

Plant Pathology, Microbial Biotechnology, and Rhizosphere Engineering for Sustainable Disease Management

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Abstract

Plant diseases continue to pose a major threat to global agricultural productivity, food security, and environmental sustainability, necessitating innovative and eco-friendly approaches for disease management. The integration of plant pathology, microbial biotechnology, and rhizosphere engineering has emerged as a promising strategy for developing sustainable crop protection systems that reduce reliance on chemical pesticides while enhancing plant health and resilience. This review paper examines recent advances in plant pathology, microbial biotechnology, and rhizosphere engineering for sustainable disease management. The study explores the interactions among plants, pathogens, and beneficial microorganisms within the rhizosphere, emphasizing the roles of plant growth-promoting rhizobacteria (PGPR), endophytic microorganisms, mycorrhizal fungi, biocontrol agents, and microbial consortia in suppressing soil-borne and foliar pathogens. Furthermore, the review discusses the application of microbial biotechnology, including microbial inoculants, biofertilizers, biopesticides, synthetic microbial communities, metagenomics, and genome-editing technologies, for improving disease resistance and maintaining rhizosphere health. Recent advances in microbiome engineering, multi-omics technologies, artificial intelligence, precision agriculture, and biosensor-based monitoring are also evaluated for their potential to optimize rhizosphere functions and enable climate-smart disease management. Despite significant progress, challenges related to microbial establishment, environmental variability, field-level consistency, regulatory frameworks, and commercialization continue to limit large-scale adoption. This review synthesizes current developments and highlights the transformative potential of integrating plant pathology, microbial biotechnology, and rhizosphere engineering to promote sustainable disease management, enhance crop productivity, and strengthen agricultural resilience.

Keywords: Plant Pathology, Microbial Biotechnology, Rhizosphere Engineering, Sustainable Disease Management, Plant Growth-Promoting Rhizobacteria, Biocontrol Agents, Endophytic Microorganisms, Mycorrhizal Fungi, Rhizosphere Microbiome, Biofertilizers, Biopesticides, Metagenomics, Precision Agriculture, Multi-Omics, Climate-Smart Agriculture.

1. Introduction

For decades, the intensive nature of global agriculture has heavily relied on synthetic fertilizers and chemical pesticides to meet the food demands of an expanding human population (Roca et al., 2024). While these inputs historically sustained high crop yields, their unchecked and continuous application

has precipitated severe ecological crises. These crises manifest as the degradation of soil physical structure, chemical pollution of aquatic environments through leaching, volatilization of greenhouse gases, and the rapid development of pesticide resistance in target pathogens (Zhang et al., 2023). Conventional disease management depends on chemical controls, employing fungicides such as prochloraz, bromuconazole, benzamides, phosphonates, and quinones to halt soilborne fungal pathogens. However, long-term dependence on these chemistries leaves persistent residues, drives target pathogens to develop resistance, and threatens non-target soil communities (Rastegari et al., 2020).

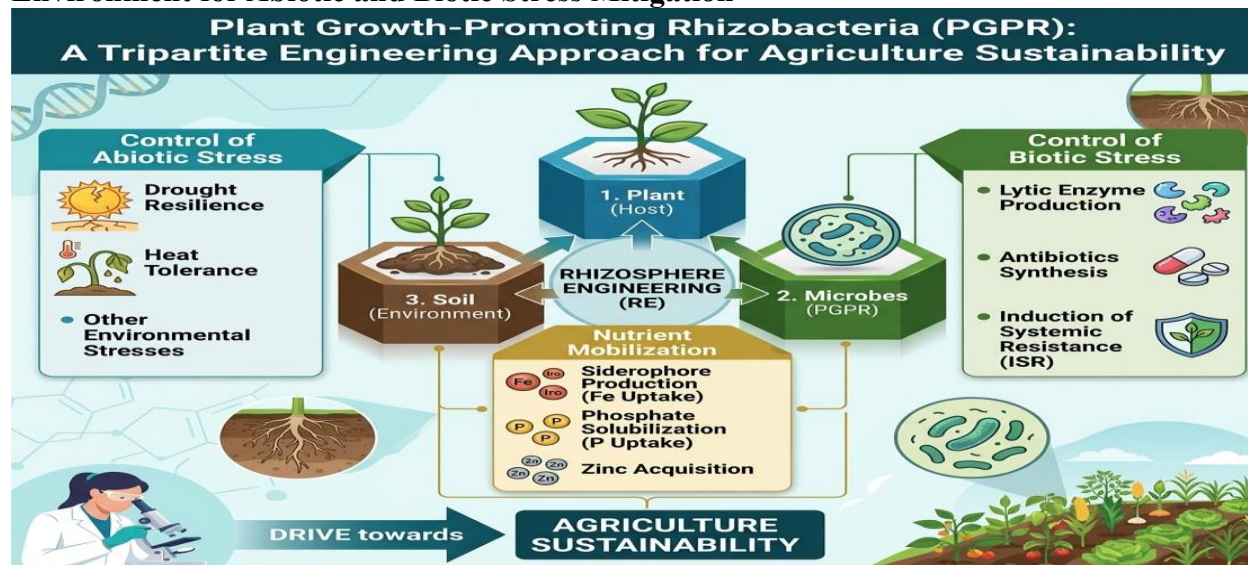
A prime example of this problem is the postharvest rot caused by *Alternaria alternata*, a storage pathogen that spoils food and produces mutagenic mycotoxins that trigger asthma and pose severe risks to human and animal health (Singh et al., 2020). In response to these challenges, modern crop protection is undergoing a transition from chemical-centric models to biological strategies that leverage the plant holobiont, which is the collective unit consisting of the host plant and its complex, associated microbiome (Dlamini et al., 2022).

Historically, the concept of plant-mediated protection has progressed over nearly a century. Chester (1933) reviewed approximately 200 scientific publications and concluded that plants acquire increased resistance to subsequent infections following an initial exposure to a pathogen, establishing early support for acquired immunity (Phour & Sindhu, 2022). This concept was demonstrated by Ross (1961), who inoculated the lower leaves of Samsun NN tobacco (*Nicotiana tabacum*) with tobacco mosaic virus (TMV) and observed that subsequent challenge inoculations on the upper leaves produced significantly smaller necrotic lesions, proving the existence of a systemic signal (Singh & Vaishnav, 2022).

Modern microbial biotechnology has since expanded this understanding, highlighting that plant-growth-promoting rhizobacteria (PGPR) and fungi (PGPF) can improve crop yields and activate systemic defense pathways, such as Induced Systemic Resistance (ISR) and Systemic Acquired Resistance (SAR) (Malik et al., 2025). Utilizing these beneficial soil microorganisms as biofertilizers and biopesticides represents an environmentally responsible approach to sustainable agriculture (Singh & Vaishnav, 2021).

This review explores rhizosphere engineering, which is the intentional manipulation of plant, microbial, and soil interactions, as a design-driven approach to replace synthetic agrochemicals with biological solutions (Sudheer et al., 2020).

Figure 1. Tripartite Engineering Interactions Among Host Plant, PGPR Microbiome, and Soil Environment for Abiotic and Biotic Stress Mitigation



2. Anatomical and Ecological Frameworks of the Root-Soil Interface

The soil surrounding plant roots is a highly complex ecological microzone containing archaea, fungi, bacteria, eukaryotes, and root systems. This microhabitat is characterized by distinct anatomical compartments that shape microbial colonization (Bano et al., 2021):

- **The Rhizosphere Proper:** The zone of soil surrounding plant roots where water, nutrients, and gases flow bidirectionally between soil, roots, and soil-dwelling organisms (Haq & Ijaz, 2020).
- **The Rhizoplane:** The interface where the root epidermis directly contacts the soil, serving as a primary site for microbial attachment and biofilm formation (Dubey & Kumar, 2022).
- **The Endorhizosphere:** The internal tissue of the root, extending from the root surface to the vascular cylinder, which endophytes colonize to establish close relationships with the host (Benaissa, 2024).

The assembly and functional diversity of the microbial communities in these compartments are shaped by rhizodeposition, which is the release of plant-derived carbon compounds. Root exudates contain a wide variety of compounds, ranging from low-molecular weight molecules like sugars, amino acids, and organic acids to high-molecular weight metabolites such as flavonoids, coumarins, and strigolactones (Mehmood et al., 2023). These exuded compounds alter the chemistry of the immediate root environment, attracting microbes to the root surface and driving microbial cell densities up to 100-fold higher than in surrounding bulk soil. This phenomenon is known as the rhizosphere effect (Hakim et al., 2021).

Rather than recruiting a random mix of soil organisms, plants select for specific microbial taxa, shaping root-associated microbiomes as extended plant phenotypes. This selection is guided by genetic associations within the host and is influenced by environmental filters, including soil pH, moisture, nutrient availability, and soil texture (Solanki et al., 2024).

For example, plant genotypes that are resistant to specific diseases select for distinct rhizosphere populations. Disease-resistant crop cultivars show different microbial densities and compositions in their rhizosphere compared to susceptible varieties (Tan et al., 2022). In tomato cultivars resistant to *Verticillium* wilt, a high density of *Trichoderma viride* enriches the rhizosphere and helps reduce wilt severity in susceptible neighboring crops. Similarly, resistant varieties of flax (*Linum usitatissimum*) release toxic glycosides and hydrocyanic acid in their root exudates to selectively suppress pathogenic fungi while supporting beneficial, tolerant species (Cheng et al., 2023).

Unintentional selection for these beneficial rhizosphere traits has occurred throughout agricultural history. Plant breeders selecting for the highest-yielding crop lines under field conditions have frequently crossed and selected for root traits that support beneficial microbe-plant associations (Guo et al., 2024).

Additionally, symbiotic partnerships, such as those with arbuscular mycorrhizae and nitrogen-fixing bacteria, are essential for primary production and ecosystem sustainability. The signaling pathway that regulates the symbiosis between legumes and *Rhizobium* proceeds through structured stages (Nadarajah & Abdul Rahman, 2023). During the preinfection stage, both partners exchange chemical signals for mutual recognition, causing the bacteria to attach to root hair cell walls. The infection process then triggers root hair curling and the formation of infection threads that transport the bacteria into the cortex. This is followed by specialized root nodule formation, and finally, the differentiation of the bacteria into nitrogen-fixing bacteroids within the nodule cells (Fazeli-Nasab & Rahmani, 2021).

3. Biochemical Signatures and the "Cry for Help" Recruitment Pathway

When plants are exposed to environmental stresses or pathogen attacks, they modify their carbon allocation and alter the quantity and composition of their root exudates (Umer et al., 2025). Under the "cry for help" hypothesis, stressed plants release specific primary and secondary metabolites to recruit

protective, disease-suppressing soil microbiomes. Nonpathogenic bacteria and their elicitors can also trigger this response, preparing the plant to resist subsequent pathogen invasions (Sharma et al., 2021). A key chemical family involved in these signaling processes is the benzoxazinoids (BXs), which are secondary metabolites produced by grass species (Poaceae). The primary BX exuded by maize roots is 2,4-dihydroxy-7-methoxy-2H-1,4-benzoxazin-3(4H)-one (DIMBOA). DIMBOA acts as an antibacterial agent and a chemoattractant (Niu et al., 2020). Chemotaxis assays and soil colonization trials show that DIMBOA recruits *Pseudomonas putida* KT2440, a beneficial colonizer of the maize rhizosphere, by upregulating bacterial genes involved in benzoate catabolism and chemotactic motility. In contrast, DIMBOA-deficient *bx1* maize mutants show significantly lower colonization by *P. putida* (Akanmu et al., 2021).

Once released, BXs degrade in aqueous environments with a half-life of under 24 hours into derivatives like 2-benzoxazolinone (BOA), 6-chloro-2-benzoxazolinone (CDHB), and 2-mercaptobenzothiazole (MBT). These compounds show direct antibacterial activity against pathogens such as *Ralstonia solanacearum*, the causal agent of bacterial wilt. MBT shows the lowest minimum inhibitory concentration (MIC) against *R. solanacearum*, followed by CDHB, DIMBOA, and BOA (Tariq et al., 2020).

However, high concentrations of DIMBOA can act as a double-edged sword; metatranscriptomic analyses indicate that excessive DIMBOA in root exudates can enrich for metabolic pathways associated with plant diseases in some contexts. Additionally, microbial species differ in their ability to metabolize and tolerate BXs (Kashyap et al., 2025). While some bacteria can degrade DIMBOA and its glucoside GDIMBOA, others show high sensitivity to DIMBOA and derived compounds like 2-aminophenol (AP) and 2-acetoamidophenol (AAP), highlighting how chemical exudates act as selective filters in the rhizosphere (Jaggi et al., 2023).

Table 1: Biochemical Profiling and Minimum Inhibitory Concentrations (MIC) of Benzoxazinoid-Derived Compounds Against *Ralstonia solanacearum*

Compound Name	Chemical Class	Plant Source	Minimum Inhibitory Concentration (MIC) against <i>Ralstonia solanacearum</i>	Primary Antibacterial / Physiological Effects
2-Mercaptobenzothiazole (MBT)	Benzothiazole Derivative	Maize Degradation Product	50 mg/L	Strongest direct bactericidal activity, inhibits biofilm formation, and restricts swarming motility
6-Chloro-2-benzoxazolinone (CDHB)	Benzoxazolinone Derivative	Maize Degradation Product	100 mg/L	Disrupts bacterial cell membranes, reduces biofilm, and limits motility
2,4-Dihydroxy-7-methoxy-2H-1,4-	Cyclic Hydroxamic Acid	Wheat, Rye, and Maize (<i>Zea mays</i>)	200 mg/L	Acts as a chemoattractant for <i>P. putida</i>

benzoxazin-3(4H)-one (DIMBOA)				KT2440, inhibits pathogen growth, and induces callose deposition
2-Benzoxazolinone (BOA)	Benzoxazolinone	Spontaneous decomposition product of DIBOA	300 mg/L	Weakest direct antibacterial agent; highly persistent due to low microbial degradation rates

Other secondary metabolites also serve as signaling cues during stress. For example, the coumarin scopoletin is exuded by *Arabidopsis thaliana* roots under iron deficiency and pathogen stress. Scopoletin reduces insoluble Fe³⁺ to bioavailable Fe²⁺ and reshapes the root microbiome by selectively inhibiting competitors while supporting beneficial, scopoletin-tolerant bacteria (Babalola et al., 2021). Exogenous coumarin application on crops like pepper and wheat under imidacloprid (IMI) stress increases the abundance of beneficial microbes, stimulates plant defense pathways, and elevates endogenous concentrations of salicylic acid, butyric acid, and ferulic acid to mitigate stress. Under pathogen attack, plants secrete coumarins, (+)-pilocarpine, and soybean glycosides to suppress pathogens and support rhizosphere colonization (Verma et al., 2025).

Furthermore, foliar pathogen infection can trigger systemic belowground recruitment. Inoculation of *Arabidopsis* leaves with *Pseudomonas syringae* pv. *tomato* (Pst) triggers the expression of the Aluminum-Activated Malate Transporter 1 (ALMT1) in roots (Gai & Wang, 2024). This transporter facilitates the secretion of malic acid, which recruits the beneficial bacterium *Bacillus subtilis* FB17. Once established, *B. subtilis* triggers systemic defenses that protect the plant against subsequent foliar attacks by Pst (Fatima et al., 2025).

Under phosphorus starvation, plant roots increase the secretion of malate, carboxylate, and oxalate. These organic acids mobilize locked phosphorus by chelating metal ions in insoluble complexes. Under toxic aluminum stress, the roots of soybean (*Glycine max*) and maize secrete citrate, which chelates harmful Al³⁺ ions to prevent root damage (Dries et al., 2021).

Plants also utilize volatile organic compounds (VOCs) and specialized metabolites for defense. Tomato roots infested with parasitic nematodes increase the biosynthesis of strigolactones. Tomato plants treated with *Bacillus amyloliquefaciens* release the volatile beta-caryophyllene, which signals neighboring plants to secrete salicylic acid into their rhizosphere, altering their microbial communities from a distance (de Faria et al., 2021). Salicylic acid biosynthesis initiates in the chloroplasts before being transported via the phloem to the roots, where it is exuded alongside camalexin to coordinate defense responses. Additionally, plants release direct defense compounds, including phenolics, terpenoids, and sulfurous volatiles like dimethyl disulfide (DMDS) and dimethyl trisulfide (DMTS), to directly inhibit invading pests and pathogens (Yang et al., 2023).

4. Molecular Mechanisms of Microbially Mediated Induced Systemic Resistance

Beneficial soil microorganisms protect their hosts from infection through both direct competitive exclusion and the activation of systemic plant defenses. Elicitation of plant systemic resistance is divided into two primary pathways: Systemic Acquired Resistance (SAR) and Induced Systemic Resistance (ISR) (Kumar, 2022).

While SAR is typically triggered by pathogenic infection and relies on salicylic acid (SA) signaling to activate pathogenesis-related (PR) genes, rhizobacteria-mediated ISR is generally independent of SA.

Instead, ISR is regulated by signaling networks dependent on the jasmonic acid (JA) and ethylene (ET) pathways. This hormonal signaling has two branches that cross-communicate with other hormonal networks, such as the abscisic acid (ABA) pathway, through shared transcription factors (Beattie et al., 2024).

The transcription factor NPR1 is required for both SA-dependent PR gene expression during SAR and the JA/ET-dependent defense responses activated during rhizobacteria-mediated ISR. Genetic studies in *Arabidopsis thaliana* using mutants such as *dde2-2* (defective in jasmonic acid synthesis) and *ein2-1* (ethylene-insensitive) confirm that intact JA and ET signaling pathways are required for ISR (Hassan & Nawchoo, 2022).

During ISR, root colonization by PGPR primes the plant's immune system, allowing a faster and stronger activation of defense-related genes upon subsequent pathogen attack. This primed state is triggered by microbial determinants known as resistance elicitors, which include (Barupal, 2025):

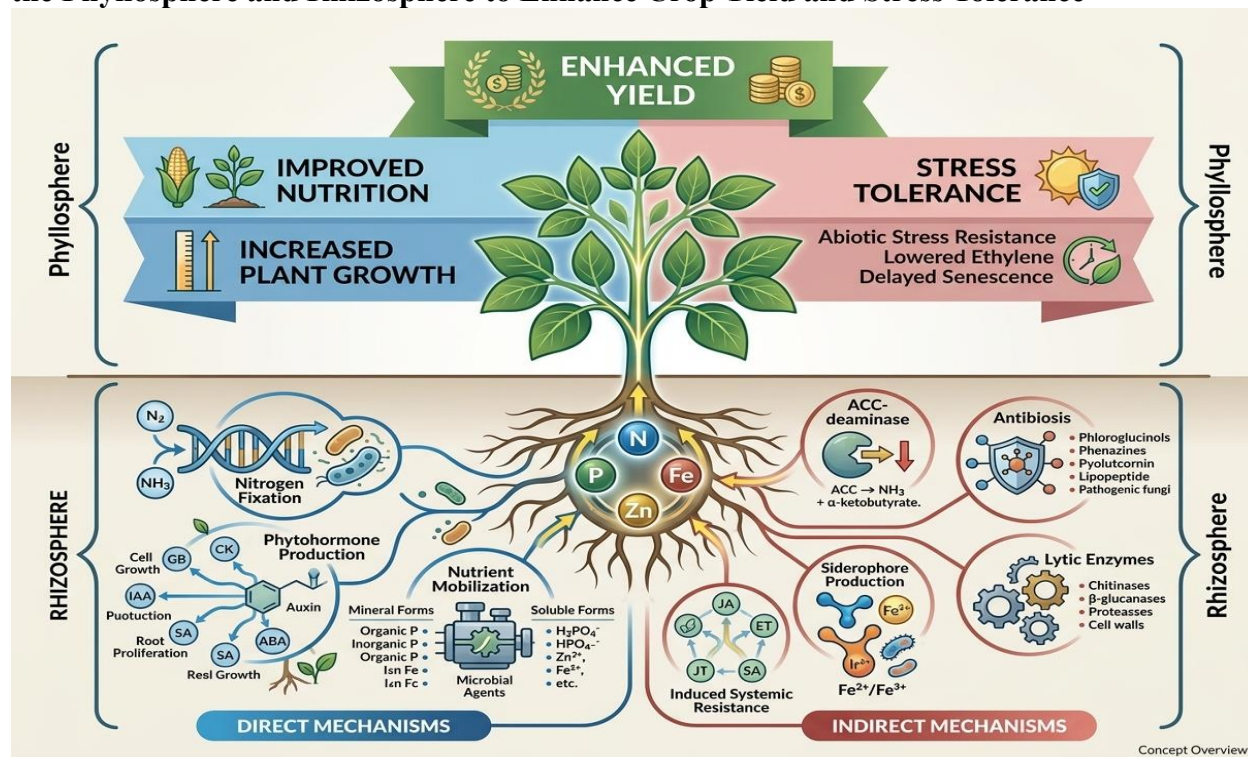
- Flagellins and flagellar proteins.
- Lipopolysaccharides, such as fucose and rhamnose.
- Siderophores and pyoverdine.
- Lipopeptides and other secondary metabolites.

The activation of ISR leads to physiological changes and the production of specialized enzymes, including (Wei et al., 2020):

- **Phenylalanine Ammonia Lyase (PAL):** A key enzyme in the phenylpropanoid pathway that supports the synthesis of phytoalexins and lignin.
- **Chitinases, beta-1,3-Glucanases, and Thaumatinins:** Pathogenesis-related (PR) proteins that directly degrade fungal cell wall polymers.
- **Peroxidase (PO) and Polyphenol Oxidase (PPO):** Oxidative enzymes that assist in cell wall reinforcement and the oxidation of phenolic compounds into quinones.
- **Superoxide Dismutase (SOD), Catalase (CAT), and Ascorbate Peroxidase (APX):** Antioxidant enzymes that scavenge reactive oxygen species (ROS) to prevent cellular damage.
- **Lipoxygenase (LOX):** An enzyme involved in the octadecanoid pathway that initiates jasmonic acid biosynthesis.
- **Proteinase Inhibitors:** Proteins that disrupt the digestive enzymes of attacking insect pests (Czajkowski et al., 2025).

In addition to suppressing diseases, microbially mediated ISR reduces the performance of leaf-chewing herbivores such as *Mamestra brassicae*. Inoculation with *Pseudomonas simiae* WCS417r (formerly *Pseudomonas fluorescens* WCS417r) alters the production of glucosinolates (GLS) and camalexin in *Arabidopsis* (Mohamed et al., 2021). Root colonization enhances the synthesis of camalexin and aliphatic glucosinolates while suppressing herbivore-induced levels of indole glucosinolates, protecting the plant against both pathogen and insect attack (Gupta, 2024).

Figure 2. Direct and Indirect Mechanisms of Plant Growth-Promoting Rhizobacteria (PGPR) in the Phyllosphere and Rhizosphere to Enhance Crop Yield and Stress Tolerance



5. Non-Ribosomal Lipopeptides and Microbial Functional Metabolites

A primary mechanism of direct pathogen suppression by biocontrol bacilli is the production of cyclic lipopeptides (cLPs) synthesized via multi-modular non-ribosomal peptide synthetase (NRPS) complexes. These lipopeptides are classified into three major families: surfactins, iturins, and fengycins (Afridi et al., 2022).

The surfactin family (approximately 1.36 kDa) consists of an amphipathic cyclic lipoheptapeptide backbone with the amino acid sequence L-Glu-L-Leu-D-Leu-L-Val-L-Asp-D-Leu-L-Leu (ELLVDLL), containing a LLDLLDL chiral sequence linked to a beta-hydroxy fatty acid chain of 12 to 16 carbon atoms (Dubey & Sharma, 2021). Surfactin biosynthesis is encoded by the *urf* operon, which contains four open reading frames that direct the surfactin synthetase multienzyme system. Surfactins have high surfactant activity and direct antibacterial properties, and they act synergistically with iturins or fengycins (Alqahtani, 2025).

The iturin family (approximately 1.1 kDa) comprises cyclic heptapeptides containing three D-amino acids (Tyr, Asn, Asn) and four L-amino acids (Pro, Ser, Asn, Gln) linked to a beta-amino fatty acid chain of 14 to 17 carbons (Chowdhary et al., 2022). This family includes iturin A, iturin C, bacillomycins (D, F, L, Lc), and mycosubtilin, which disrupt fungal membranes by interacting with lipid components, leading to cell lysis. The iturin operon spans 38 to 40 kb and contains four open reading frames (*ituD*, *ituA*, *ituB*, and *ituC*). The *ituD* gene shares homology with the malonyl-CoA transacylase *FabD*, which is involved in fatty acid synthesis in *Escherichia coli* and *B. subtilis*. The *ituB* and *ituC* genes encode large peptide synthetases of 609 and 297 kDa that assemble the peptide chain (Gosal et al., 2020).

The fengycin family includes fengycins A and B, which are cyclic decapeptides linked to a beta-hydroxy fatty acid chain that exhibit fungitoxic activity against filamentous fungi. Fengycin biosynthesis is controlled by the *fen* cluster containing five NRPS genes (*fenC*, *fenD*, *fenE*, *fenA*, and *fenB*) (Ke et al., 2021). The *fenC* gene encodes a fengycin synthetase of 2,560 amino acids (287 kDa) that activates L-glutamic acid and L-ornithine, while *fenB* activates L-isoleucine and contains a

thioesterase domain for synthesis termination. The *pps* gene group is also involved, with *ppsE* sharing 74% sequence identity with *fenE* (Behera et al., 2024).

The lipophilic tail structure is a key factor in fengycin functionality. While straight-chain saturated fatty acids are initiated by a malonyl-acyl carrier protein (ACP) and acetyl-CoA, branched-chain fatty acids require precursors like isobutyl-CoA, isovaleryl-CoA, and alpha-methylbutyryl-CoA, which are synthesized from L-valine, L-leucine, and L-isoleucine, respectively (Iqbal, 2026). This synthesis is catalyzed by the enzyme system encoded by the genes *ilvBN*, *ilvGM*, *ilvIH*, *ilvC*, *ilvD*, and *ilvE*. Fructose can induce the biosynthesis of these branched-chain amino acids by upregulating *ilvBN* by a factor of 1.5, demonstrating how carbon sources regulate lipopeptide assembly (Rai & Prasad, 2023). Other cyclic lipopeptides from *Bacillus* species show specialized functions. Licheniformin, produced by *Bacillus licheniformis*, is a surfactin-like lipopeptide that combats pathogens and dislodges persistent biofilms. Kurstakins, cyclic lipopeptides from *Bacillus subtilis*, *Bacillus cereus*, and *Bacillus thuringiensis*, also disrupt biofilms and show antibacterial and antifungal activity (Raghuvanshi et al., 2025).

These lipopeptides are produced by a wide range of plant-associated *Bacillus* species, including *B. subtilis*, *B. amyloliquefaciens*, *B. mojavensis*, *B. licheniformis*, *B. pumilus*, *B. megaterium*, *B. cereus*, and *B. thuringiensis*. Biological screenings show that the biosynthetic genes for bacillomycin (*bmyB*), surfactin (*surfAA*), and fengycin (*fenD*) are common across these species, with up to 98.4% of isolated strains producing surfactin, 90.6% producing iturin, and 79.7% producing fengycin isoforms to inhibit phytopathogens (Pratheesh et al., 2020).

6. Soil Amending, Prebiotics, and Legacy Dynamics

Rhizosphere microbiome engineering employs soil amendments and prebiotic compounds to enrich beneficial, resident microorganisms. Rhizosphere prebiotics are organic molecules that stimulate the growth of beneficial microbes without promoting pathogen growth (Berg et al., 2021). Metabolites like ribose, lactic acid, xylose, mannose, maltose, gluconolactone, and ribitol, identified from the rhizospheres of healthy plants, selectively support *Bacillus* and *Lysobacter* species to suppress tomato bacterial wilt. Similarly, adenosine enrichment in the citrus rhizosphere recruits beneficial consortia that improve both heat and disease resistance (Fasusi et al., 2021).

Prebiotics also modulate soil fertility and enzyme activities. For example, prebiotic formulations such as SPN and SPK show distinct ecological effects (Kaur, 2022):

- **SPN Formulation:** Increases the soil fungi-to-bacteria ratio and elevates alpha-glucosidase and beta-galactosidase activities.
- **SPK Formulation:** Increases the activities of arylsulfatase, phosphatase, alkaline phosphatase, and urease to improve nutrient cycling (Gurikar et al., 2022).

Additionally, biochar, a carbonaceous material produced by the pyrolysis of biomass at 300 to 700 degrees Celsius under restricted oxygen, serves as a multi-functional soil amendment (Valente et al., 2025). Composed of 70 to 80% aromatic carbon, biochar alters soil physical and chemical properties. Its porous structure decreases bulk density, increases soil aggregate stability, improves water holding capacity, and provides physical refuges that protect microorganisms from desiccation and predators. Amending soil with biochar also buffers pH, raises cation exchange capacity (CEC), and acts as a thermal buffer to regulate temperature variations around plant roots (ElSheikh & Shahein, 2025).

At the cellular level, biochar stimulates plant defenses, increasing catalase and peroxidase activities to scavenge reactive oxygen species (ROS). It also adsorbs organic pollutants like atrazine and heavy metals such as lead (Pb), helping to prevent soil contamination (Bhardwaj et al., 2024). In tomato crops, biochar amendments enrich beneficial *Pseudomonas* species that suppress *Fusarium* wilt, while reducing the swarming motility and root colonization of *Ralstonia solanacearum*. Meta-analyses show that applying 3 to 5% biochar produced at 350 to 600 degrees Celsius can reduce plant disease incidence by up to 59% (Yadav et al., 2023).

Table 2: Functional Characteristics of Prebiotics and Carbonaceous Soil Amendments

Amendment Type	Key Chemical / Physical Characteristics	Targeted Pathogen / Stress	Primary Mechanisms of Action
SPN Prebiotic	Nutrient-rich biostimulant formulation	General soilborne pathogens	Increases the fungi-to-bacteria ratio, and elevates alpha-glucosidase and beta-galactosidase activities
SPK Prebiotic	Nutrient-rich biostimulant formulation	Nutrient-deficient soils	Enhances arylsulfatase, phosphatase, alkaline phosphatase, and urease activities to improve nutrient availability
Biochar	70 to 80% aromatic carbon; highly porous physical structure	<i>Fusarium</i> spp., <i>Phytophthora</i> spp., and drought	Decreases bulk density, provides physical microbial refuges, buffers pH, and adsorbs heavy metals and organic pollutants
Adenosine	Purine nucleoside prebiotic	Soilborne pathogens and high temperatures	Selectively recruits beneficial rhizosphere taxa, and improves plant heat and disease resistance

The accumulation of these beneficial biological changes leads to soil memory, also known as the soil legacy effect. Following a disease outbreak, the "cry for help" recruitment pathway enriches the soil with antagonistic consortia that protect subsequent plant generations. Classic examples include take-all decline in wheat monocultures and the suppression of *Rhizoctonia solani* in sugar beet soils (Nyamboga et al., 2025).

However, drastic soil disinfestation practices can temporarily disrupt these biological legacies. Anaerobic soil disinfestation (AD), which uses crop residues combined with plastic covering to create anaerobic conditions, eliminates target nematodes and pathogens, but can also cause a temporary loss of general soil suppressiveness (Ayaz et al., 2023). Three months post-AD treatment, soils can show a significant shift in microbial composition, characterized by an increase in Bacteroidetes and a decrease in Acidobacteria, Planctomycetes, and Nitrospirae. This compositional shift coincides with a loss of volatile organic compounds that suppress the oomycete *Pythium intermedium*. Suppressiveness typically recovers around 15 months post-treatment as the bacterial community stabilizes, highlighting the dynamic nature of soil memory (Swetha et al., 2025).

Pathogens can also actively disrupt these beneficial legacies. To facilitate infection, soilborne pathogens produce effector proteins that target host defenses and suppress beneficial microbes in the rhizosphere. For example, the protein effectors VdAve1 and VdAMP2, secreted by the soilborne fungus *Verticillium dahliae*, suppress beneficial Sphingomonadales bacteria in the rhizosphere of cotton and tomato, demonstrating how pathogens can cause dysbiosis to overcome biological barriers (Adhikary et al., 2026).

7. Computational Workflows and AI-Guided Design of Synthetic Microbial Communities

Because single-strain microbial inoculants often show inconsistent performance under field conditions due to competition from native microbiomes, research has moved toward designing Synthetic Microbial Communities (SynComs). SynComs are defined consortia designed to simulate the functions and interactions of natural microbiomes. They leverage functional redundancy and metabolic division of labor to improve colonization stability and environmental adaptation (Jiao et al., 2026).

The design of SynComs proceeds through different strategies (Sharma & Bora, 2025):

- **Bottom-Up Approach:** Selects individually isolated strains based on specific functional traits (e.g., nutrient solubilization, pathogen suppression) and tests them in co-culture to assemble a community.
- **Top-Down Approach:** Simplifies natural, suppressive microbiomes through dilution or selective pressures while preserving core functional traits.
- **Hybrid Approach:** Combines bottom-up strain selection with top-down environmental filters to maximize functional diversity and ecological resilience.
- **Natural Microbiome (NatComs) Optimization:** Directly enriches and propagates intact microbial assemblies from suppressive soils, preserving native co-evolved networks (Scortichini, 2022).

To streamline SynCom assembly, researchers integrate multi-omics technologies and computational tools. Metagenomics, metatranscriptomics, metaproteomics, and metabolomics are used to analyze community structure, active transcription, and metabolic output. Because metabolomics targets small-molecule metabolites under 1700 Da, it directly measures final chemical phenotypes (Kaur et al., 2025).

Additionally, genome-scale metabolic models (GSMs) are used to predict individual metabolic capabilities, nutrient requirements, and cross-feeding networks (Boro et al., 2022). For example, genomic annotations can identify B-vitamin synthesis gene clusters (e.g., nicotinamide and niacin) in yeast that support lactic acid bacteria (LAB), or organic acid synthesis genes in LAB that supply nutrients to yeast. Similar modeling strategies can identify genetic markers like *lysA*, *dapF*, and *ddh* to screen and select strains that optimize nutrient production in co-culture (Araujo, 2022).

Computational design has been advanced by artificial intelligence pipelines, such as the GENIA (Genomically and Environmentally Networked Intelligent Assemblies) framework. This integrated framework combines Prospector high-throughput culturomics and Oxford Nanopore sequencing with automated annotation tools like Prodigal, PGAP, Prokka, and RAST. It processes genomic data through four modules (Rajakumar, 2022):

Genomic Encoding -> Pathway Integration -> Redundancy Reduction -> Dynamic Activation

The genomic encoding module uses graph neural networks and Node2Vec embeddings to convert genomic features into mathematical vector representations. The pathway integration module merges individual metabolic models to construct joint metabolic networks (Dubey et al., 2025). The redundancy reduction module employs Kolmogorov complexity analysis to minimize functional redundancy and reduce internal niche competition. Finally, the dynamic activation module uses dynamic environmental simulations to model community performance under changing conditions (El-Saadony et al., 2022).

This computational approach has been used to design minimal synthetic consortia that can simultaneously degrade structurally diverse persistent pollutants, including PFAS, atrazine, and lignin (Patyal et al., 2025).

Table 3: Functional Classifications and Performance Efficiencies of Synthetic Microbial Communities

SynCom Name / Focus	Host Crop Target	Microbial Composition / Key Strains	Key Mechanisms of Action	Disease Control / Stress Performance
sfSynCom (Simplified Functional)	Soybean (<i>Glycine max</i>)	<i>Bradyrhizobium elkanii</i> BXYD3 + <i>Pantoea</i> helper strains	Helper strains produce acyl-homoserine lactones to enhance core strain root colonization	Upregulates nodulation and nitrogen fixation efficiency

Watermelon SynCom	Watermelon (<i>Citrullus lanatus</i>)	16 core bacterial isolates	Reshapes the rhizosphere microbiome and enriches native beneficial <i>Pseudomonas</i>	Suppresses Watermelon <i>Fusarium</i> Wilt
Strawberry Consortia	Strawberry (<i>Fragaria x ananassa</i>)	5 <i>Bacillus</i> strains + 5 <i>Pseudomonas</i> strains	Restores soil versatility, boosts enzyme activities, and enriches beneficial <i>Burkholderia</i>	Suppresses strawberry wilt and shows a persistent legacy effect
Phytophthora Biocontrol SynCom	Pepper (<i>Capsicum annuum</i>)	5-strain multi-genus rhizobacterial consortium	Solubilizes phosphate, produces siderophores, and enriches <i>Bacillus</i> and <i>Trichoderma</i>	Direct antagonism against <i>Phytophthora capsici</i> , reducing root rot severity
Arabian Peninsula "EcoBiome"	Desert plants (Arabian Peninsula)	Multi-species desert-derived consortia	Synergistic production of IAA (84%), phosphate solubilization (73%), and biofilms (47%)	Confers drought and salinity tolerance to heterologous host crops

Another design strategy is the development of "EcoBiomes", which are multi-species synthetic microbial consortia inspired by natural desert microbiomes. Desert plants native to the Arabian Peninsula have co-evolved with microbial communities shaped by strong environmental selection (Rhouma, 2025). Screening of 75 bacterial isolates from these plants revealed that 84% produce indole-3-acetic acid (IAA), 73% solubilize phosphate, 60% synthesize siderophores, 47% form robust biofilms, and 35% express ACC deaminase (Joshi et al., 2025).

Combining these non-antagonistic, synergistic strains into desert-inspired EcoBiomes provides functional complementarity. These consortia enhance the stress tolerance of vulnerable crop species under drought, heat, and salinity. Similar approaches, such as the application of customized consortia in rice (*Oryza sativa*), help crops maintain cell turgor and reduce osmotic stress through biofilm-enclosed root zones (Cucu et al., 2025).

Furthermore, SynComs have been applied to manage diseases in cash crops and medicinal plants. In the production of *Salvia miltiorrhiza*, tailored SynComs alter root metabolism to improve both quality and yield (Argentel-Martínez et al., 2025). For Sunflower *Verticillium* Wilt, caused by *Verticillium dahliae*, co-culturing SynComs with delayed sowing strategies increases disease control efficiency by 19.08% and 37.82%, respectively, in pot experiments (Priyadarshini et al., 2025).

Under heavy metal or chemical stresses, engineered consortia can also facilitate phytoremediation and survival. Under mercury (Hg) contamination, maize recruits *Fusarium*, *Exophiala*, and *Meyerozyma* to promote IAA production and phosphate dissolution, alleviating mercury-induced phytotoxicity (Singh et al., 2022). Similarly, the grass *Vetiveria zizanioides* under antimony (Sb) and arsenic (As) stress recruits *Sphingomonas*, *Rhodospirillum*, and *Streptomyces*. These recruited genera express arsenate reductase genes to oxidize and detoxify the metals, helping the host maintain photosynthesis and biomass production (Afridi et al., 2022).

Conclusion

In conclusion, the integration of plant pathology, microbial biotechnology, and rhizosphere engineering

offers a comprehensive and sustainable approach to managing plant diseases while improving crop productivity and soil health. Beneficial microorganisms, including plant growth-promoting rhizobacteria, endophytes, mycorrhizal fungi, and microbial consortia, play critical roles in suppressing plant pathogens, enhancing nutrient availability, strengthening plant immune responses, and improving resilience to environmental stresses. Advances in microbiome engineering, multi-omics technologies, artificial intelligence, and precision agriculture have further enhanced the understanding and management of complex rhizosphere interactions, enabling more targeted and efficient disease control strategies. However, challenges such as variability in microbial performance under different environmental conditions, successful field establishment, large-scale production, regulatory approval, and long-term ecological assessment remain significant barriers to widespread implementation. Future research should focus on developing robust microbial formulations, integrating synthetic biology and artificial intelligence for microbiome optimization, validating field-scale applications across diverse agroecosystems, and establishing standardized regulatory frameworks that support sustainable commercialization. Overall, the convergence of plant pathology, microbial biotechnology, and rhizosphere engineering provides a promising pathway toward environmentally friendly, resilient, and climate-smart disease management systems capable of supporting sustainable agriculture and global food security.

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