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A review on rhizospheric bacteria for biological control of important soil borne pathogens

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ABSTRACT

Rhizospheric bacteria have emerged as effective Biological Control Agents (BCAs) against soil-borne pathogens, promoting sustainable agricultural practices. The rhizosphere, influenced directly by root exudates, is a critical zone of intense microbial interactions, housing diverse beneficial bacteria including genera such as Pseudomonas, Bacillus, Azotobacter, Rhizobium, Enterobacter, and Burkholderia. These microbes enhance plant health through multiple biocontrol mechanisms. Direct biocontrol mechanisms include competitive exclusion, antibiotic and bacteriocin production, siderophore-mediated iron sequestration, quorum sensing interference, and enzymatic pathogen degradation. Notably, Pseudomonas fluorescens produces antibiotics like phenazine-1-carboxylic acid, pyoluteorin, pyrrolnitrin, and 2,4-diacetylphloroglucinol, effectively suppressing pathogens such as Fusarium spp., Rhizoctonia solani, and Pythium ultimum. Bacillus species produce broad-spectrum antifungal antibiotics including iturin, fengycin, and zwittermicin A, significantly contributing to disease management. Bacteriocins further aid suppression by targeting closely related pathogenic strains. Indirect mechanisms involve inducing plant Induced Systemic Resistance (ISR), preparing plants against pathogen invasions through signaling pathways mediated by jasmonic acid and ethylene. Additionally, rhizospheric bacteria enhance plant growth via phosphorus solubilization, nitrogen fixation, and phytohormone synthesis, boosting plant vigor and disease tolerance. However, the practical application of these BCAs faces challenges such as inconsistent field performance due to environmental variability, limited understanding of complex microbial interactions, and difficulties in formulating stable and effective microbial consortia. Advances in molecular approaches such as metagenomics, transcriptomics, and metabolomics have deepened understanding of plant-microbe interactions, identifying key biocontrol genes and metabolites. This facilitates the development of targeted bioformulations, particularly multi-strain bacterial consortia (MSBCAs), which offer enhanced colonization efficiency and consistent pathogen suppression. Amid rising environmental concerns about chemical pesticides, rhizospheric bacteria provide sustainable alternatives, contributing significantly to the advancement of eco-friendly agricultural practices.

Keywords: *Rhizosphere, Rhizospheric bacteria, Biological control agents (BCAs), Multi-strain bacterial consortia (MSBCAs), Pseudomonas fluorescens, Bacillus subtilis, Antibiotics (e.g., phenazine-1-carboxylic acid, pyoluteorin, DAPG), Bacteriocins, Induced Systemic Resistance (ISR), Siderophores, Quorum sensing and quorum quenching, Enzymatic degradation, Biofilm formation, Plant growth promotion, Phosphorus solubilization, Nitrogen fixation, Phytohormones, Soil-borne pathogens, Fusarium spp., Rhizoctonia solani, Pythium ultimum, Sustainable agriculture*

Introduction

The rhizosphere refers to the narrow region of soil directly influenced by plant roots. This dynamic zone is a hotspot for microbial activity and is marked by intense physical, chemical, and biological interactions. It hosts a diverse microbial community that forms both symbiotic and asymbiotic associations with plants, significantly influencing plant growth and health [11]. However, it is also a critical battleground where soil-borne pathogens pose severe threats to crop productivity and global food security. These pathogens often initiate infections at the early seedling stage, particularly in nurseries, leading to systemic crop health issues throughout the growing season. They possess survival strategies that allow persistence in the soil for extended periods, either as saprophytes, in association with plant debris, or within soil organic matter [62, 98].

Dominant fungal pathogens like *Fusarium* spp. and *Alternaria* spp. are notably aggressive and require efficient control strategies [76, 85]. Other pathogens, including *Pythium*, *Phytophthora*, *Sclerotinia*, and *Verticillium* spp., can cause yield losses ranging from 50–70% [78]. Conventional practices such as crop rotation, chemical pesticides, and resistant cultivars often yield inconsistent outcomes and lack sustainability [44, 45]. Hence, there is growing interest in biological control agents (BCAs), particularly rhizospheric bacteria, due to their multifaceted mechanisms and environmental safety.

Rhizospheric bacteria exert biocontrol effects through direct and indirect mechanisms that suppress the proliferation and pathogenicity of soil-borne pathogens [37, 9].

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A primary direct mechanism is competitive exclusion, wherein beneficial microbes outcompete pathogens for nutrients and ecological niches, especially in exudate-rich root zones. These beneficial bacteria produce antagonistic compounds such as lipopeptides, biosurfactants, volatiles, and bacteriocins that inhibit pathogen metabolism, growth, and virulence [11].

BCAs can also disrupt quorum sensing (QS)—a bacterial communication system regulating virulence—by producing quorum quenching (QQ) enzymes like lactonases, chitinases, and pectinases, thereby thwarting coordinated pathogenic attacks [89]. Indirectly, they induce systemic resistance (ISR) in plants, enhancing the host's defense machinery to respond more effectively to future pathogen challenges [37, 115].

Beyond pathogen suppression, rhizospheric bacteria promote plant growth by solubilizing phosphorus, fixing atmospheric nitrogen, and synthesizing phytohormones such as auxins and cytokinins [111, 116]. Despite their vast benefits, the widespread application of BCAs is challenged by the complexity of plant-pathogen-microbe interactions, making it difficult to pinpoint specific biocontrol mechanisms [37, 116]. A comprehensive understanding of these interactions is essential for optimizing BCA formulations, tailoring application strategies, and enhancing compatibility among the biocontrol agent, host plant, and soil environment.

Recent advances in metagenomics, transcriptomics, and metabolomics provide promising tools to unravel microbial functions and interactions in the rhizosphere. These approaches help identify key genes and metabolites involved in biocontrol activities, supporting the development of next-generation bioformulations for integrated disease management [38, 114].

BCAs are prolific producers of natural antimicrobial compounds, including secondary metabolites such as antibiotics, toxins, non-ribosomal peptides, ribosomal peptides, polyketides, and volatile organic compounds (VOCs) [9, 37]. These bioactive molecules target critical cellular processes in pathogens, making them potent tools for crop protection. Given their diversity and efficacy, rhizospheric bacteria are invaluable assets in sustainable agriculture.

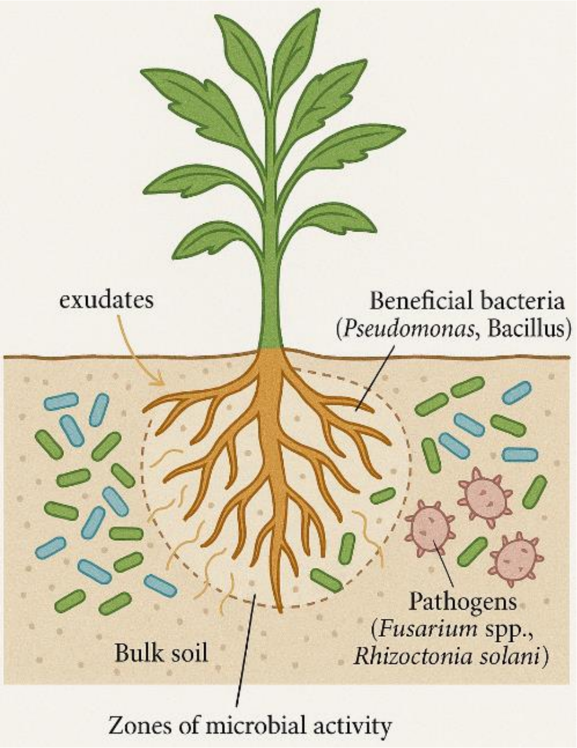

Figure-1: Structure and Function of the Rhizosphere

In contrast to the environmental and agronomic concerns posed by chemical pesticides—including residue accumulation, higher input costs, resistant pathogen strains, and disruption of beneficial soil microbiota [95]—BCAs offer eco-friendly and sustainable alternatives with long-term benefits for soil and plant health [110]. Although not a one-size-fits-all solution, integrating BCAs into disease management programs holds promise to transform plant protection practices. Continued research in formulation technology, field application, and regulatory policies will be pivotal for mainstreaming their use. Various bacterial and fungal biocontrol agents against plant pathogens are summarized in Table 1.

Table – 1: Major soil-borne diseases caused by soil-borne pathogens in crop plants

Disease	**Pathogen(s)**	**References**
Take-all of wheat	*Gaeumannomyces graminis* var. *tritici*	[51], [29]
Eyespot of wheat	*Tapesia yallundae*	[71]
Clubroot of crucifers	*Plasmodiophora brassicae*	[18]
Vascular wilt of tomato	*Fusarium oxysporum* f. sp. *lycopersici*	[18], [28]
Common scab of potato	*Streptomyces scabies*	[18]
Black root rot of tobacco	*Thielaviopsis basicola*	[18]
Rhizoctonia damping-off	*Rhizoctonia solani*	[12], [17]
Sclerotinia stem rot	*Sclerotinia sclerotiorum*	[68]
Verticillium wilt	*Verticillium dahliae, V. albo-atrum*	[71], [49]
Eyespot	*Tapesia spp.*	[25]
Rhizoctonia root rot	*Rhizoctonia solani*	[70]
Sharp eyespot	*Rhizoctonia cerealis*	[26]
Common root rot	*Cochliobolus sativus*	[15]
Fusarium crown rot	*Fusarium pseudograminearum, F. culmorum*	[90]
Black scurf	*Rhizoctonia solani* (on potato)	[105]
Root-knot	*Meloidogyne spp.*	[50]
Rhizoctonia root rot	*Rhizoctonia solani* AG-8	[94]
Damping-off	*Pythium spp., Rhizoctonia solani, Fusarium spp.*	[3]
Common root rot	*Bipolaris sorokiniana*	[27]
Crown and root rot	*Fusarium spp.* (in maize)	[79]
Phytophthora root rot	*Phytophthora spp.*	[93]
Lesion nematode damage	*Pratylenchus penetrans*	[1]
Root rot, Fusarium wilt	*Fusarium spp.*	[2], [92]
Root knot nematode	*Meloidogyne spp.*	[30]
Root rot (Beans)	*Fusarium solani* f. sp. *phaseoli, R. solani, P. ultimum, T. basicola*	[2], [109], [31]
Fusarium wilt (Beans)	*F. oxysporum* f. sp. *phaseoli*	[2], [92]
Root rot (Lettuce)	*P. ultimum, Fusarium spp.*	[74], [46]
Root rot	*Fusarium spp.*	[48], [32], [99]
Damping-off	*Pythium spp.*	[99]
Fusarium wilt	*F. oxysporum* f. sp. *phaseoli*	[2], [92]
Lesion nematode damage	*Pratylenchus spp.*	[1], [107]
Pythium root rot	*Pythium spp.*	[80], [81], [82]
Fusarium root rot	*Fusarium spp.*	[72], [73]
Root rot	*Pythium spp., Rhizoctonia solani*	[80], [81], [82]

Diversity and Ecology of Rhizospheric Bacteria

The rhizosphere is a dynamic zone of soil closely influenced by plant roots, densely populated by microbial life. Bacterial densities can range between 10^{10}–10^{12} cells/g of soil, significantly higher than in bulk soil [84]. Predominant bacterial phyla include *Proteobacteria*, *Firmicutes*, *Actinobacteria*, *Bacteroidetes*, and *Cyanobacteria* [6], [84]. Dominant genera such as *Pseudomonas*, *Bacillus*, *Azotobacter*, *Rhizobium*, and *Burkholderia* are frequently isolated from crops like wheat, maize, rice, and legumes [6], [84].

These bacteria play key ecological roles including nitrogen fixation, phosphate solubilization, potassium mobilization, and siderophore production [106]. They also produce phytohormones such as IAA, gibberellins, and cytokinins, enhancing plant development [84]. Furthermore, antibiotics, lytic enzymes (e.g., chitinases), and volatile organic compounds help suppress pathogens [6], [84].

Plant root exudates modulate these interactions by acting as chemoattractants, shaping microbial communities. Root developmental stages influence bacterial community structure, where young roots favor r-strategists and older roots support k-strategists [6]. Soil properties including pH, salinity, moisture, and organic matter significantly affect diversity [64]. Salinity and metal stress enrich for stress-tolerant species like *Bacillus* and *Paenibacillus* [106].

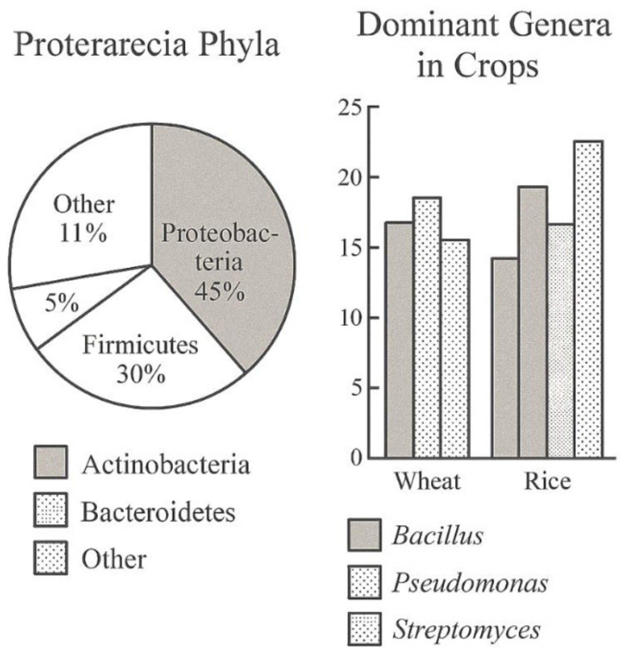

Figure-2: Diversity and Ecological Distribution of Rhizospheric Bacteria

Rhizobacteria contribute to phytoremediation and iron acquisition, essential for plant defense [114]. Functional diversity includes genes for amino acid, carbohydrate, and energy metabolism, aiding adaptation to varying habitats [64]. Community composition shifts spatially (rhizosphere vs. bulk soil) and temporally. For instance, rhizospheres in the Yellow River Delta exhibited enriched metabolizers under saline conditions [64], while seasonal shifts in Ebinur Lake showed greater diversity in summer, corresponding with root activity [114].

Mechanisms of Biological Control by Rhizospheric Bacteria

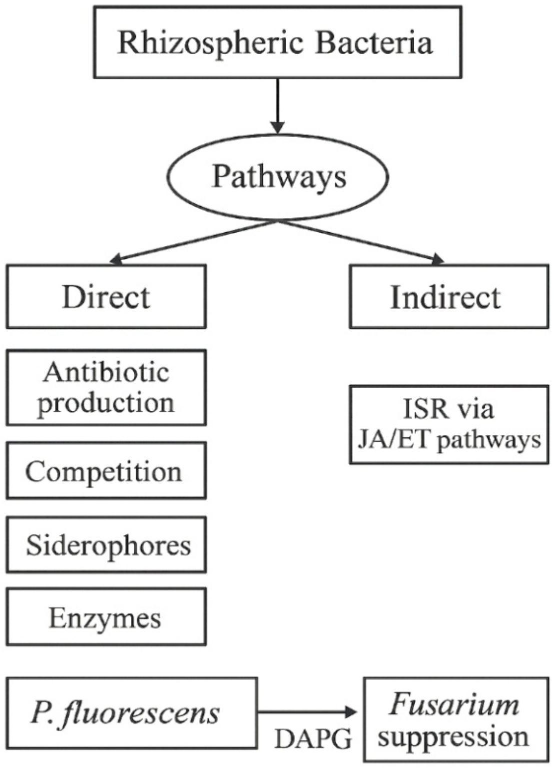

Figure-3: Mechanisms of Biocontrol by Rhizospheric Bacteria

a. Antibiotic and Bacteriocin Production

One of the primary modes of action employed by rhizospheric bacteria against phytopathogens involves the production of antimicrobial compounds such as antibiotics and bacteriocins. These secondary metabolites exert fungistatic or fungicidal effects by inhibiting spore germination, lysing fungal mycelia, or impeding pathogen metabolism [41], [104]. *Pseudomonas fluorescens* synthesizes various antibiotics including phenazine-1-carboxylic acid (PCA), pyoluteorin, pyrrolnitrin, and 2,4-diacetylphloroglucinol (DAPG), which suppress pathogens like *Gaeumannomyces graminis*, *Rhizoctonia solani*, and *Pythium ultimum* [47], [45]. *Bacillus* spp. are also prolific antibiotic producers, with *B. subtilis* producing iturin A, surfactin, and fengycin—all exhibiting strong antifungal properties [63]. Additionally, *Bacillus cereus* strain UW85 suppresses damping-off diseases via zwittermicin A and kanosamine [40]. Mutant strains with enhanced antibiotic production often show increased biocontrol efficacy. Bacteriocins such as agrocin 84 from *Agrobacterium radiobacter* K84 are used commercially to control crown gall disease caused by *A. tumefaciens* [58]. Similarly, bacteriocin-producing strains of *P. fluorescens* and *P. solanacearum* reduce disease incidence [40]. Antibiotic-deficient mutants frequently lack biocontrol ability, highlighting the importance of secondary metabolites [52], [104], [55].

b. Nutrient Competition and Niche Exclusion

Rhizobacteria suppress plant pathogens by competing for nutrients and colonization sites. Species like *Pseudomonas* deplete root and seed exudates, limiting carbon and nitrogen availability to pathogens like *G. graminis* and *Fusarium oxysporum* [101], [19], [36]. These bacteria also colonize root zones—particularly lateral root emergence sites—thus excluding pathogens through niche occupation [101].

c. Siderophore Production

Siderophores are iron-chelating compounds secreted under low-iron conditions. Fluorescent pseudomonads produce pyoverdines that bind Fe^{3+}, restricting access to pathogens such as *P. ultimum*, *F. oxysporum*, and *G. graminis* [59], [65], [16], [36]. Strains deficient in siderophore production are less effective biocontrol agents [19], [13]. Rhizobacteria also induce systemic resistance in plants involving jasmonic acid and ethylene pathways rather than salicylic acid [83]. For instance, *P. fluorescens* CHA0 protects cucumber and tobacco via ISR [53]. Regulatory genes such as *gacA* play a key role in ISR signaling [86]. Volatile organic compounds (VOCs) like 2,3-butanediol from *B. subtilis* contribute to ISR [88], and SA-related siderophores like pyochelin also support ISR [7].

d. Induced Systemic Resistance (ISR)

ISR is a plant-wide defense activated by non-pathogenic rhizobacteria. *P. fluorescens* CHA0 induces ISR in tobacco against *T. basicola* via cyanide and other elicitors [4], [97]. ISR enhances defense-related gene expression and enzyme production (e.g., peroxidases, chitinases) [59], [53]. Cross-protection effects have been seen where non-pathogenic *P. solanacearum* strains induce resistance in potato [20].

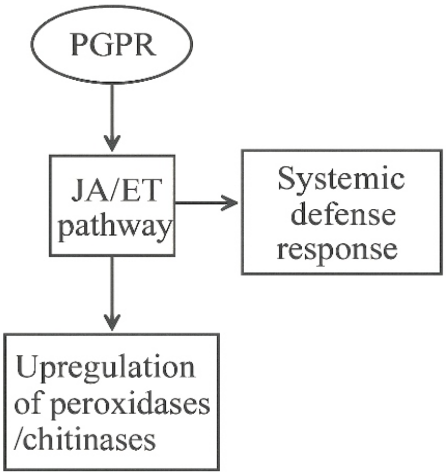

Figure-4: Induced Systemic Resistance (ISR) Signaling Pathway

e. Hydrolytic Enzyme Production

Rhizobacteria produce enzymes like chitinases, glucanases, proteases, and cellulases to degrade fungal cell walls [22]. For instance, *P. stutzeri* YPL-1 inhibits *F. solani* via chitinase and laminarinase [35]. Genetic engineering has shown that chitinase genes from *Serratia marcescens* confer enhanced protection against *R. solani* when expressed in *E. coli* or *Trichoderma* spp. [35].

f. Quorum Sensing and Quenching in Biocontrol

QS is a communication system regulating gene expression by bacterial density. Pathogens like *E. carotovora* use AHL-based QS for virulence [5]. Quorum quenching (QQ) disrupts this by degrading AIs. AHL lactonase AiiA from *Bacillus* species degrades AHLs, reducing virulence of pathogens [34]. Structural analogs such as fimbrolide inhibit QS receptors like LuxR in *P. aeruginosa* [67]. Natural inhibitors from edible plants suppress QS in *P. aeruginosa* [75], while *P. putida* IsoF and *R. erythropolis* degrade AHLs, offering protection against pathogens [39], [14].

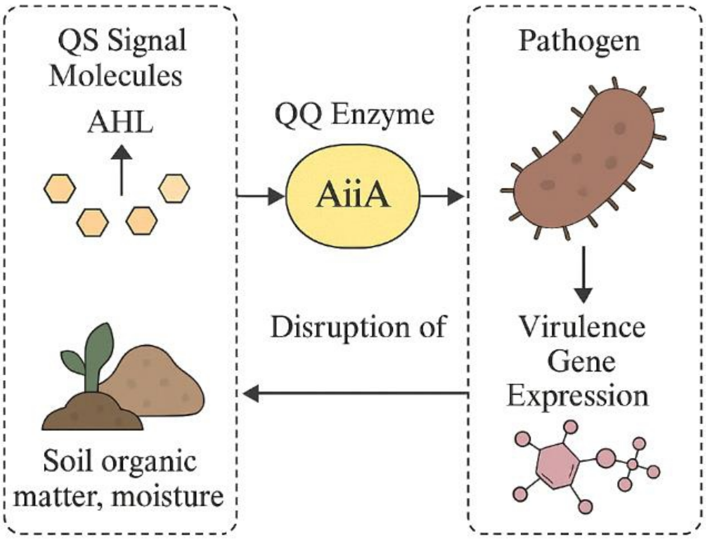

Figure-5: Quorum Sensing (QS) and Quenching (QQ) in Pathogen Suppression

g. Multi-Mechanistic Action and Environmental Modulation

Biocontrol agents use several mechanisms simultaneously, their dominance influenced by environmental factors. Siderophores are more effective in alkaline soils, whereas antibiotics are regulated by nutrient conditions [36], [55]. Compost addition enhances microbial antagonism and biocontrol potential [21], [32].

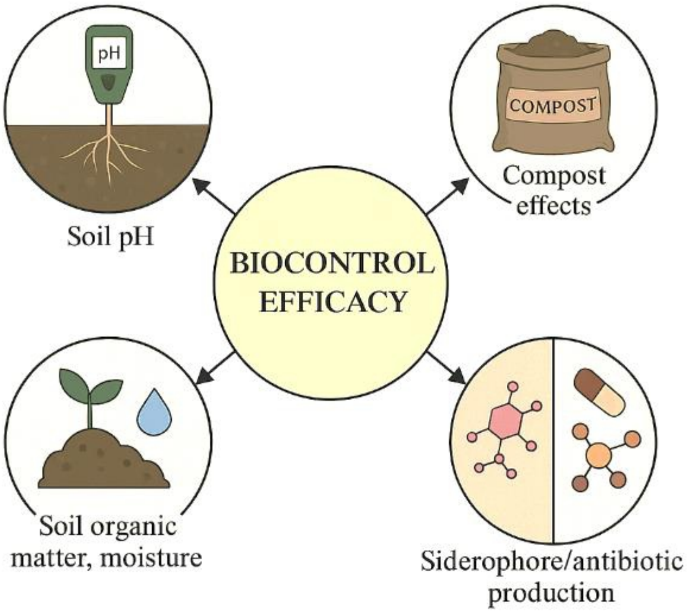

Figure-6: Environmental Factors Modulating Biocontrol Efficacy

h. Volatile Organic Compounds (VOCs) and Secondary Metabolites

VOCs like HCN, phenazines, and sulfur compounds inhibit pathogens. *P. fluorescens* strains producing HCN reduce *T. basicola* infections [108]. Compounds such as dimethyl disulfide and benzothiazole from *Paenibacillus* and *Bacillus* spp. suppress *F. oxysporum* and other pathogens [87], [113].

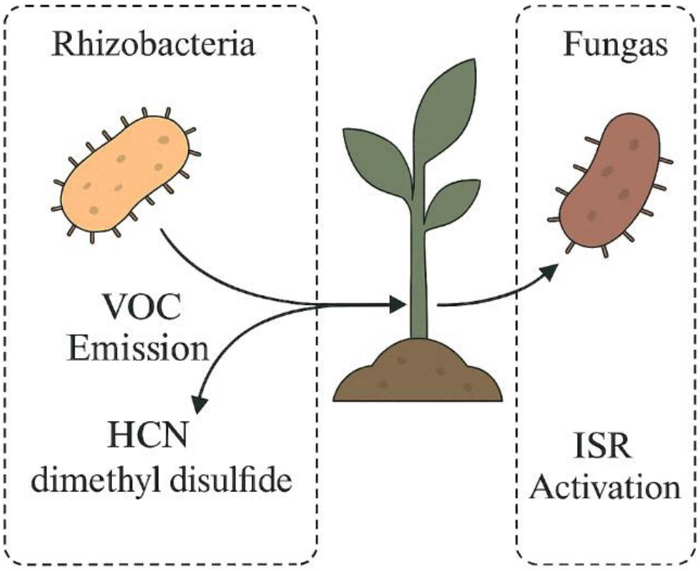

Figure-7: Volatile Organic Compounds (VOCs) in Biocontrol

Synergistic Interactions with Other Microorganisms

Rhizosphere Colonization and Microbial Interactions

Efficient rhizosphere colonization is crucial for biological control agents (BCAs) to protect plants from soilborne pathogens. Multi-strain BCAs (MSBCAs) enhance colonization, as shown by a five-strain bacterial consortium suppressing wilt in *Nicotiana attenuata* [Santhanam et al., 2019]. Diverse communities of bacteria, including *Pseudomonas* spp., improve survival and colonization, aiding in disease control such as bacterial wilt in tomatoes [Hu et al., 2016]. Interactions among microbes, such as between *Trichoderma* spp. and *Bacillus velezensis*, promote growth and biofilm formation, boosting colonization and pathogen suppression [10], [8].

Biofilm formation significantly improves microbial colonization by providing stability and resistance to environmental stress [8]. Multi-species bacterial consortia form stronger biofilms than single-species counterparts, resulting in better colonization and disease suppression [10]. Syntrophic interactions, where microbes cooperate to degrade substrates, further enhance colonization. For example, *Azospirillum brasilense* collaborates with sugar-degrading bacteria to access carbon sources, improving its survival and rhizosphere colonization [11]. Microbial motility—swimming, swarming, and gliding—facilitates migration and dispersal within the rhizosphere. Fungal mycelia can serve as "fungal highways," aiding the movement of rhizobia, such as using *Phomopsis liquidambaris* mycelia for root colonization [12]. *Paenibacillus vortex* transports non-motile fungal spores, enhancing microbial dispersal [13].

Resource Competition and Antimicrobial Production

Resource competition is a key mechanism by which BCAs suppress pathogens. They outcompete pathogens for nutrients, particularly root exudates. For instance, *Pseudomonas* spp. and non-virulent *Ralstonia* spp. inhibit *Ralstonia solanacearum* by depleting resources [6], [10]. Siderophore production improves nutrient acquisition and limits iron availability to pathogens [16]. BCAs also produce antimicrobial compounds such as lipopeptides, phenazines, and chitinases that suppress pathogens. Interactions within microbial consortia stimulate these compounds, enhancing biocontrol [40], [44].

Application Strategies in Agriculture

The use of rhizospheric bacteria, especially MSBCAs, is a potent strategy for managing soil-borne diseases. These bacteria suppress pathogens through competition, antimicrobial production, biofilm formation, and induced resistance.

Table-2: Multi-Strain Biological Control Agents for Soil-Borne Pathogens

No.	Multi-Strain BCAs	Mode of Application	Disease	Pathogens	Mode of Action	Host	Ref
1	*T. harzianum* CECT 2413 + *S. rochei*	Soil inoculation	Root rot	*P. capsici*	Hyphal disintegration; 1-propanone production	Pepper	[36]
2	*B. cereus* AR156 + *B. subtilis* SM21 + *Serratia* sp. XY21	Seedling treatment	Phytophthora blight	*P. capsici*	Alters soil bacterial community	Sweet pepper	[112]
3	*P. aeruginosa* MBAA1 + *B. cereus* MBAA2 + *B. amyloliquefaciens* MBAA3	Seed bacterization	Stem/charcoal rot	*S. sclerotiorum*, *M. phaseolina*	Ammonia, siderophores, glucanase, chitinase, cellulase	Soybean	[102]
4	*P. aeruginosa* PJHU15 + *T. harzianum* TNHU27 + *B. subtilis* BHHU100	Seed coating	White rot	*S. sclerotiorum*	ISR and ROS management	Pea	[54]
5	*Pseudomonas* sp. S1 + *Bacillus* sp. S2 + *Azotobacter* sp. S3 + *Azospirillum* sp. S4 + *P. fluorescens* S5	Seedling treatment	Vascular wilt	*F. oxysporum* f. sp. *lycopersici*	Induced systemic resistance	Tomato	[57]
6	*Glomus intraradices* + *Pseudomonas* sp. + *T. harzianum*	Seed soaking	Fusarium wilt	*F. oxysporum* f. sp. *lycopersici*	Siderophore, rhamnolipid production	Tomato	[96]
7	*B. subtilis* S2BC-1 + *B. subtilis* GIBC-Jamog	Seed bacterization + soil application	Vascular wilt	*F. oxysporum* f. sp. *lycopersici*	Biocontrol + ISR	Tomato	[91]
8	*T.* sp. NRCB3 + *T. asperellum* Prr2	Soil + root treatment	Fusarium wilt	*F. oxysporum* f. sp. *cubense*	Spore inhibition + antifungal metabolites	Banana	[103]
9	*B. subtilis* GB03 + *B. amyloliquefaciens* IN937a + *P. fluorescens* CECT 5398	Media inoculation + seed drench	Fusarium + damping-off	*F. oxysporum* + *R. solani*	Siderophores, ISR	Pepper, Tomato	[33]
10	*Bacillus* spp. EPB10, EPB56 + *P. fluorescens* Pf1	Root soaking	Fusarium wilt	*F. oxysporum* f. sp. *cubense*	Defense enzyme induction	Banana	[69]

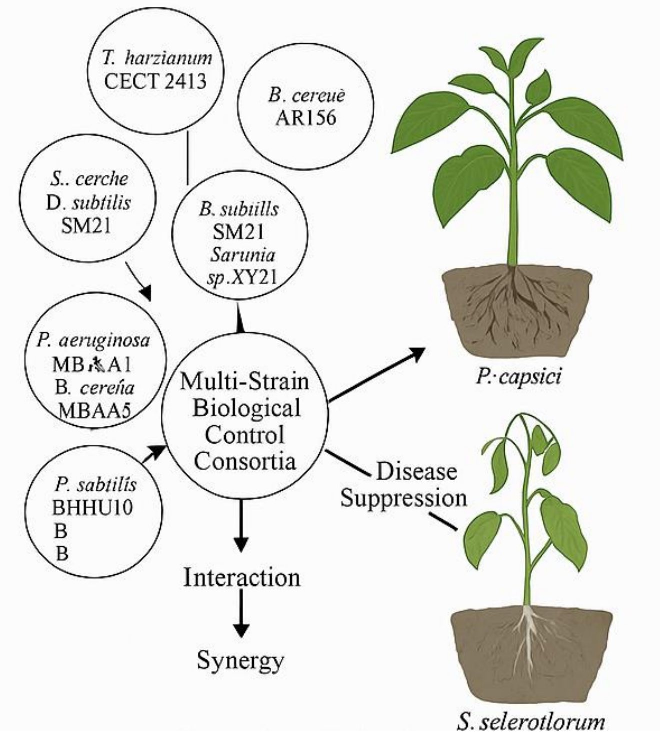

Figure-8: Multi-Strain Biological Control Consortia (MSBCAs)

Future Prospects and Sustainable Agriculture

The application of BCAs for soil-borne disease control offers an eco-friendly, sustainable alternative to chemical pesticides. BCAs promote environmental safety, reduce residue buildup, and limit pathogen resistance. Research should emphasize the mechanisms underlying BCA efficacy and their interaction with soil and plant microbiomes. Genomic and bioinformatic tools can aid in discovering novel BCAs and refining multi-strain consortia with complementary mechanisms.

Integrating BCAs into broader sustainable practices like crop rotation, organic farming, and use of resistant cultivars enhances their effectiveness as part of integrated pest management (IPM). Tailoring BCAs to environmental variables (soil pH, moisture, nutrients) and improving delivery systems will support their field-level deployment, translating lab success into agricultural resilience.

Conclusion

The role of rhizospheric bacteria as Biological Control Agents (BCAs) in the management of soil-borne diseases has become increasingly recognized for its potential in sustainable agriculture. The mechanisms through which BCAs suppress pathogens, including competition for nutrients, antimicrobial production, and the induction of systemic resistance, offer valuable alternatives to traditional chemical treatments. Multi-strain BCAs (MSBCAs), which harness synergistic interactions between different microbial species, provide a promising strategy to enhance disease suppression and improve crop yields. While challenges remain, particularly in identifying the most effective microbial strains and understanding the complex dynamics between pathogens, BCAs, and plant hosts, the future of BCAs in agricultural practices looks promising. Continued research into the optimization and application of BCAs will be key to reducing reliance on chemical pesticides, improving food security, and promoting environmentally sustainable farming practices. By fostering a deeper understanding of microbial interactions and their role in soil health, we can move closer to achieving resilient agricultural systems capable of meeting the challenges posed by climate change, soil degradation, and increasing demand for food.

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