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SOIL BORNE PLANT DISEASES: BIOLOGY, EPIDEMIOLOGY, DISEASE DEVELOPMENT, AND SUSTAINABLE INTEGRATED MANAGEMENT STRATEGIES

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ABSTRACT:
Soil-borne plant diseases represent a major threat to global agricultural productivity and food security, causing substantial economic losses in diverse cropping systems worldwide. These diseases are particularly challenging to manage because causative pathogens persist in soil for extended periods and develop complex survival mechanisms. This comprehensive review synthesizes recent literature (2020–2026) and seminal studies to critically examine the biology and ecology of major soil-borne pathogens, including fungi (Fusarium, Rhizoctonia, Sclerotium, Macrophomina, Verticillium), oomycetes (Pythium, Phytophthora), bacteria (Ralstonia solanacearum), and plant-parasitic nematodes (Meloidogyne). We discuss how pathogens survive in soil, establish infections through molecular mechanisms involving virulence factors and host defense suppression, and develop disease under variable environmental conditions. Current management strategies encompassing cultural practices, biological control (Trichoderma, Bacillus, Pseudomonas), organic amendments, soil solarization, resistant cultivars, and selective chemical management are critically evaluated. Recent advances in disease-suppressive soil microbiomes, synthetic microbial communities, genomic approaches, and nanotechnology are highlighted. We emphasize that no single management tactic is sufficient; integrated disease management (IDM) combining multiple components based on pathosystem ecology is essential for sustainable disease control. Climate change poses emerging challenges by altering disease epidemiology and pathogen distributions. Future management must shift from single-input chemical control toward ecologically informed, microbiome-based, and precision agriculture approaches. Research gaps include field validation of microbiome-based interventions, understanding synergistic pathogen interactions, and developing climate-adaptive strategies. This review provides a foundation for researchers and practitioners to design and implement effective, environmentally responsible integrated management programs.

KEYWORDS: soil-borne pathogens, disease epidemiology, biological control, rhizosphere microbiome, integrated disease management, sustainable agriculture

INTRODUCTION

Soil-borne plant diseases represent one of the most persistent and economically significant challenges in global agriculture. These diseases, caused by fungi, oomycetes, bacteria, and nematodes that survive in soil, result in devastating yield losses across diverse cropping systems worldwide (Katan, 2017; Panth et al., 2020). Unlike foliar pathogens that can be managed through relatively accessible above-ground interventions, soil-borne pathogens present a fundamentally different challenge due to their "hidden enemy" nature they reside in soil where detection is difficult and direct chemical control is problematic (Khan et al., 2023).

The global agricultural community faces increasing pressure to maintain or increase productivity despite mounting challenges from climate change, land intensification, and reduced access to conventional chemical controls. Soil-borne diseases exacerbate this predicament. For example, a 2019 analysis of disease burden in global agriculture estimated that soil-borne pathogens cause substantial annual losses, with Fusarium wilt alone affecting over 100 million hectares of cultivated land annually across multiple crops (Kiptui et al., 2020).

Historically, soil-borne disease management relied heavily on soil fumigation using broad-spectrum fumigants (methyl bromide, 1,3-dichloropropene) and systemic fungicides. However, multiple factors have rendered this approach inadequate and undesirable: (1) environmental restrictions limiting fumigant availability; (2) pathogen resistance development to fungicides; (3) non-target toxicity to beneficial soil microorganisms; (4) high

economic cost; and (5) regulatory constraints, particularly in organic and sustainable farming systems (Sarun, 2026d).

Recent advances in microbial ecology, multi-omics technologies, and understanding of plant immunity have fundamentally altered our conceptual frameworks for soil-borne disease management. Instead of viewing disease suppression as a problem to be solved through chemical annihilation of pathogens, contemporary science recognizes that disease-suppressive soils ecosystems naturally resistant to pathogenic establishment despite high pathogen inoculum represent functional outcomes of complex rhizosphere microbiome assemblies and plant-microbe-pathogen interactions (Gómez Expósito et al., 2017; Imperiali et al., 2022).

The shift toward integrated disease management (IDM) represents a fundamental reconceptualization of disease control. Rather than deploying single tactics, IDM combines cultural practices, resistant cultivars, targeted chemical inputs when justified, biological control agents, and soil and microbiome management to create an integrated system that is more robust, sustainable, and economically viable than any single approach (Khan et al., 2023).

This review synthesizes evidence from 2020–2026 literature with inclusion of foundational studies to provide a comprehensive, critical assessment of soil-borne plant disease biology, epidemiology, and management. The objective is to provide plant pathologists, researchers, agricultural professionals, and policymakers with evidence-based frameworks for understanding and managing soil-borne disease in contemporary agricultural systems facing climate change and sustainability constraints.

2. Diversity and biology of soil-borne pathogens

Soil-borne plant pathogens represent extraordinary biological diversity in morphology, infection strategies, survival mechanisms, and host ranges. Understanding the fundamental biology of major pathogen groups is essential for rational disease management.

2.1 Soil-borne fungi

Fungal pathogens dominate the soil-borne disease landscape. Key genera include Fusarium, Rhizoctonia, Sclerotium, Macrophomina, and Verticillium collectively causing some of the most economically destructive plant diseases globally.

Fusarium oxysporum represents one of the most cosmopolitan soil-borne plant pathogens, with formae speciales exhibiting remarkably narrow host specificity despite their genetic relatedness. F. oxysporum f. sp. lycopersici infects tomato; F. oxysporum f. sp. cubense causes Panama disease of banana; and F. oxysporum f. sp. vasinfectum devastates cotton. The pathogen's infection strategy involves root recognition and attachment through specialized structures, followed by penetration and colonization of the xylem vasculature, where microconidia are produced and systemically transported via the transpiration stream, resulting in vascular occlusion and wilting (Yadeta and Thomma, 2013). A recent analysis of F. oxysporum persistence in soil demonstrated that chlamydospores thick-walled resting spores represent the dominant inoculum source for long-term disease pressure, persisting for years even in the absence of susceptible hosts (Yan et al., 2023).

Rhizoctonia solani, a basidiomycete fungus and ubiquitous soil inhabitant, causes damping-off of seedlings and root rot across diverse crops including legumes, cereals, and horticultural species. Unlike Fusarium, Rhizoctonia typically colonizes roots as mycelia rather than through specialized spore types, although sclerotia do form under certain conditions. The pathogen produces cell wall-degrading enzymes and toxins that facilitate host cell death and enable tissue colonization (Banerjee et al., 2019). Damping-off caused by R. solani represents perhaps the most economically significant single soil-borne disease at the seedling stage globally, with typical stand losses of 20–40% in affected fields (Kühn et al., 2019).

Verticillium dahliae causes vascular wilt in over 400 plant species, with economic impact particularly severe in cotton, potatoes, and tree crops. The pathogen survives as microsclerotia in soil and plant debris, forming highly resistant survival structures that can persist for more than a decade in the absence of susceptible hosts. Upon root colonization, the pathogen produces phytotoxic compounds and blocks xylem vessels, leading to systemic wilt and plant death (Klimes and Dobinson, 2006).

Macrophomina phaseolina survives through microsclerotia small, dark, resting structures that permit long-term soil persistence. This pathogen causes charcoal rot of legumes and numerous other crops, with disease severity linked to soil temperature and moisture conditions that favor pathogen development over host growth (Kaur et al., 2012).

Sclerotium/Sclerotinia species produce true sclerotia large, melanized survival structures visible to the naked eye that permit soil persistence for years. These sclerotia germinate under specific environmental conditions to produce apothecia that release ascospores, initiating epidemics of diseases like lettuce drop and white mold of beans and canola (Bolton et al., 2006).

2.2 Oomycetes

Despite superficial resemblance to fungi, oomycetes represent a distinct evolutionary lineage within Stramenopila and possess fundamentally different molecular, biochemical, and ecological characteristics. Pythium and Phytophthora species are quintessentially aquatic pathogens whose life cycles depend on free water for zoospore mobility and infection.

Pythium species cause damping-off, root rot, and wilt across all major crop categories. At least 27 Pythium species have been identified from soybean roots alone, with species-specific responses to fungicide seed

treatments (NDSU, 2025). Pythium typically produces sporangia that release motile zoospores capable of swimming through soil water films to reach infection sites. Oospores provide long-term survival, though with considerably shorter longevity than Fusarium chlamydospores.

Phytophthora species are more host-specific than Pythium and have received renewed research attention due to emerging species like P. capsici affecting vegetables and P. cinnamomi causing widespread tree decline. Both zoosporic and oosporic survival stages enable disease perpetuation and dispersal.

2.3 Soil-borne bacteria

Ralstonia solanacearum, a Gram-negative bacterium, ranks among the top 10 plant pathogens globally based on scientific and economic importance. This vascular pathogen infects over 310 plant species across 42 families, with primary importance to solanaceous crops (tomato, potato, eggplant, pepper) and banana (Moko disease). The pathogen enters roots through wounds or natural openings, colonizes xylem vessels where it forms biofilms that obstruct water transport, and produces type III secretion system effectors that suppress plant defenses while promoting bacterial virulence (Mondal et al., 2024). Bacterial wilt caused by R. solanacearum can result in 100% crop loss under favorable conditions and remains a quarantine-regulated pathogen in many countries due to its destructive potential and ability to persist in soil and water (Kumar et al., 2024).

2.4 Plant-parasitic nematodes

Root-knot nematodes (Meloidogyne spp.) represent the most economically important plant-parasitic nematodes, with global yield losses estimated at $118 billion annually. The infective second-stage juveniles (J2s) penetrate roots, establish feeding sites (giant cells), and reproduce, with each female producing 300–500 eggs. Females produce a gelatinous egg matrix that protects eggs until juvenile development permits new infection cycles. Although nematodes are animals rather than microorganisms, they profoundly alter soil pathogen complexes by creating entry wounds for fungi and bacteria, thereby facilitating secondary pathogenic invasions (Sikora et al., 2018). Other economically important genera include Pratylenchus (root-lesion nematodes) and Heterodera/Globodera (cyst nematodes), each with specific geographic distributions and host preferences.

Table 1. Major Soil-Borne Pathogens, Hosts, Diseases, and Key Characteristics

Pathogen Group	Species	Major Hosts	Disease	Survival Structures	Infection Strategy	Primary Symptoms	References
Fusarium	F. oxysporum f. sp. lycopersici	Tomato	Vascular wilt	Chlamydospores, microconidia	Root colonization, xylem invasion	Wilting, yellowing, vascular discoloration	Yadeta and Thomma (2013); Yan et al. (2023)
Fusarium	F. oxysporum f. sp. cubense (Foc) race 1	Banana	Panama disease	Chlamydospores	Root colonization, vascular occlusion	Wilting, premature fruit drop	Dita et al. (2018)
Fusarium	F. oxysporum f. sp. cubense (Foc TR4) race 4	Banana	Panama disease TR4	Chlamydospores	Root colonization, xylem invasion	Severe systemic wilt	Dita et al. (2018)
Rhizoctonia	R. solani AG 4	Legumes, cereals, vegetables	Damping-off, root rot	Mycelium, sclerotia	Direct root invasion	Pre/post-emergence seedling death, lesions	Karpova et al. (2019)
Rhizoctonia	R. solani AG 3	Potato, beet	Black scurf, root rot	Mycelium, sclerotia	Tissue colonization	Dark lesions on roots/tubers	Leggett et al. (2003)
Verticillium	V. dahliae	Cotton, potato, tree crops	Vascular wilt	Microsclerotia	Root colonization, xylem occlusion	Systemic wilting, V-shaped yellowing	Klimes and Dobinson (2006)
Macrophomina	M. phaseolina	Legumes, grains, oils	Charcoal rot	Microsclerotia	Tissue colonization	Black tissue discoloration	Kaur et al. (2012)
Sclerotium	S. rolfsii	Vegetables, legumes,	Basal rot, damping-off	True sclerotia	Tissue invasion	Soft rot at soil line	Bolton et al. (2006)

		ornamentals					
Sclerotinia	S. sclerotiorum	Beans, canola, vegetables	White mold, stem rot	True sclerotia	Tissue colonization, systemic spread	White mycelial growth, watery lesions	Bolton et al. (2006)
Pythium	P. ultimum	Most crops	Damping-off, root rot	Oospores, sporangia	Zoospore infection through water films	Seedling collapse, pre-emergence rot	Keinath et al. (2021)
Pythium	P. irregulare	Vegetables, ornamentals	Root rot, damping-off	Oospores	Zoospore-mediated infection	Root tissue necrosis	NDSU (2025)
Phytophthora	P. capsici	Peppers, cucurbits	Crown/root rot	Oospores, chlamydospores	Zoospore infection, soil contact	Crown girdling, plant collapse	Keinath et al. (2021)
Phytophthora	P. cinnamomi	Trees, shrubs	Root rot	Oospores, chlamydospores	Zoospore-mediated	Root necrosis, tree decline	Hardham and Blackman (2018)
Ralstonia	R. solanacearum	Solanaceous crops, banana	Bacterial wilt/brown rot	Vegetative cells in debris/water	Root invasion via wounds, xylem colonization, biofilm formation	Rapid systemic wilting, bacterial ooze	Mondal et al. (2024); Kumar et al. (2024)
Meloidogyne	M. incognita	Most crops (polyphagous)	Root-knot disease	Eggs in gelatinous matrix	Root penetration, giant cell formation	Galls on roots, stunting, wilting	Roberts et al. (2009)
Meloidogyne	M. javanica	Vegetables, fruits	Root-knot disease	Eggs in gelatinous matrix	Root invasion, feeding site establishment	Root knotting, nutrient deficiency	Sikora et al. (2018)
Meloidogyne	M. hapla	Temperate crop roots	Root-knot disease	Eggs	Root penetration, syncytia formation	Root galls, plant stress	Roberts et al. (2009)
Pratylenchus	P. vulnus, P. penetrans	Tree crops, vegetables	Root-lesion disease	Free-living in soil	Root penetration, migration	Necrotic root lesions, plant decline	Sikora et al. (2018)
Heterodera/Globodera	H. glycines, G. rostochiensis	Soybean, potato	Cyst disease	Cysts with eggs	Vermiform penetration, syncytia formation	Root cyst formation, systemic stress	Sikora et al. (2018)

3. Survival and persistence of soil-borne pathogens

The capacity of soil-borne pathogens to survive unfavorable conditions including absence of susceptible hosts, environmental stress (temperature, moisture, UV radiation), and antagonism from soil microorganisms represents the fundamental property enabling their agricultural importance and management difficulty.

3.1 Survival structures

Survival structures represent the result of millions of years of pathogenic evolution, conferring resistance to desiccation, freezing, enzymatic degradation, and antagonism. Fusarium chlamydospores consist of thick walls containing melanin and protective compounds that enable decade-long viability in field soil, even under high temperature and moisture stress (Pegg et al., 2019). In contrast, macroconidia and microconidia of Fusarium lack these protective walls and deteriorate rapidly, playing roles in secondary spread rather than long-term survival.

Rhizoctonia sclerotia, though produced less reliably than in other sclerotia-forming pathogens, confer survival capacity measured in years. Recent studies demonstrate that sclerotial depth in soil and soil moisture substantially affect longevity, with sclerotia buried deep in soil and maintained at intermediate moisture levels surviving longest (Leggett et al., 2003).

Macrophomina microsclerotia are small (10–100 μm) aggregates of thick-walled cells that withstand environmental stress better than most fungal propagules. Field studies demonstrate at least 75% survival over 12 months in natural soil at 26°C and 50–55% moisture-holding capacity, though survival decreases substantially in very acidic soil (pH 4.5) or under prolonged flooding (Sinclair and Dhingra, 1995).

Verticillium microsclerotia similarly persist for extended periods in field soil and plant residue, presenting particular challenges for disease management because deep soil incorporation and crop rotation alone cannot eliminate inoculum.

Sclerotium/Sclerotinia true sclerotia are larger (>1 mm) and more visibly distinct than microsclerotia, with even greater environmental tolerance. S. sclerotiorum sclerotia can persist 5–8 years in field soil, and germination is primarily dependent on sclerotial maturation rather than immediate environmental conditions.

Pythium and Phytophthora oospores provide survival but with lower longevity than fungal sclerotia, typically persisting 1–3 years in soil. The reliance on free water for zoospore infection makes these pathogens particularly responsive to soil moisture fluctuations.

Ralstonia solanacearum survives primarily as vegetative cells within plant debris, soil organic matter, and in association with plant roots or nematode root lesions. The bacterium also survives in water sources (irrigation water, surface water) and in alternative hosts, but cannot form specialized resting structures and thus relies on host availability and moisture for extended survival (Kumar et al., 2024).

Meloidogyne eggs within females and within egg masses demonstrate substantial environmental tolerance, with some survival documented for months even under temperature extremes and desiccation stress (Roberts et al., 2009).

3.2 Inoculum Sources and Dissemination

Soil serves as a primary inoculum reservoir, with pathogen population density (inoculum density or ID) directly influencing disease incidence and severity in a relationship often described by disease progress curves or logistic models. Additionally, plant debris containing propagules represents a critical inoculum source, particularly in crop residues where pathogens continue reproduction until complete tissue decomposition. Management of these sources through sanitation, crop residue destruction, and soil treatment remains fundamental to disease suppression.

Seed transmission of soil-borne pathogens occurs, though less frequently than for foliar pathogens. Fusarium species contaminate seeds externally or internally, and transmission via seed represents a primary dispersal mechanism for range expansion of specific formae speciales. Similarly, Ralstonia solanacearum occasionally contaminates seed lots, and quarantine measures targeting infected seed represent critical regulation points.

Irrigation water and drainage water serve as important dissemination routes, particularly for oomycetes whose zoospores actively seek water films. Contaminated water has been documented as a source of long-distance pathogen dispersal and introduction to new geographic regions.

Farm machinery, contaminated soil on equipment, and soil-adhered propagules on transplants represent significant dispersal pathways within and between farms, emphasizing the importance of field sanitation practices.

4. Disease development and epidemiology

Soil-borne disease development represents a complex sequence beginning with pathogen survival in the soil, followed by inoculum activation, root recognition and chemotaxis, root attachment, penetration, colonization, toxin or effector production, host defense suppression, symptom development, pathogen reproduction, and finally return to the soil. Throughout this process, environmental conditions, host physiology, and pathogen genetics interact to determine whether infection occurs and to what severity disease develops.

4.1 Inoculum potential and disease threshold

The concept of inoculum potential (IP) or inoculum density (ID) describes the pathogenic capacity of soils, with disease severity often showing sigmoidal relationships with ID. Threshold inoculum levels exist below which disease does not develop, even with susceptible hosts, and above which disease severity increases proportionally to ID. For example, Fusarium wilt incidence may be negligible at ID < 1–2 propagules per gram of soil but increases dramatically above this threshold.

The relationship between ID and disease is not simply linear; host resistance, soil conditions, and environmental factors modify threshold levels. Disease-suppressive soils often maintain high pathogen populations while disease remains minimal, indicating that pathogen presence alone does not predict disease development (Gomez Exposito et al., 2017).

4.2 Environmental factors governing disease development

Temperature profoundly influences soil-borne disease development through direct effects on pathogen growth rates, survival, reproduction, and host susceptibility. Each pathogen exhibits characteristic temperature optima; for example, Fusarium oxysporum shows optimal growth at 24–30°C, explaining its greater prevalence in warm-season crops and tropical climates. Verticillium dahliae, conversely, exhibits more moderate temperature

optima and causes greater disease in temperate crops. Climate change represents a substantial threat because the global temperature increase is projected to expand suitable geographic ranges for many pathogens and intensify disease severity in currently affected regions (Singh et al., 2023; Kumar et al., 2025).

Soil moisture directly governs Pythium and Phytophthora diseases (which require high soil water potential for zoospore infection), influences Fusarium and Rhizoctonia disease development indirectly through effects on root exudation and host stress physiology, and is critical for Ralstonia solanacearum survival and movement. Conversely, extremely high soil moisture (waterlogging) suppresses certain pathogens like Verticillium while favoring water mold diseases. Intermediate soil moisture (50–75% of soil water-holding capacity) typically favors maximum disease development for many soil-borne pathogens, reflecting optimal conditions for both pathogen activity and susceptible host root extension into pathogen-infested soil zones.

Soil pH affects disease development through multiple pathways: altered pathogen growth rates, changes in solubility of key nutrients affecting host resistance, and shifts in rhizosphere microbial community composition and antagonism toward pathogens. Macrophomina sclerotial survival is reduced in very acidic soil (pH < 4.5), while Pythium incidence increases in acidic soils. These pH effects underscore the complexity of soil-borne disease prediction and management.

Soil organic matter and carbon: nitrogen ratio influence disease through effects on rhizosphere microbiome assembly, saprophytic microbial competition with pathogens, and production of volatile and soluble compounds with antimicrobial activity. High soil organic matter typically correlates with greater soil disease suppressiveness, though this relationship is not absolute and depends on organic matter type and quality.

4.3 Host factors and disease development

Plant age and root developmental stage influence susceptibility to root pathogens. Seedlings typically show maximum susceptibility to damping-off pathogens (Rhizoctonia, Pythium) because of immature defense systems and delicate root tissues. Established plants often tolerate root colonization by soil-borne pathogens that would kill seedlings, reflecting both physiological maturation and developed defense responses.

Host nutrition profoundly influences disease development, with effects often crop-specific. Nitrogen deficiency increases susceptibility to some pathogens but decreases susceptibility to others. Silicon application, often through mineral amendments, has been demonstrated to reduce root rot severity through enhanced mechanical barriers and induced defense responses in some pathosystems.

Plant genetic resistance represents the most economically viable management component when available. Resistance typically involves both major gene (R gene) resistance qualitative resistance showing gene-for-gene interactions and quantitative resistance (polygenic) conferring partial reduction in disease severity without complete immune response.

Table 2. Environmental and Soil Factors Influencing Soil-Borne Disease Development

Factor	Effect on Pathogen	Effect on Host	Disease Consequence	Optimal Conditions for Disease	References
	Pathogen growth rate increases with increasing temperature (species-specific optima)	Host development rate, root extension into pathogen-infested soil zones	Increased disease at optimal temperatures (e.g., F. oxysporum 24–30°C)	20–30°C for many temperate fungi; 25–35°C for warm-season pathogens	Yadeta and Thomma (2013)
High (>100% water-holding capacity)	Favors zoosporic oomycetes; inhibits some fungi	Anaerobic stress, reduced root vigor	Very high moisture favors Pythium/Phytophthora, inhibits Verticillium	Intermediate moisture (50–75% WHC) optimal for most pathogens	Singh et al. (2023)
Intermediate (50–75% WHC)	Optimal for most pathogenic fungi and bacteria	Good root growth and respiration	Maximum disease development for Fusarium, Rhizoctonia, Ralstonia	50–75% WHC	Panth et al. (2020)
Low (< 25% WHC)	Inhibits zoosporic pathogens; slows growth of most fungi	Stress response, reduced growth	Reduced disease severity overall	Not optimal for disease	Kumar et al. (2024)
Very acidic (< 4.5)	Inhibited growth of many pathogens; altered microbial community	Nutrient deficiency; aluminum toxicity	Generally reduced disease; reduced Macrophomina survival	pH 5.5–7.5 optimal for most	Sinclair and Dhingra (1995)

Neutral (6.5–7.5)	Optimal growth for most pathogens	Optimal nutrient availability and plant performance	Maximum disease severity for many pathogens	6.5–7.5	Panth et al. (2020)
Alkaline (> 8.0)	Some pathogen growth reduced; altered microbial composition	Micronutrient deficiency	Reduced disease for some pathogens; increased colonization by antagonists	Not optimal; soil suppressiveness often increased	Roychowdhury et al. (2024)
High (> 5%)	Substrate for saprophytic competitors; favors antagonistic microbes	Improved water retention; enhanced nutrient availability	Typically, reduced disease; enhanced suppressiveness	Long-term high organic matter	Deng et al. (2021)
Low (< 1%)	Limited substrate; reduced antagonistic populations	Reduced water retention; nutrient limitation	Increased disease severity; conducive soil conditions	Monoculture, low-input systems	Mitsuboshi et al. (2018)
Sandy	Rapid drainage; low water retention	Drought stress; limited root development	Generally reduced disease (low moisture); variable Pythium response	Clay-loam optimal for most	Panth et al. (2020)
Clay-loam	High water retention; complex pore space; rich microbial habitat	Good water/nutrient availability; variable aeration	Typically, high disease severity; high biological activity	Clay-loam 40–50% clay	Singh et al. (2023)
Low	Some pathogens limited; reduced virulence	Host stress; reduced defense; suppressed growth	Conflicting effects: reduced host growth may limit disease; reduced defense may increase it	N-deficient optimal varies by pathogen	Kumar et al. (2024)
High	Increased virulence for some pathogens	Increased vegetative growth; sometimes reduced defense	Increased disease for many pathogens through enhanced susceptibility	Excess N generally increases disease	Panth et al. (2020)
Silicon	Limited direct pathogen effect	Enhanced mechanical defenses; induced resistance	Reduced disease severity in many pathosystems when adequate	Silicon-fortified systems	Roychowdhury et al. (2024)
Iron	Competition between pathogen and antagonists for iron	Essential for host photosynthesis; plant stress if deficient	Siderophore-producing antagonists reduce pathogenic iron availability	Balanced iron availability	Imperiali et al. (2022)

5. Host pathogen soil interactions and plant immunity

Understanding how plants defend against soil-borne pathogens, how pathogens suppress these defenses, and how soil microbial communities modulate these interactions is fundamental to rational disease management. The classical disease triangle (host × pathogen × environment) has been reconceptualized as a multidimensional framework including soil, rhizosphere microbiome, and molecular signaling (Khan et al., 2023).

5.1 Plant Immunity: PTI and ETI

Plants recognize pathogens through two primary immune layers. Pattern-Triggered Immunity (PTI) results from perception of conserved pathogen-associated molecular patterns (PAMPs) such as bacterial flagellin, lipopolysaccharides, or fungal cell wall components by Pattern Recognition Receptors (PRRs) located on plant cell surfaces. This recognition activates signaling cascades involving Mitogen-Activated Protein Kinases (MAPKs), calcium ion influx, Reactive Oxygen Species (ROS) production, and biosynthesis of defense hormones, particularly salicylic acid (SA). PTI provides basal defense against a broad spectrum of pathogens (Boutrot and Zipfel, 2017).

Effector-triggered immunity (ETI) represents a second, more potent defense layer activated when plants recognize pathogen effector proteins (virulence factors) through intracellular Nucleotide-Binding, Leucine-Rich Repeat (NB-LRR) immune receptors. This recognition typically triggers a Hypersensitive Response (HR)

programmed cell death at infection sites that physically restricts pathogenic spread (Jones and Dangl, 2006). ETI is typically more durable than PTI because it targets specific pathogenic virulence factors, though ETI can be overcome by pathogen mutation or acquisition of effector variants.

5.2 Defense hormone signaling: SA, JA, and ET

Salicylic acid accumulates rapidly following pathogen attack and functions as a master regulator of defense gene expression through NPR1 (Non-Expressor of PR genes 1), which coordinates transcriptional activation of Pathogenesis-Related (PR) genes encoding antimicrobial proteins, hydrolytic enzymes, and phenolic compounds (Roychowdhury et al., 2024). SA-mediated defenses are particularly effective against biotrophic pathogens that require living host tissue.

Jasmonic acid (JA) and ethylene (ET) signaling pathways activate distinct sets of defense genes, particularly effective against necrotrophic pathogens and herbivorous insects. The JA and SA signaling pathways generally show antagonistic interactions, reflecting the evolutionary trade-off between defense against different pathogen types.

During effector-triggered immunity, SA and JA signaling are coordinately activated rather than antagonistic, creating enhanced defense responses. This non-canonical interaction occurs through SA receptors (NPR3/NPR4) that promote degradation of JA-responsive transcriptional repressors (JAZs), enabling both SA- and JA-responsive gene expression (Pieterse et al., 2023).

5.3 Pathogen suppression of plant immunity

Successful soil-borne pathogens have evolved sophisticated mechanisms to suppress host defenses. Type III secretion systems (TTSS) in Ralstonia solanacearum deliver effector proteins directly into plant cells, where they interfere with kinase signaling, ubiquitin-proteasome pathways controlling transcription factor stability, and synthesis of antimicrobial compounds (Mondal et al., 2024). Fusarium toxins and secondary metabolites directly kill host cells or interfere with plant hormone signaling.

5.4 Rhizosphere microbiome-mediated defense

Recent research demonstrates that the rhizosphere microbial community influenced by root exudation, plant genotype, and soil environmental conditions profoundly influences disease suppression. Disease-suppressive soils suppress pathogens through action of specific antagonistic bacteria (Pseudomonas spp., Bacillus spp., Streptomyces spp.) that produce antibiotics, siderophores competing for iron, and lytic enzymes degrading pathogenic cell walls, or through general suppression involving competition for nutrients and rhizosphere space (Imperiali et al., 2022). Mechanistic studies employing metagenomics and metabolomics have identified specific microbial taxa and metabolic pathways associated with disease suppression, including Non ribosomal peptide synthetase (NRPS) gene clusters encoding antifungal peptides (Imperiali et al., 2022).

6. Role of soil properties in disease development

6.1 Soil Texture and Structure

Soil texture (sand: silt: clay ratios) influences disease through effects on water retention, aeration, root penetration, and microbial habitat availability. Clay soils retain moisture longer, favoring Pythium and Phytophthora diseases but sometimes suppressing Fusarium diseases in excessively wet conditions. Soil structure aggregation of soil particles influences pore space, water movement, and biological activity, with well-structured soils typically supporting greater microbial diversity and disease suppression capacity.

6.2 Soil pH and buffering capacity

Soil pH operates across multiple scales: it directly affects pathogen growth optima, modifies nutrient availability to both host and pathogen, and fundamentally reshapes rhizosphere microbial communities. Most soil-borne pathogens show pH optima around neutral (pH 6–7), though with species-specific variation. Acidic soils (pH < 5.5) support greater populations of bacteria and fungi that antagonize Macrophomina, reflecting altered microbial ecology rather than direct pathogen sensitivity to pH.

6.3 Soil organic matter and soil suppressiveness

Soils receiving long-term inputs of organic amendments (compost, manure, crop residues) typically develop greater disease suppressiveness to specific pathogens (Fusarium, Rhizoctonia) regardless of inoculum density. Organic matter provides substrate for antagonistic microorganisms, promotes microbial diversity, and generates volatile and soluble compounds with antimicrobial activity (Deng et al., 2021; Mitsuboshi et al., 2018). However, the relationship between total organic matter and disease suppressiveness is not linear; certain types of organic matter (e.g., alfalfa hay at 0.8% w/w reduced Macrophomina sclerotial survival by 75%) confer suppressiveness through specific mechanisms beyond simple carbon provision (Sinclair and Dhingra, 1995).

6.4 Soil nutrient status

Nitrogen, phosphorus, potassium, and micronutrient status influence disease development indirectly through effects on host physiology and directly through microbial nutrient demand and microbial antagonism. Low nitrogen availability can increase susceptibility or resistance depending on pathogen and host; high nitrogen sometimes increases disease severity through enhanced root growth into pathogen-infested soil zones or suppression of plant defense responses.

6.5 Soil microbial biomass and diversity

The biomass and taxonomic diversity of soil microorganisms correlate positively with disease suppressiveness in many pathosystems. Soils with high bacterial and fungal diversity, assessed through molecular techniques

(16S rRNA amplicon sequencing, shotgun metagenomics), typically show reduced disease despite high pathogen populations (Gomez Exposito et al., 2017). This finding suggests that redundancy in antagonistic function multiple different microorganisms capable of suppressing pathogens provides disease control robustness more resistant to environmental perturbations than reliance on single antagonistic species.

6.6 Continuous cropping and disease build-up

Long-term monoculture or continuous cropping in the same field leads to pathogen population build-up in soil, often resulting in severe disease that persists for years even after host removal or switching to non-host crops. This phenomenon reflects pathogen adaptation to cropping system soil conditions, selection for aggressive pathogenic lineages, and possibly alterations in rhizosphere microbial communities that reduce natural disease suppression. Continuous cropping with Chinese medicinal herbs, for example, results in severe soil-borne disease problems that substantially reduce productivity and are difficult to remediate (Hong et al., 2026).

7. Major management strategies

Management of soil-borne diseases has evolved from single-tactic approaches (e.g., soil fumigation) toward integrated systems combining multiple methods based on pathosystem-specific biology and local environmental, economic, and social contexts.

7.1 Cultural practices

Crop rotation remains one of the most economically viable long-term disease suppression tactics. By removing the susceptible host, crop rotation breaks pathogen reproduction cycles and allows inoculum decay. The effectiveness depends on rotation duration and choice of non-host or poor-host crops. Fusarium wilt is best managed through rotations of 5–7 years with non-host crops; however, pathogens with wide host ranges (Rhizoctonia, Pythium, Macrophomina) require longer rotations or selection of crops resistant to multiple pathogens.

Field sanitation removal and destruction of infected plant debris, cleaning machinery, and preventing pathogen entry via contaminated soil represents foundational disease management. However, sanitation alone cannot eliminate deeply embedded inoculum in soil or address continuous cropping systems where sanitation is impractical.

Planting time modification to avoid conditions maximizing disease occurs in some systems; for example, delayed planting of legumes to avoid conditions favoring Rhizoctonia damping-off, or late-season planting of tomato to avoid peak Fusarium pressure in some regions.

Irrigation management, particularly avoiding excessive irrigation that promotes root diseases caused by oomycetes and Rhizoctonia, represents a simple yet often underutilized management tactic.

Plant density and spatial arrangement influence disease through effects on canopy microclimate, root density and competition, and soil aeration. Wider spacing and reduced plant density often suppress Rhizoctonia root rot by reducing root contact with infected soil particles and reducing host stress that increases disease susceptibility.

7.2 Physical Methods

Soil solarization, involving covering soil with transparent polyethylene film for 4–8 weeks in sunny weather, heats soil to temperatures lethal for most pathogens. Peak soil temperatures often reach 45–60°C at shallow depths, killing chlamydospores, sclerotia, and actively growing mycelium. Beyond direct thermal killing, solarization triggers beneficial microbial shifts creating residual disease suppressiveness post-treatment (Gamliel and Katan, 2020). However, solarization is economically viable primarily for high-value crops (vegetables, nursery plants) because of plastic and labor costs.

Soil steaming and hot water treatment similarly kill pathogens through thermal stress but are even more expensive than solarization, limiting application to small-scale or high-value situations.

Anaerobic soil disinfestation (ASD) represents an emerging approach involving soil saturation creating anaerobic conditions that favor fermentation and production of organic acids and other antimicrobial compounds. ASD shows promise for suppressing multiple pathogens simultaneously and appears to leave disease-suppressive microbial communities intact, unlike chemical fumigation that indiscriminately kills soil microorganisms (Gamliel and Katan, 2020).

7.3 Biological Control

Biological control exploits naturally antagonistic microorganisms to suppress pathogens, offering sustainability advantages over chemical control and avoiding pesticide resistance selection.

Trichoderma species represent the most widely researched and commercialized fungal biocontrol agents. These ascomycete fungi suppress soil-borne pathogens through multiple mechanisms: (1) mycoparasitism/hyperparasitism, actively feeding on pathogenic fungi; (2) antibiosis, producing antibiotics (gliotoxins, peptaibols, gliovirin) that inhibit pathogenic growth; (3) production of lytic enzymes (chitinases, glucanases, proteases) degrading pathogenic cell walls; (4) competition for nutrients and ecological niches; (5) Induced systemic resistance (ISR), stimulating plant defense responses through secretion of secondary metabolites and volatile organic compounds (VOCs). Field efficacy of Trichoderma varies considerably (10–90% disease reduction) depending on strain identity, formulation, environmental conditions, and rhizosphere establishment capacity. Recent field studies demonstrate that Trichoderma-amended soil can suppress Fusarium wilt, Rhizoctonia damping-off, and other soil-borne diseases, though performance consistency remains problematic (Malik et al., 2024; Hossain, 2025).

Bacillus species, particularly B. subtilis and B. amyloliquefaciens, represent Plant-growth-promoting rhizobacteria (PGPR) with demonstrated biocontrol activity against soil-borne pathogens. Bacillus suppresses pathogens through antibiosis, siderophore production competing for iron, and induction of systemic resistance, while simultaneously promoting plant growth through phytohormone production and nutrient solubilization.

Pseudomonas species (P. fluorescens, P. aeruginosa) produce fluorescent siderophores and antibiotics inhibiting diverse pathogens. A recent study demonstrated that P. rhodesiae HAI-0804 effectively suppressed Pythium damping-off and root rot in cucumber through efficient root colonization and siderophore-mediated iron competition, with efficacy enhanced by glutamate amendment (Fira et al., 2024).

Streptomyces species represent terrestrial actinobacteria producing diverse antimicrobial compounds. Recent studies document that chitinase-producing Streptomyces strains, such as Streptomycess cellulosae, effectively reduce Rhizoctonia damping-off and root rot through enzymatic hydrolysis of fungal cell walls (Abo-Zaid et al., 2024).

Mycorrhizal fungi (arbuscular mycorrhizae, ectomycorrhiza) form symbiotic associations with plant roots, increasing nutrient uptake and triggering systemic defense responses against pathogens. AM fungi reduce colonization by Fusarium, Rhizoctonia, and plant-parasitic nematodes through both direct antagonism and induced plant defense.

Despite substantial research demonstrating biocontrol efficacy in controlled environments, field performance remains inconsistent and often disappointing relative to laboratory results. Factors limiting field biocontrol include: (1) environmental variability affecting biocontrol agent survival and activity; (2) inconsistent rhizosphere colonization by biocontrol agents; (3) need for antagonistic strain selection (most commercial strains show lower antagonism than laboratory-isolated strains); (4) inadequate formulation technology leading to poor shelf-life and stability; (5) regulatory limitations in some regions; and (6) market resistance from growers accustomed to chemical pesticides (Kumar and Singh, 2023).

Future biocontrol efficacy improvement depends on: combining biocontrol agents in consortia providing functional redundancy and broader pathogen suppression; developing improved formulations preserving strain viability; integrating biocontrol with compatible management tactics (organic amendments, resistant cultivars); and employing strain selection and genetic improvement to enhance colonization and antagonism capacity.

7.4 Organic amendments and soil health management

Organic amendments (compost, manure, crop residues, biochar) modify soil biology and chemistry, often reducing disease severity through multiple mechanisms. Long-term application of organic amendments (5–10 years of continuous input) develops disease-suppressive microbiomes capable of suppressing specific pathogens (Fusarium, Rhizoctonia) regardless of inoculum density. The mechanistic basis involves: (1) direct substrate provision favoring antagonistic microorganisms; (2) production of volatile and soluble antimicrobial compounds; (3) improvement of soil physical structure enhancing water retention and biological habitat; (4) modification of nutrient availability affecting host physiology and pathogen virulence.

Compost-based soil amendments reduce disease incidence of soil-borne pathogens across multiple pathosystems. In one study, tomato plants grown in compost-amended soil showed reduced Fusarium wilt and enhanced plant growth due to disease-suppressive microbial communities dominated by Bacillus and Pseudomonas species (Deng et al., 2021).

Biochar (charred plant biomass produced through pyrolysis) improves soil structure, increases organic carbon content, and adsorbs phytotoxic compounds while providing habitat for soil microorganisms. Recent research demonstrates that 2% biochar amendment to tomato soil inoculated with Ralstonia solanacearum significantly reduced bacterial wilt severity, increased soil organic carbon and nutrient content, and shifted rhizosphere bacterial community composition toward enrichment of disease-suppressive Bacteroidetes and Pseudomonas (Ren et al., 2020).

Vermicompost (compost processed through earthworm digestion) shows enhanced disease suppression compared to conventional compost, likely due to selective colonization and enzyme production by compost-dwelling microorganisms. However, vermicompost efficacy for soil-borne disease suppression remains insufficiently studied.

Green manure (cultivation and incorporation of legume or other cover crops) provides organic matter input while potentially benefiting from N-fixation in legume systems. Green manure implementation can reduce Macrophomina and other soil-borne diseases, though effects are often modest without combining with other management tactics.

Despite substantial evidence supporting organic amendment benefits for disease suppression, the mechanism(s) underlying suppressiveness remain incompletely understood and variable across soil types and amendment types, limiting predictive capability and farmer adoption confidence.

7.5 Biofumigation

Biofumigation involves incorporation of plant residues with biocidal properties (glucosinolate-containing Brassica crops, allelopathic residues) into soil, where residue decomposition releases volatile and semi-volatile compounds suppressing pathogens and pests. The approach has shown promise in suppressing Rhizoctonia, Fusarium, Sclerotinia, and plant-parasitic nematodes in greenhouse and small-scale field studies, though field-

scale efficacy remains limited by inconsistent residue quality, inoculum persistence, and interactions with soil biology.

7.6 Chemical management

Chemical fungicides remain important soil-borne disease management tools when used judiciously within IDM frameworks. Seed treatments (mefenoxam for Pythium/Phytophthora, carbendazim for Rhizoctonia, thiram for general protection) provide early-season protection of seedlings during high-risk damping-off periods. Soil application of fungicides is less common due to cost and persistence concerns, though some situations (high-value crops, severe disease history) warrant treatment.

Systemic fungicides (triazoles, succinate dehydrogenase inhibitors) translocate within plants and provide internal protection, potentially suppressing vascular colonization by Fusarium and Verticillium more effectively than contact fungicides. However, systemic fungicide use selects for resistant pathogen populations; resistance to azoles has been documented in Fusarium and Phytophthora, and to benzimidazoles (carbendazim) in numerous pathogens.

Resistance management requires: (1) rotating fungicides with different modes of action; (2) using lower-risk fungicides (biological agents, resistance inducers) as first options when feasible; (3) monitoring pathogen resistance status; and (4) limiting applications to periods of greatest disease risk rather than calendar-based schedules.

Non-chemical alternatives to conventional fungicides are increasingly important. Resistance inducers (acibenzolar-S-methyl, phosphorous acid formulations) trigger plant defense responses, providing partial disease reduction when combined with other tactics. Recent studies document that acibenzolar-S-methyl application increases expression of PR genes and enhances resistance to Fusarium wilt and other soil-borne diseases (Conrath, 2009).

7.7 Host resistance and resistant cultivars

Host resistance represents the most sustainable, cost-effective, and farmer-accessible management component when available. Resistance is typically controlled by single major resistance genes (R genes, showing gene-for-gene interactions with pathogen avirulence genes, Avr) or quantitative resistance (polygenic) providing partial disease reduction without complete immunity.

Major gene resistance is often pathogen-race-specific, meaning pathogen strains carrying matching avirulence genes remain avirulent while strains lacking these genes overcome resistance. Historical examples abound: Panama disease of banana caused by Fusarium oxysporum f. sp. cubense (Foc) race 1 was managed by cultivar resistance for decades until emergence of Foc race 4 (Foc TR4) overcoming resistance in otherwise resistant cultivars, necessitating identification and development of new resistance sources (Dita et al., 2018).

Quantitative resistance, inherited polygenic resistance conferring partial but durable disease reduction, offers advantages of broader pathogen spectrum suppression and lower selection pressure for resistance breakdown. However, quantitative resistance reduces (but does not eliminate) disease severity, making its deployment more complex in high-disease-pressure environments.

Modern breeding approaches combine conventional pedigree selection with molecular marker-assisted selection (MAS) and genomic selection, accelerating resistance accumulation and incorporating multiple resistance genes (stacked resistance) providing enhanced durability and pathogen spectrum suppression.

Recent genomic advances using RNA-seq and CRISPR/Cas9 genome editing have identified susceptibility genes whose silencing confers enhanced resistance without yield penalties. For example, silencing susceptibility genes controlling pathogen virulence factor-induced immune suppression has shown promise in multiple pathosystems, though regulatory acceptance of genome-edited crops remains limited in many countries.

Table 3. Management strategies for soil-borne diseases

Management Strategy	Target Pathogen(s)	Mechanism of Action	Advantages	Limitations	References
Crop Rotation (5–7 years with non-host)	Fusarium, Verticillium, Sclerotinia	Breaks pathogenic life cycles; allows inoculum decay	Cost-effective; long-lasting effect; no environmental toxicity	Pathogens with wide host range; land use constraints; farmer adoption	Panth et al. (2020)
Field Sanitation	All soil-borne pathogens	Removes inoculum source; prevents dissemination	Reduces initial inoculum	Cannot eliminate deep soil inoculum; labor-intensive	Katan (2017)
Planting Time Modification	Rhizoctonia, Pythium	Aligns planting with unfavorable disease conditions	Minimizes intervention costs; integrates with other tactics	Requires knowledge of local disease phenology; variable effectiveness	Singh et al. (2023)
Resistant Cultivars	Fusarium, Rhizoctonia,	Pathogen-specific R genes	Cost-effective; sustainable;	Race-specific resistance may break down;	Roberts et al. (2009)

	Verticillium, Meloidogyne, etc.	or quantitative resistance	farmer-accessible	limited availability for some crops	
Irrigation Management	Pythium, Phytophthora, Rhizoctonia	Reduces soil moisture; avoids waterlogging conditions	Conserves water; prevents disease; improves aeration	Requires monitoring; effectiveness variable by soil type	Kumar et al. (2024)
Soil Solarization	Fusarium, Rhizoctonia, Sclerotium, etc.	Thermal killing of propagules; beneficial microbial shifts	Broad-spectrum efficacy; creates suppressiveness post-treatment	High cost (plastic, labor); requires 4–8 weeks; limited to high-value crops	Gamliel and Katan (2020)
Soil Steaming	All soil-borne pathogens	Thermal sterilization of soil	Complete pathogen control	Very expensive; requires specialized equipment; kills all microbes	Khan et al. (2023)
Anaerobic Soil Disinfestation (ASD)	Fusarium, Ralstonia, Pythium	Fermentation under anaerobic conditions; organic acid production	Preserves beneficial microbiome; cost-effective; can be integrated with field practices	Requires sustained anaerobic conditions; variable efficacy	Singh et al. (2023)
Trichoderma spp. (as biocontrol agents)	Fusarium, Rhizoctonia, Sclerotium, Verticillium	Mycoparasitism, antibiosis, lytic enzymes, ISR	Environmentally safe; multiple mechanisms; can promote plant growth	Field efficacy inconsistent (10–90% reduction); colonization variable; formulation issues	Malik et al. (2024); Hossain (2025)
Bacillus spp. (PGPR)	Fusarium, Rhizoctonia, Ralstonia, nematodes	Antibiosis, siderophore competition, ISR	Enhances plant growth; sustainable; rhizosphere establishment efficient	Field performance variable; strain-specific efficacy; regulatory approval limited	Panth et al. (2020)
Pseudomonas spp. (PGPR)	Pythium, Fusarium	Siderophore production, antibiotic synthesis, biofilm formation	Specific targeting of oomycetes; iron competition effective	Environmental sensitivity; colonization inconsistent	Fira et al. (2024)
Streptomyces spp.	Rhizoctonia, Fusarium	Chitinase production; cell wall degradation	Broad antagonism; novel bioactive compounds; sustainable	Limited commercial development; formulation challenges	Abo-Zaid et al. (2024)
Mycorrhizal Fungi	Fusarium, Rhizoctonia, Meloidogyne	Enhanced nutrient uptake; induced systemic resistance; direct antagonism	Addresses multiple crop constraints (nutrition + disease); durable	Establishment variable; interaction effects with soil microbes unpredictable	Imperiali et al. (2022)
Compost (2–5% w/w application)	Fusarium, Rhizoctonia	Substrate for antagonistic microbes; direct bioactive compounds	Cost-effective; improves soil structure; long-term suppressiveness	Requires prolonged application (5–10 years); quality variable; disease suppression not guaranteed	Deng et al. (2021)
Biochar (2–5% w/w application)	Ralstonia, Fusarium, Pythium	Adsorption of phytotoxic metabolites; microbial habitat; nutrient cycling	Improves soil physicochemical properties; persistent effect; carbon sequestration co-benefit	Production cost; field efficacy variable; environmental effects of high application rates unclear	Ren et al. (2020)
Vermicompost	Fusarium,	Selective	Enhanced	Higher production cost	Mitsuboshi et

	Rhizoctonia	microbial enrichment; enzyme production	biological activity; nutrient availability; plant growth promotion	than conventional compost; field validation limited	al. (2018)
Brassica incorporation (5–10 t/ha)	Rhizoctonia, Sclerotium, Meloidogyne	Glucosinolate decomposition to volatile isothiocyanates	Broad-spectrum suppression; integrated into crop rotation	Efficacy inconsistent; residue quality variable; requires adequate soil moisture; labor-intensive	Singh et al. (2023)
Seed Treatment (Fungicide)	Pythium, Rhizoctonia, Fusarium	Preventive fungicide application at sowing	Protects seedlings at high-risk period; cost-effective for large-scale crops	Only protects early season; systemic fungicide resistance selection risk	Panth et al. (2020)
Soil Application (Fungicide)	Fusarium, Sclerotium	Direct soil-incorporated or applied fungicide	Targets soil-resident inoculum; broad-spectrum potential	High cost; limited depth penetration; non-target soil microbe effects	Khan et al. (2023)
Resistance Inducers (Acibenzolar-S-methyl)	Fusarium, Rhizoctonia	Activation of plant defense pathways; PR gene upregulation	Integrated into crop management; no direct pathogen targeting; safety profile	Only partial disease reduction; requires combination with other tactics	Conrath (2009); Roychowdhury et al. (2024)
Silver Nanoparticles (Ag-NPs) (10–50 ppm)	Fusarium, Rhizoctonia, Pythium	ROS generation; cell membrane disruption; enzyme inhibition	Lower effective dose than conventional fungicides; multiple mechanisms	Phytotoxicity risk; soil microbiome effects unclear; field validation limited	Singh et al. (2022)
Zinc Oxide Nanoparticles (ZnO-NPs)	Fusarium, Rhizoctonia	Oxidative stress; cell wall disruption	Nutrient co-benefit (zinc); antimicrobial efficacy	Environmental accumulation concerns; non-target effects	Kumar et al. (2024)

8. Disease-suppressive soils

Certain soils suppress soil-borne diseases despite high pathogen populations, representing extraordinary biological phenomena with immense practical potential for sustainable disease management.

8.1 General vs. Specific Suppressiveness

Disease-suppressive soils are classified into two categories. General (non-specific) suppressiveness results from high overall soil biological activity, diverse antagonistic microorganisms, and/or high soil organic matter, conferring resistance to a broad spectrum of pathogens. Specific (selective) suppressiveness involves targeted suppression of particular pathogens through specific antagonistic microorganisms or compounds, typically developing after repeated pathogen exposure or targeted management practices.

8.2 Mechanistic Basis

Multi-omics studies employing metagenomics (taxonomic characterization), meta transcriptomics (functional gene expression), and metabolomics (small-molecule metabolite characterization) have identified core antagonistic microbial taxa consistently associated with disease suppression: members of Proteobacteria (especially γ-Proteobacteria), Firmicutes (Bacillus, Streptomyces), and Actinobacteria (Streptomyces). These taxa produce antibiotic compounds (often encoded by NRPS biosynthetic gene clusters), lytic enzymes, iron-chelating siderophores, and volatile organic compounds suppressing pathogenic growth.

Recent mechanistic studies employing PhyloChip-based metagenomics identified that upon pathogenic attack, plants recruit specific rhizosphere bacteria through root exudation of particular amino acids and organic acids, effectively creating a "call for help" that mobilizes natural enemies of pathogens (Chapelle et al., 2016).

9. Microbiome-based disease management

Emerging evidence supports that rationally managing rhizosphere microbiome composition and function represents a paradigm shift in disease management, moving from pathogen killing toward pathogen suppression through ecological manipulation.

9.1 Rhizosphere engineering and synthetic microbial communities

Synthetic microbial communities (SynComs) constructed from defined, characterized bacterial strains capable of suppressing pathogens represent experimental approaches to replace complex, uncharacterized soil microbiomes with simplified, reproducible communities. Early studies demonstrate that simple SynComs (3–12 bacterial strains) can suppress Fusarium wilt in model plants (Arabidopsis thaliana) and crops, though translating laboratory SynCom success to field performance remains challenging due to environmental variability, strain colonization inconsistency, and interaction complexity.

9.2 Limitations and Future Directions

Current microbiome-based management approaches face substantial challenges: (1) field performance inconsistency compared to greenhouse results; (2) strain colonization failure in some soil types and climate conditions; (3) regulatory uncertainty regarding microbial product registration and liability; (4) lack of standardization in SynCom design, microbial characterization, and formulation; and (5) intellectual property and commercial viability concerns limiting private sector investment.

Future microbiome management success requires: improved mechanistic understanding of strain-strain interactions and plant-microbe signaling; development of improved formulations stabilizing strain viability and ensuring rhizosphere establishment; integration with complementary management tactics (resistant cultivars, organic amendments); and field validation across diverse cropping systems, soil types, and climate conditions.

10. Omics and molecular approaches

Multi-omics technologies have revolutionized understanding of host-pathogen interactions, enabling identification of virulence mechanisms and plant defense pathways amendable to manipulation.

10.1 Genomics and Transcriptomics

Genome sequencing of major soil-borne pathogens (Fusarium oxysporum, Rhizoctonia solani, Ralstonia solanacearum, Phytophthora spp.) has revealed remarkably large genomes containing thousands of effector genes and secondary metabolite biosynthetic gene clusters. Comparative genomics among pathogenic and non-pathogenic strains of the same species identifies genes associated with pathogenicity, enabling targeted breeding approaches and rational resistance deployment.

Transcriptomic analysis of pathogen-infected roots versus uninfected controls identifies virulence genes induced during infection, host defense genes upregulated as defense responses, and trade-off genes reflecting pathogen suppression of host defenses. These data inform mechanistic understanding and suggest novel intervention points (e.g., silencing genes encoding effectors or pathogen virulence-related secondary metabolites).

10.2 CRISPR-Based Genome Editing

CRISPR/Cas9 genome editing technology enables precise, targeted modifications of plant and pathogen genomes, offering potential for rapid development of disease-resistant crops without traditional breeding timelines. CRISPR-mediated editing of susceptibility genes (genes required for pathogen infection) shows promise for generating durable, broad-spectrum resistance without yield penalties (Shmakov et al., 2022). However, regulatory acceptance, public perception, and liability concerns limit current deployment of genome-edited crops, particularly in regions with stringent GMO regulations.

11. Integrated disease management (IDM) framework

No single management tactic is sufficient for sustainable soil-borne disease suppression. IDM synthesizes multiple compatible tactics into holistic systems designed for specific pathosystems, local environments, farmer capabilities, and economic contexts.

11.1 IDM Principles

Effective IDM combines:

1. Host genetics: Deployment of disease-resistant or tolerant cultivars as the foundation, utilizing both major genes (high effect, potentially race-specific) and quantitative resistance (partial effect, durable)
2. Cultural practices: Crop rotation, field sanitation, planting time/density modification, irrigation management, and soil solarization or other physical methods based on economic feasibility
3. Biological control: Integration of antagonistic microorganisms (Trichoderma, Bacillus, Pseudomonas, Streptomyces) as biocontrol agents or rhizosphere-resident organisms enhanced through organic amendment and microbiome management
4. Organic amendments: Long-term soil health improvement through organic matter addition, creating naturally disease-suppressive microbiomes
5. Targeted chemical intervention: Judicious use of fungicides/bactericides for seed treatment or early-season protection when disease risk is high, with fungicide rotation to delay resistance development
6. Microbiome management: Enhancement of rhizosphere antagonistic communities through root exudate manipulation, beneficial strain inoculation, or environmental modification favoring desired microbial traits

11.2 Integration and synergistic interactions

IDM components interact, sometimes synergistically and sometimes antagonistically. For example, resistant cultivars in a crop rotation system with organic amendment input can suppress disease more effectively than any single component alone. Conversely, certain combinations may show antagonism; for example, chemical fungicides can temporarily suppress beneficial rhizosphere microorganisms, reducing biocontrol agent efficacy.

Successful IDM requires understanding these interactions and designing integrated systems where components complement rather than antagonize each other. This necessitates pathosystem-specific research and farmer adaptive management.

12. Challenges and limitations

Despite substantial research and management innovation, soil-borne disease management faces persistent challenges limiting practical implementation.

12.1 Pathogen persistence and inoculum survival

The capacity of soil-borne pathogens to survive for years in soil, even in the absence of susceptible hosts, creates fundamentally intractable management scenarios in some situations. Deep soil-embedded inoculum cannot be accessed by surface applications or shallow soil treatment, requiring either accepting disease coexistence with managed inoculum levels or implementing expensive, environmentally disruptive fumigation approaches.

12.2 Pathogen complexes

Many crops are affected by multiple soil-borne pathogens simultaneously, with different optimal management strategies, host resistance sources, and environmental optima. Managing multiple pathogens within single cropping systems requires substantially more complex and expensive IDM, increasing adoption barriers.

12.3 Genetic variability and pathotype diversity

Large pathogenic populations in soil generate substantial genetic diversity within species, with different pathotypes or races showing altered virulence profiles, fungicide sensitivity, and host range. This diversity limits the utility of single resistance genes or fungicide chemistries, necessitating constant identification of new resistance sources and fungicide alternatives.

12.4 Climate change impacts

Rising global temperatures and altered precipitation patterns are shifting geographic distributions of soil-borne pathogens, intensifying disease in currently affected regions, and introducing pathogens into previously unaffected areas. These changes occur faster than breeding programs can generate adapted resistant cultivars, creating acute management crises in some regions. For example, Fusarium wilt TR4 (race 4 of F. oxysporum f. sp. cubense) has spread to previously unaffected banana-growing regions, threatening global banana production.

12.5 Regulatory and practical constraints

Regulatory restrictions limiting soil fumigant availability (methyl bromide phased out internationally; 1,3-dichloropropene restricted in many jurisdictions) have eliminated effective broad-spectrum chemical alternatives to cultural and biological management approaches. Additionally, regulatory pathways for approving biocontrol agents and other biological products remain slow and expensive, limiting product development and commercialization.

12.6 Inconsistent biological control efficacy

Despite substantial research demonstrating biocontrol efficacy in controlled environments, field performance remains inconsistent and often disappoints relative to laboratory predictions. This gap between theory and practice reflects environmental complexity, strain colonization inconsistency, and interactions among biocontrol agents, endogenous soil microbes, and abiotic factors insufficiently understood.

12.7 Climate-driven microbiome changes

Climate change-driven alterations in soil moisture and temperature regimes, coupled with potential shifts in plant-driven root exudation profiles, may modify rhizosphere microbiome assembly and disease-suppressive capacity unpredictably. This creates uncertainty regarding reliance on microbiome-based disease management under future climate scenarios.

13. Future perspectives and research directions

13.1 Microbiome engineering and synthetic communities

Future development of defined, characterized, commercially viable synthetic microbial communities represent a promising avenue for sustainable disease management. Advances required include: (1) improved mechanistic understanding of strain-strain and plant-strain interactions enabling predictive SynCom design; (2) development of improved formulations and application methods ensuring consistent rhizosphere establishment; (3) integration with complementary management tactics (resistant cultivars, organic amendments) within IDM frameworks; and (4) field validation across diverse environments and cropping systems.

13.2 Precision microbiome management

Rather than replacing native microbiomes with defined SynComs, future approaches may involve "precision microbiome management" selectively enriching specific antagonistic lineages already present in soil through targeted organic amendments, root exudate modification through plant breeding or applied compounds, and environmental manipulation (soil pH adjustment, aeration management).

13.3 Disease-suppressive soil development

Strategic research toward understanding and deliberately creating disease-suppressive soils through specific organic amendment sequences, biocontrol organism inoculation, and cultivation practices represents a high-priority research area with substantial practical potential for sustainable disease management.

13.4 AI-assisted disease forecasting
Integration of remote sensing, soil sensors, weather data, crop phenology, and pathogen biology within machine learning frameworks enable development of farmer-accessible, location-specific disease forecasting tools supporting precision management decision-making and intervention timing.
13.5 Climate-resilient resistance breeding
Accelerated breeding and genomic selection programs are essential for developing cultivars combining disease resistance with climate stress tolerance (drought, heat, flood), ensuring agricultural productivity under increasingly variable future conditions.
13.6 Integrating Biological and Chemical Tools
Future IDM success depends on developing systems that strategically integrate biological control agents, resistant cultivars, organic amendments, and targeted chemical interventions in ways maximizing synergistic interactions while minimizing antagonisms. This requires multidisciplinary research integrating plant pathology, microbiology, chemistry, ecology, and agricultural engineering.
14. Research gaps and major unanswered questions
Despite substantial progress, significant knowledge gaps limit disease management optimization:
1. What are the specific mechanisms enabling disease-suppressive soil formation and development? How can these mechanisms be deliberately engineered into currently conducive soils?
2. How do climate change-driven shifts in soil temperature and moisture regimes affect rhizosphere microbiome assembly, disease-suppressive capacity, and pathogen ecology?
3. What factors determine biocontrol agent rhizosphere colonization and persistence? Can colonization consistency be improved through formulation, strain selection, or environmental manipulation?
4. How do multiple soil-borne pathogens interact, and can these interactions be manipulated to reduce overall disease pressure?
5. What is the relative contribution of genetic resistance, cultural practices, biological control, and microbiome effects to disease suppression in field IDM systems?
6. How can resistance durability be enhanced and resistance breakdown prevented as pathogenic populations evolve under management?
7. Can nanoparticle-based disease management be developed safely with acceptable environmental and health profiles for farmer use?
8. How can farmer knowledge, decision-making, and adoption of complex IDM approaches be improved through extension, digital tools, and incentive programs?

15. CONCLUSION
Soil-borne plant diseases represent complex, multifactorial challenges fundamentally different from foliar diseases due to pathogen persistence in soil and inaccessibility to management interventions. Historical reliance on chemical fumigation and systemic fungicides is unsustainable environmentally and economically, and increasingly ineffective due to regulatory restrictions and pathogenic resistance development.
Contemporary soil-borne disease management has shifted from single-input approaches toward ecologically informed, integrated disease management combining compatible multiple tactics: host resistance as foundation, cultural practices disrupting pathogenic life cycles, targeted use of biological control agents, soil health enhancement through organic amendments and microbiome management, and selective chemical intervention based on economic thresholds and resistance management principles.
Emerging technologies multi-omics characterization of host-pathogen-microbiome interactions, development of disease-suppressive microbial communities, precision agriculture enabled by remote sensing and AI, and nanotechnology applications offer new management possibilities requiring further development, validation, and integration into practical, farmer-accessible systems.
Future success requires: (1) continued fundamental research understanding disease mechanisms and suppressive soil development; (2) applied research translating laboratory findings to field-scale systems; (3) extension and farmer education supporting IDM adoption; (4) policy frameworks encouraging sustainable disease management through economic incentives and regulatory support; and (5) international collaboration addressing soil-borne diseases threatening food security in diverse agroecological regions and socioeconomic contexts.
The agricultural community faces an imperative to develop sustainable, resilient disease management approaches compatible with climate change adaptation, soil conservation, and food security objectives. Soil-borne disease management exemplifies this imperative and offers opportunities for transformative change toward more sustainable, productive, and ecologically sound agricultural systems.

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