing have revealed that suppressive soils harbor elevated abundances of *Pseudomonas*, *Streptomyces*, *Lysobacter*, *Burkholderia*, *Bacillus* and *Trichoderma* relative to conducive soils [6,7]. The network connectance and resilience of microbial communities in suppressive soils is typically greater than in conducive soils, suggesting that ecological complexity itself confers stability of the suppressive phenotype. Perturbation experiments using heat treatment, fumigation, or antibiotic addition consistently demonstrate that disrupting microbial diversity compromises suppressiveness, even when the target pathogen and physicochemical conditions remain unchanged.

Microbiome engineering for sustainable disease management

Advances in understanding the soil microbiome have opened new avenues for engineering suppressive communities to enhance crop protection. Strategies range from the selection and application of individual biocontrol agents to consortia-based approaches and holistic management of the soil environment to favor suppressive communities [34]. Individual biocontrol agents such as *Trichoderma harzianum*, *Bacillus subtilis*, *Pseudomonas fluorescens*, and *Coniothyrium minitans* are commercially available in many countries and have demonstrated efficacy against multiple pathogens in field conditions.

Synthetic microbial communities (SynComs)—rationally designed consortia of microorganisms with complementary biocontrol functions—represent a frontier approach that may overcome the limitations of single-agent inoculants [35]. By combining organisms with different mechanisms (antibiosis, ISR, mycoparasitism), SynComs can provide broader-spectrum protection and may be more resilient to environmental variability. Coupling SynCom application with organic amendments and crop management practices that favor persistence of introduced microorganisms is critical to field success.

Microbiome transplantation—the transfer of disease-suppressive soil microbiomes to conducive soils—represents a more holistic approach analogous to fecal microbiome transplantation in human medicine [7]. While logistically challenging at field scale, this concept has demonstrated proof-of-principle and informs strategies for restoring suppressive potential in degraded soils. Precision agriculture tools, including remote sensing, soil sensors, and machine learning integration with microbiome datasets, are increasingly being applied to spatially map and target zones of suppressive potential within fields.

Despite its conceptual appeal, microbiome transplantation faces several practical challenges that currently limit its widespread adoption. From a scalability perspective, the physical transfer of sufficient quantities of suppressive soil to treat commercial-scale agricultural fields is logistically demanding and technically complex, as the structural integrity and microbial viability of the transplanted community must be maintained during collection, storage, and application [7]. Economic feasibility presents an equally significant barrier: the costs associated with identifying and sourcing high-quality suppressive soils, processing and formulating transplant materials, and applying them at field scale often render the approach commercially unviable compared to conventional biocontrol inoculants or fungicides, particularly for smallholder farmers in developing agricultural economies [34]. Regulatory considerations add a further layer of complexity, as the deliberate introduction of non-native or undefined microbial consortia into agricultural soils may trigger biosafety assessment requirements in many jurisdictions, with regulatory frameworks in the European Union, United States, and other major agricultural regions currently lacking harmonized guidelines specifically for microbiome transplantation technologies [4]. Addressing these challenges through the development of standardized formulation protocols, cost-reduction strategies, and fit-for-purpose regulatory pathways will be essential to translating the proof-of-principle success of microbiome transplantation into accessible field-scale disease management tools.

Challenges and future directions

Despite significant progress, several challenges remain in translating microbiome science into reliable disease management outcomes. The context-dependency of biocontrol—the frequent failure of agents effective in laboratory or greenhouse trials to deliver consistent performance in the field—remains a central problem [4]. This variability reflects the complexity of soil environments, the competitive pressure from native microbiota, and the influence of environmental conditions including temperature, moisture, and soil chemistry on both the biocontrol agent and the pathogen.

Regulatory frameworks for the approval of new biocontrol agents and microbial consortia are often slower than technological developments, limiting the commercial availability of next-generation products. The ecological risks of introducing non-native microorganisms—including displacement of native beneficial species and horizontal gene transfer of antibiotic resistance genes—require careful evaluation [34]. Integrating microbiome-based approaches with precision plant breeding to develop cultivars with enhanced ability to recruit suppressive microbiomes represents a promising but underexplored frontier [36].

Future research should prioritize longitudinal studies of microbiome dynamics under different management regimes to identify the conditions under which suppression is most stable and resilient. Multi-omics approaches integrating metagenomics, metatranscriptomics, metaproteomics, and metabolomics will provide unprecedented mechanistic resolution of the interactions governing pathogen suppression. Standardization of experimental methods and data sharing will accelerate comparative studies and the development of predictive models linking microbiome composition to functional outcomes.

Conclusion

The soil microbiome naturally defends against soil-borne pathogens through antibiosis, competition, induced resistance, mycoparasitism, and volatiles. Shaped by soil properties, management, and plant interactions, suppressive microbial communities offer broad-spectrum, resilient protection unmatched by chemical pesticides. Disease-suppressive soils prove that sustainable, ecosystem-level control is possible. Leveraging this via microbiome engineering, biocontrol, and targeted practices can transform crop protection. Advances in microbiome science now enable agriculture to align with ecological principles for global food security.

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