

Rhizospheric fungi for sustainable wilt disease management: from plant-microbe interactions to microbial biotechnology and agro-aquaculture applications

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Abstract. *Fusarium* wilt and other soil-borne vascular diseases remain major constraints to sustainable crop production because their causal agents persist in soil, interact intimately with host roots, and are difficult to eradicate using conventional management practices. Increasing concerns regarding pesticide residues, environmental contamination, pathogen resistance, and deterioration of soil biological health have stimulated interest in rhizosphere-based biological control. Rhizospheric fungi, particularly *Trichoderma*, *Clonostachys*, arbuscular mycorrhizal fungi, selected *Penicillium* spp., and non-pathogenic *Fusarium* isolates, can suppress soil-borne pathogens through complementary mechanisms including mycoparasitism, competition, antibiosis, hydrolytic enzymes, volatile organic compounds, nutrient mobilization, root colonization, induced systemic resistance, hormonal modulation, and restructuring of the soil microbiome. Recent research indicates that disease suppression should increasingly be viewed as an emergent property of the plant–pathogen–microbiome–environment continuum rather than as the consequence of direct antagonism by a single microorganism. Disease-suppressive soils, microbiome engineering, synthetic microbial communities, multi-omics, precision formulation, and controlled delivery are consequently emerging as important directions for next-generation biocontrol. Recent studies further demonstrate that root exudates and agricultural practices can reshape rhizosphere communities associated with *Fusarium* suppression, while advances in formulation technology are improving the stability and applicability of fungal inoculants. Beyond terrestrial agriculture, fungal biotechnology offers an emerging connection with agro-aquaculture through nutrient recycling, agricultural-residue valorization, wastewater treatment, fungal–microalgal systems, and circular bioeconomy approaches. However, direct introduction of terrestrial fungal biocontrol agents into aquatic production systems remains premature and requires independent ecological, toxicological, and regulatory assessment. This review critically synthesizes the ecology, mechanisms, biotechnology, formulation, field constraints, climate-resilience potential, and agro-aquaculture prospects of rhizospheric fungi, and proposes a systems-level framework for their integration into sustainable disease management.

Keywords: rhizosphere, *Trichoderma*, *Fusarium* wilt, biological control, plant-microbe interaction, microbiome engineering, microbial biotechnology, synthetic microbial communities, climate resilience, agro-aquaculture.

Introduction. Wilt diseases are among the most economically important soil- and vascular-borne diseases of agricultural crops. *Fusarium oxysporum* and related pathogenic *Fusarium* lineages are particularly important because they infect roots, colonize vascular tissues, interfere with water transport, and induce chlorosis, wilting, vascular discoloration, stunting, and, under severe conditions, plant death (Gordon & Martyn, 1997; Dean et al., 2012). The capacity of *Fusarium* to survive as persistent soil-borne inoculum, including

chlamydospores, contributes to the long-term epidemiological stability of wilt diseases and makes eradication extremely difficult. A recent comprehensive synthesis similarly emphasizes the ecological persistence, host interactions, and management complexity of *Fusarium* wilt (Uysal et al., 2026).

Conventional management has relied on resistant cultivars, sanitation, crop rotation, soil disinfestation, chemical fungicides, and cultural practices. Although these measures can reduce disease pressure, their effectiveness is frequently constrained by pathogen persistence, host specificity, environmental variability, and the difficulty of completely eliminating soil-borne inoculum. Excessive dependence on synthetic pesticides can additionally affect non-target organisms, soil microbial communities, environmental quality, and human health. Consequently, contemporary plant pathology increasingly emphasizes integrated disease management in which biological, cultural, genetic, and ecological approaches are combined rather than used independently.

The rhizosphere provides a particularly promising biological interface for this purpose. It represents the zone of soil directly influenced by living roots and is characterized by intense chemical and biological interactions among plants, fungi, bacteria, archaea, and other soil organisms. Root exudates containing sugars, amino acids, organic acids, phenolics, flavonoids, and secondary metabolites act as substrates and signaling molecules that influence microbial recruitment and community assembly (Bais et al., 2006; Sasse et al., 2018). Beneficial rhizospheric microorganisms can consequently influence nutrient acquisition, root architecture, plant immunity, stress tolerance, and pathogen resistance (Berendsen et al., 2012; Philippot et al., 2013; Chiriack, 2013).

Among beneficial fungi, *Trichoderma* has become the most extensively developed fungal biocontrol platform. Its success is related to rapid growth, rhizosphere competence, metabolic versatility, production of antimicrobial metabolites, secretion of hydrolytic enzymes, mycoparasitism, competition, and stimulation of plant defense (Harman et al., 2004; Vinale et al., 2008ab; Saldaña-Mendoza et al., 2023). Recent literature further emphasizes that *Trichoderma* should be considered a multifunctional plant-beneficial microorganism rather than simply an antagonist of fungal pathogens. It can promote nutrient acquisition, root development and tolerance to abiotic stresses, while its metabolites influence plant growth and physiological responses.

Importantly, the efficacy of fungal biocontrol is highly context-dependent. Recent work on *Trichoderma* against banana *Fusarium* wilt emphasizes that disease suppression is an emergent outcome of several interacting mechanisms, including mycoparasitism, secondary metabolites, competition, induced systemic resistance, and rhizosphere microbiome modulation. It also highlights the persistent gap between promising greenhouse results and reliable field performance (dos Santos, 2025).

This review therefore moves beyond a conventional pathogen-antagonist perspective and considers rhizospheric fungal biocontrol as a component of an integrated plant–fungus–pathogen–microbiome–environment system. Particular emphasis is placed on fungal diversity, mechanisms of wilt suppression, disease-suppressive soils, microbial consortia, multi-omics, formulation and commercialization, climate resilience, and the emerging connection between fungal biotechnology and agro-aquaculture.

Rhizospheric Fungi: Diversity, Ecology and Functional Importance

The rhizosphere as a microbial hotspot. The rhizosphere is one of the most biologically active compartments of soil. Root-derived carbon continuously creates nutrient-rich microsites that support intense microbial growth and metabolic exchange. Root exudates regulate microbial recruitment, while microorganisms reciprocally influence root physiology, nutrient acquisition, immune responses, and developmental processes (Bais et al., 2006; Berendsen et al., 2012; Sasse et al., 2018).

Plants therefore should not be considered passive substrates for microbial colonization. They actively shape their microbial environment through exudation, root architecture, immune signaling, and physiological responses. During pathogen attack, these processes may result in selective recruitment of protective microorganisms, often conceptualized as a plant "cry for help" response. Such plant-mediated microbiome

assembly provides an important ecological basis for microbiome-assisted disease management.

Functional diversity of rhizospheric fungi. Rhizospheric fungi encompass mycorrhizal, saprophytic, endophytic and antagonistic groups. Arbuscular mycorrhizal fungi (AMF) establish symbiotic associations with plant roots and improve phosphorus and micronutrient acquisition while influencing root architecture and stress tolerance (Smith & Read, 2008; Begum et al., 2019; Rollon et al., 2017ab; Alizadeh, 2012). Non-mycorrhizal fungi, including *Trichoderma*, *Clonostachys*, *Penicillium*, *Aspergillus* and selected non-pathogenic *Fusarium*, may contribute to pathogen suppression and plant growth promotion.

The functional diversity within *Trichoderma* is particularly significant. Species- and strain-level differences determine root colonization, metabolite production, stress tolerance, enzyme secretion and antagonistic activity. Therefore, modern biocontrol development should emphasize strain-level functional characterization, rather than assuming that all isolates belonging to a particular species will exhibit equivalent efficacy. Recent reviews continue to identify *Trichoderma* as a versatile biocontrol and plant-growth-promoting fungus, while also emphasizing environmental dependence and formulation challenges (Gutiérrez-Moreno et al., 2025; Awal et al., 2024; Otithi et al., 2026).

Root colonization and plant-fungus communication. Root colonization is a prerequisite for many beneficial effects of rhizospheric fungi. Following application, a fungal strain must germinate, locate suitable root surfaces, compete with indigenous microorganisms and establish sufficiently persistent populations. Root exudates provide both nutrients and chemical signals influencing these processes.

Successful colonization may modify root morphology, nutrient uptake, hormone signaling, and defense pathways (Tătar, 2013). Beneficial fungi can influence jasmonic acid (JA), ethylene (ET), salicylic acid (SA), auxin and other signaling pathways, resulting in altered growth and immune responses (Pieterse et al., 2014; Poveda, 2021; Chiriach, 2013).

Thus, the most effective fungal inoculant is not necessarily the isolate with the strongest inhibition zone in a Petri dish, but rather the strain that combines rhizosphere competence, ecological fitness, pathogen suppression, plant compatibility and environmental resilience.

Fusarium Wilt: Pathogen Biology and Plant-Microbiome Interactions

Epidemiology and persistence. *Fusarium oxysporum* comprises pathogenic and non-pathogenic populations occupying diverse ecological niches. Pathogenic lineages may display strong host specialization and cause wilt diseases in tomato, banana, chickpea, cotton, cucumber, watermelon and numerous other crops. Infection commonly begins at the root, followed by vascular colonization and disruption of plant water relations (Gordon & Martyn, 1997).

The persistence of chlamydospores allows the pathogen to remain viable in soil for prolonged periods. Dissemination can occur through infected planting material, soil movement, irrigation water, agricultural equipment and contaminated residues. These characteristics explain why chemical control alone is rarely sufficient.

Infection process and vascular colonization. *Fusarium* wilt begins with the interaction between pathogen propagules and susceptible roots. Root exudates provide nutrients and chemical signals that stimulate spore germination and directional growth toward the root surface. After attachment, the pathogen penetrates the epidermis and cortex and eventually reaches the xylem, where it proliferates and interferes with water and mineral transport (Gordon & Martyn, 1997; Dean et al., 2012). Vascular colonization is accompanied by complex host responses involving deposition of structural barriers, production of reactive oxygen species (ROS), hormonal changes and alterations in water relations. These responses, together with fungal biomass and vessel occlusion, contribute to the characteristic wilting symptoms.

The persistence of *Fusarium* in soil further complicates disease management because chlamydospores can survive in the absence of a susceptible host. Consequently, effective biological control should not be restricted to direct inhibition of the pathogen in soil but should also interfere with root infection, enhance root health and stimulate systemic resistance. Recent reviews emphasize that *Fusarium* wilt is controlled most effectively when pathogen suppression is combined with improvement of plant physiological resistance and manipulation of the rhizosphere environment (Uysal et al., 2026) (Figure 1A).

Pathogen-host-microbiome interactions. *Fusarium* wilt is increasingly recognized as a disease resulting from interactions among the pathogen, host genotype, resident microbiome and environment. Plants continuously influence rhizosphere microbial assembly through root exudates, mucilage and immune responses, while microorganisms reciprocally regulate plant growth and defense (Berendsen et al., 2012; Philippot et al., 2013).

Recent microbiome studies demonstrate that *Fusarium* infection can reproducibly alter rhizosphere microbial composition. Su et al. (2026), using large-scale analyses of *Fusarium*-wilt rhizospheres, showed consistent shifts in microbial communities associated with diseased plants, demonstrating that disease development involves substantial modification of the rhizosphere microbiome.

Importantly, greater microbial diversity alone does not necessarily guarantee disease suppression. Instead, functionally specialized microbial communities possessing competitive, antimicrobial or plant-defense-promoting activities appear to be more important (Farooq et al., 2026; Weller et al., 2002; Todorović et al., 2023). Thus, modern biological control should aim to establish a functionally suppressive rhizosphere, rather than simply increase microbial abundance (Figure 1B).

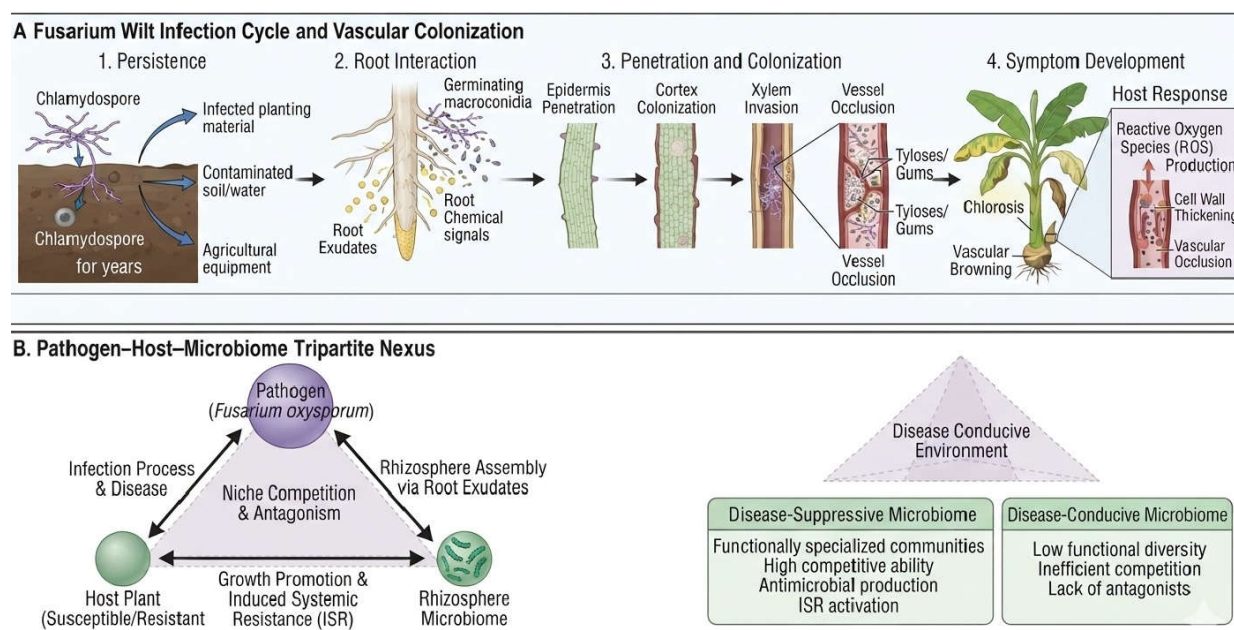


Figure 1. Multi-stage infection process of *Fusarium oxysporum* inside plant vascular systems and the tripartite ecological interactions between the host, pathogen, and rhizosphere microbiome.

Evidence for Rhizospheric Fungi in Sustainable Wilt Disease Management

***Trichoderma* spp. as principal fungal biocontrol agents.** *Trichoderma* represents the most extensively studied fungal genus for biological management of soil-borne pathogens. Its effectiveness derives from rapid growth, rhizosphere competence, mycoparasitism, competition, antibiosis, hydrolytic enzyme production, secondary metabolites and stimulation of plant defense (Harman et al., 2004; Vinale et al., 2008ab; Woo et al., 2014; Contreras-Cornejo et al., 2009).

Importantly, *Trichoderma* strains differ substantially in their biological performance. A strain showing strong inhibition of *Fusarium* in dual culture may not necessarily colonize roots effectively or survive under field conditions. Bandara and Kang (2024) demonstrated that different *Trichoderma* application methods produced different effects on tomato growth, rhizosphere microbiome composition and soil suppressiveness against *F. oxysporum*, emphasizing that application strategy can be as important as strain selection. Recent reviews similarly emphasize that the future of *Trichoderma*-based biocontrol depends on understanding strain-specific mechanisms, ecological fitness and formulation stability rather than treating the genus as a uniform biological entity (Villavicencio-Vásquez et al., 2025).

Other beneficial fungi. Although *Trichoderma* dominates the literature, other fungi possess significant biocontrol potential. *Clonostachys*, *Penicillium*, *Aspergillus*, arbuscular mycorrhizal fungi (AMF) and selected non-pathogenic *Fusarium* isolates can contribute through competition, mycoparasitism, nutrient mobilization or stimulation of host resistance (Li et al., 2024; Liu et al., 2026; Jung et al., 2012).

AMF improve phosphorus acquisition and root development and may reduce disease susceptibility through changes in root physiology and defense signaling (Smith & Read, 2008; Begum et al., 2019). Non-pathogenic *Fusarium* isolates are particularly interesting because they may occupy ecological niches similar to pathogenic populations and therefore interfere with pathogen establishment. However, molecular characterization and pathogenicity testing are essential before their agricultural deployment.

Mechanisms of Rhizospheric Fungi-Mediated Wilt Suppression. Rhizospheric fungi suppress wilt pathogens through multiple, interconnected mechanisms rather than a single mode of action (Figure 2).

Mycoparasitism and direct antagonism. Mycoparasitism involves recognition of pathogen hyphae, attachment, coiling, penetration and degradation. *Trichoderma* produces chitinases, glucanases and proteases that contribute to destruction of fungal cell walls (Benítez et al., 2004; Harman et al., 2004). This mechanism can operate together with antibiosis and competition.

Competition for nutrients and space. Rapid colonization of the rhizosphere allows beneficial fungi to compete with pathogens for carbon, nitrogen, micronutrients and infection sites. Root-colonizing strains may occupy susceptible sites before *Fusarium* establishes infection. However, the strength of competition depends on soil pH, temperature, nutrient status, moisture and indigenous microbial communities (Uysal et al., 2026).

Antifungal metabolites and volatile compounds. *Trichoderma* produces numerous secondary metabolites, including terpenoids, polyketides, peptaibols and other bioactive compounds capable of inhibiting phytopathogens (Vinale et al., 2008ab). Recent research has expanded the known chemical diversity of *Trichoderma* natural products and emphasized their potential for biological control and agricultural biotechnology (Jin & Alberti, 2025).

Fungal volatile organic compounds provide an additional mechanism because they can act without direct physical contact. However, metabolite activity observed under laboratory conditions requires validation in soil and field environments.

Cell-wall-degrading enzymes. Chitinases, β -1,3-glucanases and proteases contribute to degradation of pathogen cell walls (Benítez et al., 2004). Their activity is often induced during direct fungal interactions, suggesting that beneficial fungi can adjust their antagonistic responses according to environmental and microbial signals.

Induced systemic resistance and hormonal regulation. Root colonization by beneficial fungi can prime plants for enhanced defense through induced systemic resistance

(ISR). This process involves interactions among jasmonic acid, ethylene, salicylic acid and other signaling pathways (Pieterse et al., 2014; Poveda, 2021). *Trichoderma* may therefore provide protection even when direct physical contact with the pathogen is limited.

ROS regulation, root development and nutrition. Beneficial fungi can regulate antioxidant enzymes such as superoxide dismutase, catalase and peroxidase, thereby maintaining redox balance during pathogen attack. They may also improve root architecture and nutrient acquisition through hormonal modulation and nutrient mobilization.

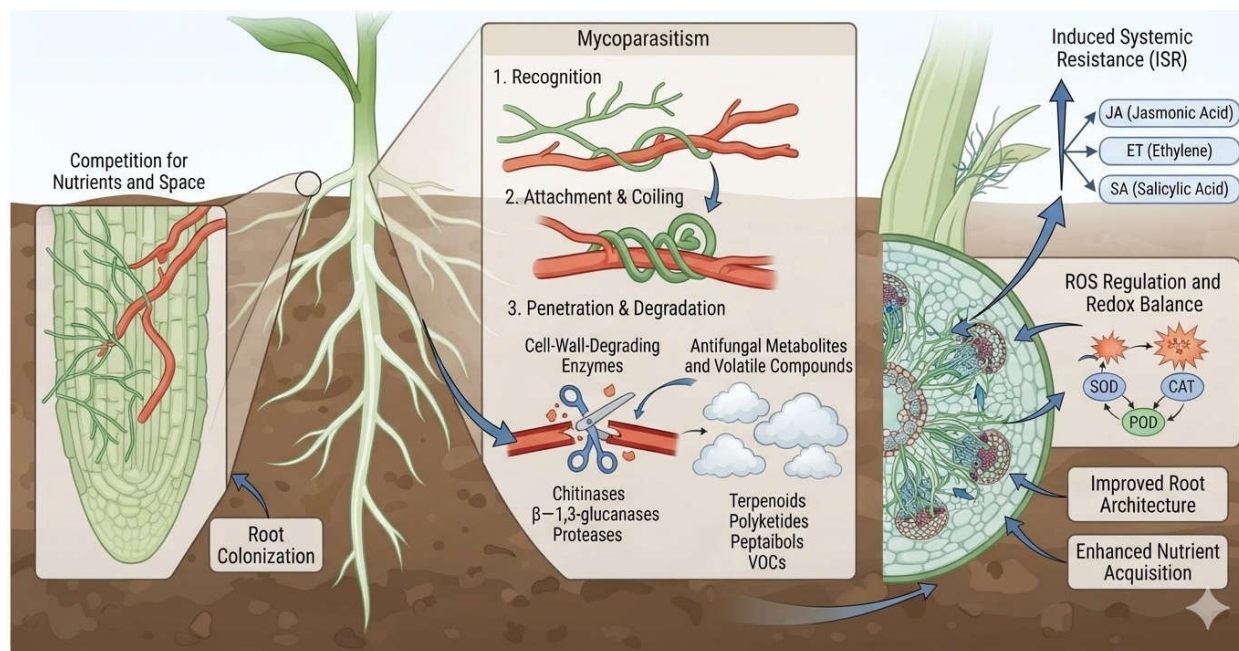


Figure 2. Mechanisms of rhizospheric fungi-mediated wilt suppression.

From Single-Strain Biocontrol to Microbial Consortia. The variable performance of individual fungal inoculants has stimulated interest in multi-microbial formulations. Single strains may perform effectively under controlled conditions but encounter strong ecological competition after introduction into field soils.

Fungal–fungal combinations can provide complementary functions, whereas fungal–bacterial consortia may combine mycoparasitism with siderophore production, antibiosis, nutrient mobilization and root colonization. Kredics et al. (2024) reviewed the increasing development of multicomponent *Trichoderma*-containing inoculants and emphasized that compatibility and functional complementarity are critical for successful consortium development.

However, simply combining several microorganisms does not necessarily improve disease control. Consortium members may compete with each other, alter metabolite production or display different growth rates. Consequently, future synthetic communities should be designed using ecological and genomic information to select organisms with complementary rather than redundant functions.

Microbiome Engineering and Disease-Suppressive Soils. Disease-suppressive soils provide a natural model for biological disease control. Such soils restrict disease despite the presence of a susceptible host and pathogen. Suppression may involve microbial competition, antibiosis, parasitism, nutrient limitation and stimulation of plant immunity (Table 1).

Root exudates play an important role in recruiting beneficial microorganisms. This plant-driven microbial assembly may become stronger after pathogen attack, thereby helping plants enrich microorganisms capable of suppressing disease. Recent studies

indicate that *Trichoderma* application can influence both rhizosphere microbiome composition and soil suppressiveness against *F. oxysporum* (Bandara & Kang, 2024).

This concept suggests a shift from microbial inoculation toward microbiome engineering, in which soil amendments, crop diversification, organic inputs and selected microbial inoculants are combined to create a stable disease-suppressive environment.

Table 1

Functional diversity and mechanisms of rhizospheric fungi involved in sustainable wilt disease management

Rhizospheric fungal group / representative taxa	Major functional traits	Principal mechanisms of wilt suppression	Plant-health benefits	Major target/ pathogen examples	Biotechnological significance	Representative references
<i>Trichoderma</i> spp.	Rapid growth; rhizosphere competence; root colonization; metabolic versatility	Mycoparasitism; competition for nutrients and space; antibiosis; hydrolytic enzymes; volatile and non-volatile metabolites; induced systemic resistance	Enhanced root growth; nutrient acquisition; defense priming; tolerance to abiotic stresses	<i>Fusarium oxysporum</i> , <i>Rhizoctonia solani</i> , <i>Pythium</i> spp., <i>Sclerotium</i> spp.	Most extensively developed fungal biocontrol platform; suitable for seed treatment, soil application and bioformulations	Harman et al. (2004); Vinale et al. (2008ab); Woo et al. (2014)
<i>Clonostachys</i> spp.	Mycoparasitism; competitive colonization; secondary metabolism	Direct parasitism; antimicrobial metabolites; enzymatic degradation	Improved root protection and potential growth promotion	<i>Fusarium</i> spp. and other soil-borne fungi	Promising component of multifunctional fungal consortia	Hermosa et al. (2012); Kredics et al. (2024)
Arbuscular mycorrhizal fungi (AMF)	Root symbiosis; extensive extraradical hyphal networks; nutrient mobilization	Improved nutrient acquisition; competition for infection sites; altered root physiology; defense priming	Enhanced P and micronutrient acquisition; improved root development; stress tolerance	<i>Fusarium</i> spp., <i>Phytophthora</i> spp. and other soil-borne pathogens	Useful as a component of integrated microbial inoculants and soil-health management	Smith & Read (2008); Begum et al. (2019)
Non-pathogenic <i>Fusarium</i> isolates	Root/rhizosphere colonization; niche occupation	Competition with pathogenic <i>Fusarium</i> ; induced resistance; ecological interference	Increased resistance to vascular infection	<i>F. oxysporum</i> formae speciales	Potential for pathogen-specific biological control; requires stringent biosafety assessment	Gordon & Martyn (1997); Bubici et al. (2019)
<i>Penicillium</i> spp.	Phosphate solubilization; secondary-metabolite production; rhizosphere competence	Competition; antibiosis; nutrient mobilization; antimicrobial metabolites	Improved nutrient availability and plant vigor	<i>Fusarium</i> spp. and other soil-borne pathogens	Potential multifunctional biofertilizer–biocontrol agents	Vinale et al. (2008ab); Poveda (2021)
<i>Aspergillus</i> spp.	Organic-acid production; nutrient solubilization; metabolic versatility	Competition; antimicrobial metabolites; nutrient mobilization	Improved nutrient acquisition and plant growth	Selected <i>Fusarium</i> and soil-borne pathogens	Potential for biofertilizer and biocontrol applications	Poveda (2021)
Endophytic and rhizospheric beneficial fungi	Internal or root-associated colonization; metabolic plasticity	ISR; competition; antimicrobial compounds; modulation of plant signaling	Enhanced systemic resistance and stress tolerance	Vascular and soil-borne pathogens	Valuable source of novel strains and metabolites	Berendsen et al. (2012); Pieterse et al. (2014)
Fungal consortia / synthetic microbial communities	Functional complementarity; niche differentiation; multi-trait activity	Combined mycoparasitism, antibiosis, competition, nutrient mobilization and ISR	More comprehensive plant protection and potentially greater field stability	<i>Fusarium</i> spp. and complex soil-borne disease complexes	Next-generation microbiome engineering and precision biocontrol	Kredics et al. (2024); Woo et al. (2014).

Omics and Microbial Biotechnology. Modern omics technologies are transforming fungal biocontrol research. Genome sequencing enables identification of genes associated with secondary metabolism, hydrolytic enzymes, stress tolerance and root colonization. Transcriptomics reveals genes activated during fungus–pathogen and fungus–plant interactions, whereas metabolomics identifies bioactive compounds responsible for pathogen suppression.

Integration of genomics, transcriptomics, proteomics and metabolomics can therefore provide a mechanistic basis for strain selection. Instead of selecting fungi only according to inhibition zones, researchers can identify strains possessing genetic and metabolic traits associated with rhizosphere competence and disease suppression.

The incorporation of artificial intelligence and machine learning may further enable prediction of fungal performance based on soil characteristics, crop genotype, climatic

conditions and microbiome composition. Such approaches could significantly reduce the time required for screening and field validation.

Formulation, Delivery and Commercialization. Formulation is one of the major determinants of successful commercialization. A biologically effective strain must survive production, storage, transport, application and establishment in the rhizosphere.

Current technologies include wettable powders, granules, liquid formulations, seed coatings, carrier-based products and encapsulated preparations. Martinez et al. (2023) emphasized the importance of carrier selection, drying technology and microencapsulation for improving *Trichoderma* viability, shelf life and field performance.

Freeze drying, spray drying, fluidized-bed drying and encapsulation provide opportunities to protect fungal propagules against environmental stress. Future formulations should additionally incorporate controlled-release systems capable of delivering viable propagules directly to the root zone.

Quality control should include accurate taxonomic identification, viable propagule concentration, genetic stability, absence of contaminants, shelf-life testing and efficacy under relevant environmental conditions.

Field-Level Constraints and Challenges. The principal limitation of fungal biocontrol is the inconsistency between laboratory efficacy and field performance. Environmental variability, host genotype, indigenous microbiota and pathogen diversity can all influence biological control.

Soil temperature, moisture, pH, salinity and organic matter affect fungal survival and activity. Similarly, plant genotype influences root exudation and microbial recruitment. Pathogen populations also vary genetically and may differ in susceptibility to individual antagonists.

Recent research reinforces the importance of environmental context. The 2026 comprehensive review of *Fusarium* wilt emphasizes that microbial biological control is highly context dependent and that functional microbial communities, rather than diversity alone, are associated with disease suppression (Uysal et al., 2026).

Long-term ecological effects must also be evaluated because repeated introduction of microbial strains could modify native microbial communities and nutrient cycling.

Climate Change and Climate-Resilient Production. Climate change is expected to alter the epidemiology and severity of soil-borne diseases by modifying temperature, precipitation patterns, soil moisture, atmospheric CO₂, and plant physiological status (Petrescu-Mag et al., 2022, 2026; Afriana, 2025; Prayudha et al., 2023; Pandey et al. 2026a). These changes can influence pathogen survival, host susceptibility, rhizosphere microbial interactions, and the efficacy of biological control agents. *Fusarium* wilt is particularly sensitive to environmental conditions because pathogen infection, root colonization, vascular development, and disease expression are strongly influenced by temperature, soil moisture, host genotype, and soil properties (Gordon & Martyn, 1997; Uysal et al., 2026). Consequently, future wilt-management strategies should not consider the pathogen, host, and biocontrol agent independently, but rather as components of a dynamic plant–soil–microbiome–climate system.

Rhizospheric fungi may contribute to climate-resilient crop production through multiple complementary functions (Alizadeh & Parsaeimehr, 2011; Chang et al., 2020; Păpuc & Bora, 2023). *Trichoderma* spp., for example, can enhance root development, nutrient acquisition, antioxidant activity, and tolerance to drought, salinity, and temperature stress while simultaneously suppressing soil-borne pathogens. A recent meta-analysis demonstrated that *Trichoderma*–plant interactions can improve several physiological and biochemical traits associated with tolerance to abiotic stress, although responses vary according to host, fungal strain, and environmental conditions (dos Santos et al., 2025). Similarly, recent reviews emphasize that the effectiveness of *Trichoderma* is strongly context-dependent and influenced by soil characteristics, crop genotype, environmental conditions, and native microbial communities (Gutiérrez-Moreno et al., 2025).

Climate-resilient biological control should therefore emphasize locally adapted fungal strains, stress-tolerant inoculants, compatible microbial consortia, and formulations capable of maintaining viability under fluctuating environmental conditions. Integration with organic amendments, conservation agriculture, biochar, crop diversification, resistant cultivars, and precision irrigation may further improve disease suppression. Rather than treating climate change solely as a constraint, microbial biotechnology can exploit beneficial plant–microbe interactions to develop adaptive production systems capable of maintaining crop health under increasingly variable environments.

Microbial Biotechnology in Agro-Aquaculture Systems. The application of rhizospheric fungi can be extended beyond terrestrial agriculture into integrated agro-aquaculture systems. Although crop production and aquaculture represent distinct production environments, both generate organic residues, nutrient-rich waste streams, and microbial resources that can potentially be linked through circular biological processes (Ulfah & Dewi, 2025; Setijaningsih et al., 2025; Lesmana et al., 2024; Castro-Gonzales et al., 2023; Aguirre et al., 2023; Deswati et al., 2023; Utomo et al., 2023). This creates an opportunity to develop integrated systems in which microbial biomass, agricultural residues, plant nutrients, and aquaculture wastewater are converted into useful biological resources (Glockow et al., 2024; Chary et al., 2024).

Conceptual link between rhizospheric fungi and aquaculture. Many fungi used in agriculture possess extracellular enzymes, nutrient-transforming abilities, biosynthetic pathways, and stress-tolerance mechanisms that are potentially useful in environmental biotechnology. Their ability to degrade complex organic substrates and interact with bacteria and algae makes them attractive components of integrated bioprocesses. Consequently, fungal biotechnology may serve as a bridge between soil disease management, organic-waste valorization, wastewater treatment, and sustainable aquaculture.

Fungal biotechnology for sustainable production. Fungal biomass and fungal metabolites have potential applications in enzyme production, organic-waste decomposition, bioconversion, biosorption, biofertilizer development, and bioremediation. *Trichoderma* and other beneficial fungi can also function as plant-growth-promoting and disease-suppressive microorganisms, thereby supporting the agricultural component of integrated production systems. The development of multifunctional microbial inoculants containing compatible fungal and bacterial species may further improve nutrient cycling and biological disease suppression (Kredics et al., 2024).

Fungi-microalgae systems for aquaculture water management. One promising application is the development of fungi–microalgae and microalgae–bacteria–fungi consortia for aquaculture wastewater treatment. Such systems exploit complementary metabolic functions: microalgae assimilate inorganic nutrients and capture CO₂, bacteria transform organic and inorganic compounds, whereas fungi can contribute extracellular enzymes, biomass formation, pollutant adsorption, and microbial-community stabilization. Experimental evidence indicates that fungi–microalgae consortia can improve nutrient removal and influence bacterial community structure more effectively than individual organisms in aquaculture water-treatment systems (2024).

More specifically, Xu et al. (2024a) demonstrated that a *Chlorella vulgaris*–bacterium–*Clonostachys rosea* consortium enhanced nutrient removal from aquaculture wastewater, with substantial removal of inorganic nitrogen and phosphate under optimized illumination conditions. Another study showed that microalgae–bacteria–fungi consortia could simultaneously reduce nutrients and selected antibiotics from aquaculture wastewater, demonstrating the potential of fungal partners in multifunctional water-treatment systems (Xu et al., 2024b).

These findings suggest that beneficial fungi traditionally investigated for plant disease management may also contribute to circular agro-aquaculture biotechnology. However, direct extrapolation from plant-associated biocontrol to aquaculture should be avoided.

Strain identity, environmental safety, host specificity, metabolite production, persistence, and effects on aquatic organisms must be evaluated before practical deployment.

Circular bioeconomy perspective. An integrated agro-aquaculture model could connect crop residues, fungal biotechnology, nutrient recovery, wastewater treatment, microbial biomass production, and agricultural bioinputs within a circular bioeconomy framework. In such systems, agricultural residues may serve as substrates for microbial cultivation, while treated aquaculture wastewater may provide recoverable nutrients for crop production. Fungal-microalgal systems could simultaneously contribute to nutrient recovery and biomass generation, thereby reducing waste discharge and improving resource-use efficiency.

Thus, the future role of rhizospheric fungi may extend beyond direct disease suppression toward multifunctional microbial platforms capable of supporting plant health, waste valorization, nutrient recovery, and environmentally sustainable aquaculture.

Integrated Disease Management and Precision Biological Control. The future management of *Fusarium* wilt should move from single-agent biocontrol toward integrated and precision-based disease management. *Fusarium* wilt is a complex disease in which pathogen genotype, host resistance, soil characteristics, environmental conditions, and microbial-community structure interact to determine disease development (Uysal et al., 2026). Therefore, no single biological control agent is likely to provide universally reliable protection across all crops and environments.

An effective integrated strategy should combine resistant or tolerant cultivars with rhizospheric fungal inoculants, organic amendments, crop rotation, sanitation, optimized irrigation, soil-health management, and rational use of chemical fungicides when necessary. Biological control should consequently be viewed as a component of integrated disease management rather than a complete replacement for all other management approaches.

Precision biological control can further improve efficacy by matching the microbial strain or consortium to specific soil, crop, pathogen, and climatic conditions. High-throughput sequencing, quantitative PCR, metagenomics, metabolomics, and predictive modelling can identify microbial signatures associated with disease suppression. Recent meta-analytical evidence indicates that *Fusarium* infection reproducibly alters rhizosphere bacterial communities, suggesting that disease-associated microbiome signatures may eventually contribute to disease-risk prediction and targeted microbial intervention (Su et al., 2026).

Microbial consortia represent another important component of precision disease management. Combining microorganisms with complementary mechanisms - such as mycoparasitism, antibiosis, nutrient competition, induced resistance, and plant-growth promotion - may provide greater functional stability than single-strain inoculants. However, microbial compatibility, ecological fitness, formulation stability, and interactions with indigenous microorganisms must be experimentally validated before field application (Kredics et al., 2024).

A practical precision-biological-control pipeline can therefore be organized into five stages: (i) diagnosis of pathogen and soil conditions; (ii) characterization of the indigenous microbiome; (iii) selection of functionally compatible fungal strains; (iv) formulation and targeted delivery; and (v) monitoring of disease, microbial establishment, and crop performance. Such an approach could transform biological control from a largely empirical practice into a predictive and site-specific biotechnology.

Biosafety, Ecological Risk and Regulatory Considerations. Despite the considerable potential of rhizospheric fungi as biological control agents, their large-scale application requires systematic assessment of biosafety and ecological consequences. A fungal strain that performs well under laboratory conditions may behave differently following introduction into complex agricultural ecosystems. Potential concerns include persistence beyond the intended application site, horizontal ecological effects, competition with

indigenous microorganisms, alteration of microbial community structure, production of secondary metabolites, and unintended effects on non-target organisms.

Risk assessment should therefore be conducted at the strain level, rather than assuming that all members of a particular genus have identical biological properties. Particular attention should be given to taxonomic identity, genome characteristics, toxin or metabolite profiles, pathogenicity potential, environmental persistence, host range, and interactions with native microbial communities. This is particularly important for widely used genera such as *Trichoderma*, because species and strains can differ considerably in ecological and physiological characteristics.

The increasing use of multicomponent microbial inoculants also introduces additional regulatory complexity. When several fungal and bacterial strains are combined, their individual safety profiles may not adequately predict the behaviour of the complete consortium. Compatibility, stability, persistence, metabolite production, and ecological interactions should therefore be assessed for the final formulation rather than solely for individual components (Kredics et al., 2024).

Regulatory frameworks should consequently encourage standardized characterization of microbial products, including strain authentication, genome-based identification, contaminant testing, viability, stability, efficacy, environmental fate, and non-target safety. Harmonization of these requirements would facilitate responsible commercialization while preventing poorly characterized products from entering agricultural markets.

An important principle for future microbial biotechnology is therefore “efficacy with ecological responsibility.” The objective should not simply be to maximize pathogen suppression but to achieve disease control while maintaining soil biodiversity, ecosystem functioning, food safety, and environmental integrity.

Research Gaps and Future Perspectives. Although substantial progress has been achieved in understanding rhizospheric fungi and their role in *Fusarium* wilt suppression, several major research gaps remain.

Bridging the laboratory-to-field gap. The most important challenge is the inconsistency between laboratory or greenhouse performance and field efficacy. Controlled experiments provide valuable mechanistic information but cannot fully reproduce the complexity of agricultural soils. Field performance is influenced by soil type, temperature, moisture, crop genotype, native microbiota, agricultural practices, and pathogen population structure. Recent analyses of *Trichoderma* applications emphasize this context dependency and the need for locally adapted strains and multi-environment validation (Gutiérrez-Moreno et al., 2025).

Future studies should therefore prioritize multi-location, multi-season experiments using standardized disease-assessment criteria and commercially realistic formulations.

Mechanism-guided selection of biocontrol fungi. Selection of fungal biocontrol agents should move beyond qualitative screening based solely on inhibition zones or pathogen antagonism. Strains should be characterized according to functional traits such as root colonization, mycoparasitism, metabolite production, nutrient competition, induced resistance, abiotic-stress tolerance, and microbiome compatibility. Recent advances in *Trichoderma* biotechnology emphasize the value of combining multiple functional traits when selecting strains for agricultural applications (Gutiérrez-Moreno et al., 2025).

Microbiome-informed disease suppression. The rhizosphere should increasingly be treated as a functional microbial ecosystem rather than merely a habitat for individual biocontrol organisms. *Fusarium* infection can reproducibly restructure rhizosphere microbial communities, indicating that disease development and microbial community assembly are closely interconnected (Su et al., 2026).

Future research should identify keystone taxa, functional genes, microbial metabolites, and ecological networks associated with disease-suppressive soils. Rather than introducing large numbers of microorganisms indiscriminately, microbial interventions could be designed to stimulate or restore naturally occurring disease-suppressive functions.

Integration of multi-omics, artificial intelligence and predictive biology. The combination of metagenomics, transcriptomics, metabolomics, proteomics, and spatial microbiome analysis provides an opportunity to connect microbial identity with biological function. Multi-omics approaches can identify fungal genes involved in secondary metabolism, host colonization, mycoparasitism, and stress adaptation, while metabolomics can identify metabolites associated with pathogen inhibition and plant defence.

Artificial intelligence and machine-learning approaches could subsequently integrate microbial, environmental, genomic, and phenotypic datasets to predict which fungal strains or consortia are most likely to succeed under particular field conditions. Such predictive systems may ultimately allow site-specific recommendations for microbial inoculants rather than relying on universal formulations.

Climate-specific microbial biocontrol. Future fungal biocontrol programmes should incorporate climate scenarios into strain selection and formulation. Stress-tolerant fungi capable of maintaining root colonization and antagonistic activity under drought, heat, salinity, or irregular soil moisture will be particularly valuable. Evidence from recent meta-analysis indicates that *Trichoderma* can enhance plant tolerance to several abiotic stresses, but the magnitude and direction of the response remain dependent on plant–fungus combinations and environmental context (dos Santos et al., 2025).

Development of stable and functionally defined consortia. Microbial consortia should be designed according to complementary ecological functions rather than simply increasing the number of microorganisms. Compatible fungal–fungal or fungal–bacterial combinations may provide broader and more stable disease suppression than single strains, but antagonism among consortium members, formulation instability, and inconsistent colonization remain major challenges (Kredics et al., 2024).

Future research should therefore focus on functionally defined synthetic microbial communities, in which each member has a clearly demonstrated ecological role and compatibility within the consortium.

Integration with agro-aquaculture and circular bioeconomy. The connection between agricultural biocontrol and aquaculture biotechnology represents an emerging research frontier. Fungal–microalgal and microalgae–bacteria–fungi systems have already demonstrated potential for nutrient recovery and treatment of aquaculture wastewater (Xu et al., 2024ab).

Future research should investigate whether beneficial agricultural fungi can be integrated safely into circular production systems in which crop residues, aquaculture wastewater, microbial biomass, and recovered nutrients are interconnected. Such systems could simultaneously contribute to disease management, waste reduction, nutrient recycling, and sustainable food production.

Overall, the next generation of fungal biocontrol research should progress from “isolate and test” toward “characterize, predict, engineer, formulate, validate, and monitor.” This transition will be essential for converting the considerable biological potential of rhizospheric fungi into dependable agricultural technologies.

Conclusion. Rhizospheric fungi represent a powerful biological resource for developing sustainable strategies against *Fusarium* wilt and other soil-borne diseases. Their importance extends beyond direct antagonism of pathogens because they can simultaneously influence root colonization, nutrient acquisition, plant defence, stress tolerance, soil microbial communities, and overall rhizosphere functioning. This multifunctionality provides a major advantage over approaches that target the pathogen through a single mechanism.

The future of fungal biocontrol will depend on understanding and managing the complete plant–pathogen–fungus–microbiome–environment continuum (Pandey et al., 2026b). Single-strain inoculants will remain valuable, but their effectiveness can be strengthened through compatible microbial consortia, microbiome-informed interventions,

improved formulations, precision delivery, and integration with resistant cultivars and other components of integrated disease management.

Climate change further emphasizes the need for resilient biological solutions capable of functioning under variable temperature, moisture, salinity, and soil conditions. At the same time, advances in genomics, metabolomics, microbiome science, artificial intelligence, and microbial biotechnology provide unprecedented opportunities to identify superior strains and design predictable microbial communities.

The emerging connection between rhizospheric fungal biotechnology and agro-aquaculture also broadens the scope of sustainable microbial applications. Fungi may contribute not only to plant disease suppression but also to nutrient recovery, wastewater treatment, biomass production, and circular bioeconomy systems. However, these opportunities must be accompanied by rigorous biosafety assessment, ecological monitoring, standardized formulation, and appropriate regulatory oversight.

Ultimately, the successful deployment of rhizospheric fungi will require a transition from empirical biological control toward mechanism-based, microbiome-informed, climate-resilient, and precision microbial biotechnology. Such an integrated framework can help reduce dependence on synthetic agrochemicals, improve soil and plant health, enhance resource-use efficiency, and contribute to more resilient and sustainable food-production systems.

Authors Contributions. SNT, AT, PP and AY wrote the original draft of the manuscript. IVP and IBD read and reviewed the manuscript. All authors reviewed, edited, and approved the final version of the manuscript.

Conflict of Interest. The authors declare that there is no conflict of interest.

Data Availability. Not applicable.

Funding. This research received no external funding.

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Received: 21 August 2026. Accepted: 25 September 2026. Published online: 25 September 2026.

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How to cite this article:

Tripathi, S. N., Tripathi, A., Pandey, P., Yadav, A., Petrescu-Mag, I. V., Bănăţean-Dunea, I. (2026). Rhizospheric fungi for sustainable wilt disease management: from plant-microbe interactions to microbial biotechnology and agro-aquaculture applications. *Aquaculture, Aquarium, Conservation & Legislation*, 19(5), 2199–2215.