Review

Rhizobiome and Its Architecture in the Crop Improvement and Resistance Towards Pathogens

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Rhizobiome and Its Architecture in the Crop Improvement and Resistance Towards Pathogens

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Abstract: Rhizobiome is a network of beneficial microbes (fungi, bacteria, nematodes, actinomycetes, mycorrhizae) and to study their interaction is fascinating in producing higher crop yield and increase resistance against phytopathogens. The interactions could be competitive, neutral, commensal and mutualistic. Beneficial interactions chiefly colonize roots and maximize plant growth parameters like plant height, leaves number & fruit/pod/seed number. The positive microinoculants fix nitrogen, solubilize P and Fe, produce phytohormones, improve plant defense chemicals and enzyme machinery in root tissues upon pathogen invasion. The rhizomicroinoculants also increase photosynthetic and nutritional proficiency by maximizing total chlorophyll, carotenoid, carbohydrates, amino acids and proteins in plants. They play a crucial role in preventing disease outbreak under stressful situations like drought, metal stress, salinity, high temperature, soil erosion, change in rainfall and humidity. Understanding rhizomicrobiome interaction and preparing novel rhizospheric microbial formulations could be good strategy to improve plant growth parameters, fruit yield and defense ability towards pathogen.

Keywords: beneficial microbes; rhizobiome; root interactions; plant growth; plant resistance

1. Introduction

Root is a vital organ which absorb minerals and transport water to aerial parts of the plants. The root structural information is important to know and build beneficial microflora in the vicinity of root activity. The occurrence of soil microbes varies and is influenced by root exudates, chemical components, pH value and edaphic factors. Rhizobiome is a zone where group of microbes interacts with one another. The two main kinds of microbial interactions prevail in rhizobiome include microbe to microbe and microbe to plant. Microbes communicate and compete continuously with each other for space and nutrients to form population and spread colony in rhizobiome [1]. A microbe can antagonise the growth of other microbe to support plant growth or in combination they produce toxins to form infection symptoms in plants. *Ustilago maydis* (biotrophic pathogen) inhibited wilt pathogen *Fusarium verticillioides* to support the growth of maize plants [6]. We can observe that, microbe [*Albugo laibachii*] of one host plant type [*A. thaliana*] produce infection symptoms and prevent the growth of non-host pathogens [*Phytophthora infestans*] [2]. Crude elicitors (oligosaccharides, proteins, and sphingolipids) extracted from pathogenic microbe (*C. capsici*) can induce plant growth and resistance in chilli plants [109]. Communication can be stopped by inhibiting AHL lactone enzyme in pathogenic microbes by rhizobacteria [4]. *Trichoderma* spp. and *Bacillus amyloliquefaciens* negatively impact on soil borne pathogen (*F. oxysporum*) colony to prevent wilt infection and improve growth in tomato plants [108]. Various organic amendments were applied in soil in the form of compost, manure and plant extracts to increase microbial functionality and soil fertility to produce higher crop yield. For example: *Phytophthora capsici* positively support the *B. subtilis*, *T. gamsii* and *T. asperellum* growth when compost is drenched in rhizobiome and negatively foster fruit rot/ blight disease severity in zucchini plants [107]. Certain microbes particularly viruses whose virulency is much higher that it will overcome the beneficial effects of useful microbes and prevent nitrogen accumulation in plants. Higher application of urea negatively affects virus and bacterial colony growth [81]. It was interestingly observed that, the root exudate trehalose secreted by leguminous plants helps in the colonization of rhizobia and mycorrhizae which increase growth potency and drought tolerance ability in leguminous plants [5]. Useful root resident microbes secrete secondary metabolites/phytohormones to prevent the growth and division of soil borne pathogens [67]. Overall microbe-microbe interaction is dependent on soil factors, habitat, host plant type, root exudates and environmental calamities.

Microbe to plant interaction may be saprophytic or parasitic. Mostly the interactions are saprophytic. The positive or negative interaction is dependent on the amount of rainfall, light intensity, soil moisture, temperature, soil type, mineral availability, root structure and root health [1]. The beneficial fungal colony namely *Penicillium, Aspergillus* sp., *Talaromyces* and *Trichoderma* interacts with plant roots to promote fruit setting in chilli, water melon and cucumber plants [8,10,75]. Certain mycorrhizae and free nitrogen fixing bacteria (*Bradyrhizobium japanicum*) lies in soil to stimulate tomato plant growth [71]. Priming treatments with *Trichoderma* sp. prevent over ripening or premature-ripening of melon fruits by declining ethylene concentration and increasing ACC deaminase [11,104]. The information from transcriptome, genomic and proteomic analysis could be useful in identification of organic acids, fatty acids, chemotaxis and stess tolerant gene from beneficial microbes in order to improve yield, height, nutritional parameters and antagonise noxious pathogen growth and division [12,23,24,64,82]. The mechanism behind rhizobacteria and rhizofungi in influencing plant productivity and plant health is by phytohormones production, siderophore production, complex phosphorous, mineral solubilization, lignin, callose and phenol production, PAL, POX, PPO and other antioxidant enzyme production [SOD, CAT] against different biotic, abiotic stressors [7,8,46]. Beneficial microbes were added manually to soil roots chiefly to improve farming methods, increase plant productivity and prevent plants from harmful effects of agrochemicals. The challenging aspect of using biocontrol agents as inducers lies in mass producing and marketing them as biopesticides, bioherbicides and biofertilizers. Henceforth, beneficial microbes’ recognition and their interactions with soil microflora is most important for choosing positive strains to develop novel bioformulations that can stimulate growth and manage diseases in plants.

2. Microbial Interactions with Plants Roots and Their Beneficial Roles

Plant diseases pose serious threat to global food scarcity and cause malnutrition problems. In order to address the problem, beneficial microbial inoculants serve as good source of inducer to achieve sustainable crop yield and manage plant diseases. Microbial colonies vary based on soil type, climatic factor, host plant and kind of interaction. Beneficial interactions of *P. fluorescens* reduced *F. monoliforme* infection, induce maize plants growth and improve mineral cycling by phosphate and zinc solubilization [58]. Rhizospheric fungus *Trichoderma virens* [ZT05] enhances root length (25.11), root surface area (98.19), average root diameter (5.66), root tip number (45.89) and root branch number (74.42%) in *Pinus sylvestris* var. mongolica plants [15]. *Aspergillus ustus* promote growth by secondary roots formation and protected *A. thaliana* plants from infectious pathogens [16]. Different strains of *Chaetomium globosum* increase IAA, GA production and copper tolerance to improve growth and sustainable capacity in chilli and maize plants [18,19]. Parasitic fungus *Sphaerodes mycoparasitica* and rhizospheric fungus-*T. harzianum* treatments increased seed germination %, total plant biomass and suppressed infection of *Fusarium graminearum*, *Pythium ultimum* and *Colletotrichum graminicola* in wheat and maize plants under phytotron conditions [20,35]. *Penicillium* spp. increase photosynthetic efficiency and nutritional parameters like chlorophyll content, lignans, amino acids and proteins in *Sesamum indicum* [17]. Application with *T. harzianum*, *Phoma multirostrata*, and *Penicillium chrysogenum* in tomato plants maximized ACC deaminase levels and nitrogen uptake in plants [21]. *Fusarium oxysporum* prevented nematodes [*Pratylenchus goodeyi*, *Helicotylenchus multicinctus*] growth and the priming treatments were also promising in improving banana fruit yield [22]. Mycorrhizae like *G. mosseae, G. etunicatum, G. claroideum, G. microaggregatum, G. geosporum* and *R. irregularis* improve fruit

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yield, plant weight, water uptake and leaf water potential in tomato plants [14]. *Funneliformis mosseae* application augment growth parameters like fresh weight, dry weight, ca concentration and lowered oxidative damage in tomato plants [13]. Transcriptome studies revealed that mycorrhizal inoculation in *Medicago truncatula* roots increased aquaporins, ATPases, metal adherence, proteins, mineral transporter, and osmoregulatory proteins in root nodules [24]. Rhizomicrobial interactions improve soil health by scavenging toxic metals and toxic pesticides-Fenvalerate, Chlorpyrifos, Cypermethrin from *Stenotrophomonas maltophila*, *Sphingobacterium thalpophilum* plant roots [25]. *Talaromyces wortmannii* produced terpenoid-like volatile and β-caryophyllene to stimulate turnip plants growth [36]. The flower setting is important for fruit production in all kinds of plants. *Penicillium simplicissimum* treatment increase size and weight of marigold flower [27]. Free living non-parasitic nematodes improve soil quality by pathogen inhibition, mineral cycling, and controlling soil borne pathogens. The nematodes can sense environmental disturbances and serve as food for microflora to improve soil health [106]. *Pochonia chlamydosporia* and *Piriformospora indica* induce premature flowering in *A. thaliana, Coleus forskohlii, Lagenaria siceraria* and *Nicotiana tabacum* [30]. *T. harzianum*, *F. equiseti, T. harzianum* T22 treatments stimulate ISR in cucumber plants against anthracnose pathogen-*C. orbiculare* [34]. Certain volatile compounds namely alcohols, alkanes, ketones and terpenoids helps in rhizomicrobial communication in soil [1]. *F. oxysporum* suppressed *Pratylenchus goodeyi* and *Helicotylenchus multicinctus* (nematodes) growth [37]. *Saccharothrix yanglingensis* induced chitinase production which antagonize *Valsa mali* reducing apple canker disease infection [40]. Actinomycetales, *Microbispora*, and *Nonomuraea* prominently displayed antifungal activity in tomato plants against *A. solani, P. parasitica, R. solani*, and *P. irregulare* [42]. *Streptomyces albogriseolus* produced fungichromin that work competently against nematode infection in banana plants [38]. The actinomycetes and mycorrhizal consortium increased growth parameters like plant height, stem diameter, radical size, leaf area and number and total plant biomass. The bioinoculants antagonise *P. capsici* pathogen to reduce wilt infection on chilli plants [39]. Bean seedling growth was improved by *Cladosporium cladosporioides*, *Penicillium simplicissimum* and *Trichoderma* sp. [41]. Root resident microbes were potent enough to increase salt tolerance ability by inducing higher level of catalase, PO, SOD, APO, monodehydroascorbate reductase, GR, GST, GPX and ascorbic acid in *Brassica juncea* plants [26]. Application of *Aspergillus versicolor* reduced fruit rot symptoms in tomato plants [43] and inoculation of rhizobacteria and rhizofungi prevent toxin accumulation, inhibit root knot pathogen and cyst nematodes [45]. Talc based formulations performed well compared to vermiculite-based formulations in providing better tomato yield [44]. Treatment with *Alternaria* sp. *Aspergillus* sp. maximize seedling germination performance of *Astragalus utahensis* [48]. Treatment with *T. longipile* and *T. tomentosum* improved photosynthetic proficiency by 58 to 71% by leaf area expansion in cabbage and lettuce plants [74]. *Aspergillus* spp. PPA1 and *Fusarium* spp. PPF1 were amended in soil that maximize chlorophyll accumulation in cucumber and Indian spinach leaves [75,76]. It is suggested that increased in leaf number, area and chlorophyll contents would increase photosynthesis and carbohydrates synthesis in plants [76]. AMF combined treatments with PGPR managed proline and relative water content levels to increase drought stress tolerance level in *Melissa officinalis* plants [46]. *Trichoderma* sp., trigger SA, ET and JA signalling defense responses to improve resistance in plants [47,75]. Actinobacteria namely *Acidiferrimicrobium*, *Micrococcus*, *Arthrobacter sinomonas*, *Nocardia*, *Streptomyces*, *Frankia* sp., *Rhodococci* sp., invade plant roots, expand mycelial hyphae to stimulate growth and defense responses in plants [54]. The cucumber and muskmelon plants sprayed with *T. harzianum* showed early seed emergence, increase % germination, seedling vigour and % transplantation rate [49,50]. Hypovirulent *R. solani* strains increased fresh leaf and stem weight in tomato plants under pot culture experiments [51]. *Microbispora*, *Actinomadura*, *Streptomyces*, *Mesorhizobium cicero* increased grain yield, nitrogen content via nodule formulation and improved root colonization efficiency by flavonoid content synthesis in *Cicer aeriatinum* plants [55]. *Exophiala* sp. produced gibberellins to reprogrammed cucumber plants growth under salinity and drought conditions [53]. *Streptomyces* strains (Rhizobacteria) lowered fungal infection of *Dactylonectria* sp., *Ilyonectria* sp., *Phaeoacremonium chlamydospora*, and *Phaeoacremonium* sp. in grapevine plants under

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nursery and field conditions [56]. *Micromonospora aurantiaca* and *Streptomyces griseus* increased N, P uptake to promote wheat plants growth and reduce damping-off (*Pythium ultimum*) infection [85]. Genome analysis of *Dermacoccus abyssi* identified salt tolerant gene to promote tomato plants growth under halophytic conditions [56]. Thus, beneficial microbes residing in roots help the plant to bear lower water content, scavenge toxic metals from soil and protect plants from adverse natural calamities to finally stimulate higher productivity and flexibility in plants [**Figure 1**]. The important rhizospheric fungi that promote plant growth and stimulate resistance in various plant crops has been listed in Table 1.

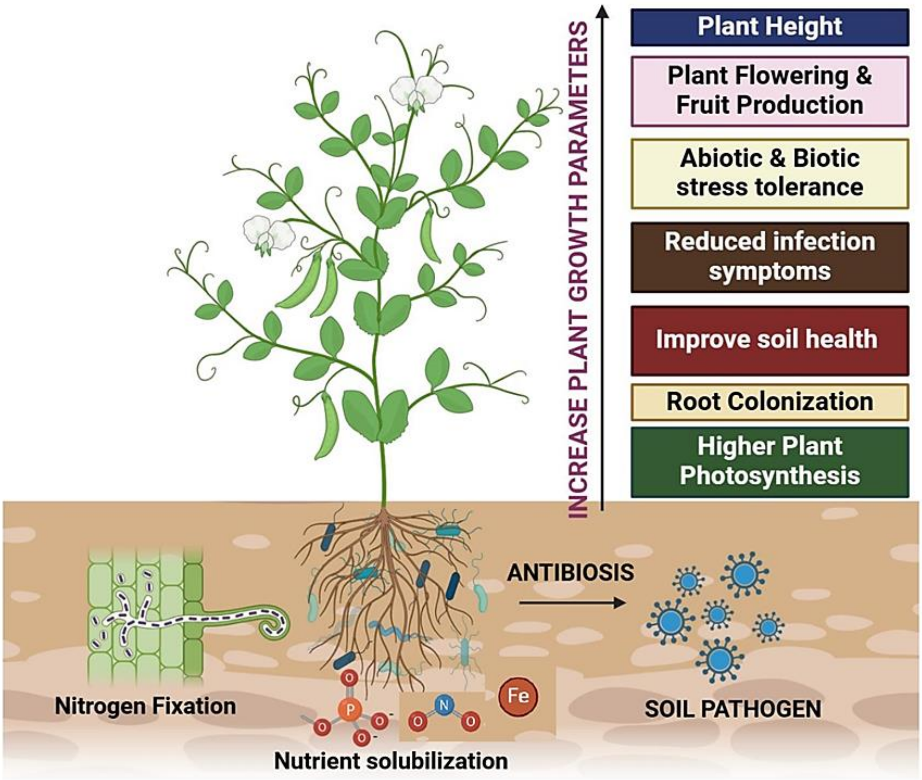

Figure 1. A Graphical Representation of Mutualistic/ Saprophytic Interaction in Plant Rhizobiome.

Table 1. Evaluation of Rhizospheric Microbes in the Promotion of Plant growth and Increased Resistance.

Plant host	Rhizosphere Microbes	Plant growth Mechanism	Resistance Mechanism	Abiotic Pressure	Pathogen	Reference
		Growth Promoting Bacteria/ Actinobacteria				
Wheat (*Triticum aestivum*)	*P. putida*	Produce more tiller, grain/ spike formation & 100 seed weight	Higher antioxidant activity, Proline, Total proteins, Sugars & Amino acids	Heat Stress	-	[102]
Tomato (*Lycopersicon esculentum*)	*Pseudomonas* strains R62 & R81	Increase dry root weight, shoot weight & fruit yield under field conditions	Control wilt disease incidence	-	*Fusarium oxysporum* f.sp. *lycopersici*	[44]

-	*Streptomyces albogriseolus*	Higher 6-methyl-fungichromin	-	-	*Meloidogyne incognita* & *Meloidogyne javanica*	[38]
Chilli (*Capsicum annuum*)	Actinomycetes	Increase plant height, stem diameter, leaves number & leaf area	Increased radical volume & reduce disease severity	-	*Phytophthora capsici*	[39]
Wheat (*Triticum aestivum*)	*Arthrobacter protophormiae* (SA3) & *Dietzia natronolimnaea* (STR1)	Promote IAA content & reduced ABA/ACC content	-	Increase (ABA) & ACC under salt & drought stress	-	[67]
Tomato (*Solanum lycopersicum*)	*Paenibacillus lentimorbus*	-	Expression of defense-related & autophagy-related genes	-	*Sclerotium rolfsi*	[101]
Cucumber (*Cucumis sativus*)	*Saccharothrix yanglingensis*	-	Antifungal activity & Chitinase Production	-	*Valsa mali*	[40]
Potato (*Solanum tuberosum*)	*Lysinibacillus* sp.	-	Antibiosis	-	*Ralstonia solanacearum*	[99]
Helianthus annuus	*Bacillus subtilis*	Increase Plant Biomass, Phosphate & iron solubilization,	Phytohormone production	-	*Fusarium oxysporum*	[104]
Solanum tuberosum Oryza *sativa, Zea mays* & *Phaseolus vulgaris*	*Serratia* spp.	Higher phytase activity	AHLs- acyl homoserine lactone & phytohormone production	-	-	[100]
Limonium sinense	*Bacillus flexus* KLBMP 4941	Increase root length, shoot length & fresh weight	Organic acids production	Mitigated salt stress by producing organic acids (stearic, palmitic, palmitoleic & oleic acids	-	[64]
Wheat (*Triticum turgidum*)	*Bacillus cabrialesii*	Increase chlorophyll content & Roots colonization	Increased antibacterial metabolites such as Bacillaene, Bacilysin, Bacillibactin & subtilosin-A	-	*Bipolaris sorokiniana*	[28]

Solanum lycopersicum	*Dermacoccus abyssi*	Phosphate solubilization, Phytohormone (IAA) production, more total soluble sugar & total chlorophyll content	Mitigated salt stress & osmoregulate by soluble sugars. Increase H_2O_2 scavenging activity	-	-	[57]
Zea mays	*Pseudomonas fluorescens*	-	Reduced ear rot disease incidence	-	*Fusarium moniliforme*	[58]
			Growth Promoting Fungi/ Mycorrhizae			
Tagetes erecta	*Penicillium citrinum* & *Penicillium simplicissimum*	Maximized the carbohydrates & reducing sugars. Increased size, dry matter & flower early.	Produced root exudated & enhanced polygalacturonase, & cellulase enzymes activity	-	-	[27]
Cucumis melo	*Trichoderma harzianum* *Trichoderma ghanense* & *Trichoderma hamatum*.	Maximize leaves number, root and shoot weight, & IAA production	Inhibitory activity, Decrease wilt Incidence, Increase in SA & JA.	More ACC deaminase	*Fusarium oxysporum*	[10]
Sesamum indicum	*Penicillium sp.* NICS01	Increased plant length, amino acid content & plant weight.	-	Salt stress	-	[17]
Tomato (*Solanum lycopersicon*)	*Funneliformis mosseae.*	Increased biomass (Root and Shoot Fresh weight)	Improving Antioxidant Machinery	Lowered Ascorbate, glutathione, redox ratio & L-galactono-1,4- lactone dehydrogenase ratio	-	[13]
Pinus sylvestris var. *mongolica*	*G. mosseae, G. etunicatum, G. claroideum, G.microaggregatum, G. geosporum & R. irregularis*	Promoted Lycopene & β-Carotene contents	Increased antioxidant potential by enhancing ascorbic acid content	Improved Leaf water content (%) under water stress.	-	[14]
Pinus sylvestris var. *mongolica*	*Trichoderma harzianum E15* *Trichoderma virens* & *S. luteus*	Improved root structure by increasing	Lower proline content & MDA content	Increase superoxide dismutase-SOD &	-	[15,103]

		root length & surface area. Increased fresh & dry weight.		peroxidase-POX) activity to withstand drought stress		
Chilli (*Capsicum annuum* L.)	*Talaromyces funiculosus*	Phosphate solubilization, Siderophore, HCN, IAA, Chitinase & Cellulase production, Increase chlorophyll, fruit weight & plant Biomass.	Higher antagonistic activity, Disease Protection, PAL, POX, Chitinase, ISR, Lignin & Callose production	-	*Colletotrichum capsici*	[08]
Drum stick (*Moringa Oleifera*)	*P. chrysogenum* & *T. viride*	-	Maximize Antagonistic behaviour	-	*Fusarium oxysporum*, *Penicillium digitatum*, & *Aspergillus wentii*	[09]
Rape Mustard (*Brassica juncea*)	*Trichoderma harzianum*	Plant height, Root Length & Plant Dry weight	Maximized SOD, POD, APX, GR, GST, GPX, GSH & GSSG activities	Plant tolerant to saline stress [Proline 59.12%, H_2O_2 69.5% & MDA contents by 36.5%]	-	[26]
Maize (Zea mays)	*Trichoderma harzianum*	Promoted root growth size, area & root hair area	Reduced anthracnose symptoms by maximizing β,1-3 glucanase, exochitinase & endochitinase in roots & shoots.	-	*Pythium ultimum*, & *Colletotrichum graminicola*	[35]
Brassica campestris L. var. *perviridis.*	*Talaromyces wortmannii*	Increased growth by high levels of β-caryphyllene contents	Reduce infection symptoms	-	*Colletotrichum higginsianum*	[36]
Chilli (*Capsicum annuum*)	*Arbuscular Vesicular Mycorrhizae* (AMF)	More plant height, stem diameter, leaves number & leaf area	Increased radical volume & reduced disease severity	-	*Phytophthora capsici*	[39]
Phaseolus vulgaris	*Trichoderma* sp.	Enhanced root length & aerial parts	Indole-3-acetic acid (IAA)	-	-	[41]

Tomato (*Solanum lycopersicon*)	*Rhizoctonia* G1, L2, W1 & W7	Increase Plant weight (stems & leaves).	Reduced Disease Severity	-	*Fusarium oxysporum f. sp. lycopersici*	[51]
Cucumber (Cucumis melo)	*Funneliformis mosseae*	More fresh weight & dry weight was noticed	Increased Phenols, flavonoids, lignin, DPPH activity & phenolic compounds	Increased tolerance to temperature stress by maximizing glucose-6-phosphate dehydrogenase (G6PDH), shikimate dehydrogenase (SKDH), (PAL), cinnamyl alcohol dehydrogenase (CAD), (PPO), guaiacol peroxidase (G-POD), caffeic acid peroxidase (CA-POD) & chlorogenic acid peroxidase (CGA-POD).	-	[72]
Maize	*Pseudomonas putida*	-	Benzoxazinoids Allelochemical/ antimicrobial effect	-	-	[60]
Cucumis sativus	*Exophiala sp.* LHL08	GA production	Induce defense response by SA production	Increased abscisic acid (ABA) & other phytohormone production under salinity & drought	-	[53]

3. Rhizomicrobiome Interaction with Secondary Metabolite, Signalling Proteins and Their Relationship in Plants

Plants secrete secondary metabolites within root region surrounded by soil that can manipulate rhizomicrobiome and have direct role in induction of plant growth promotion and defense responses. To improve soil nutritional efficiency, the survival of beneficial microflora and their colonization ability are the key factors. Root exudates secreted by plants were utilized by beneficial microbes to fulfil nutritional deficiency. Coumarin secreted by plant roots to attract *Pseudomonas simiae* colony overcome iron deficiency in *Arabidopsis* plants [59]. *Pseudomonas fluorescence* JM-1 produced 2,4-

Diacetylphloroglucinol to lowered the ear rot infection in *Zea mays* plants [58]. Certain root secretions help the beneficial microbes to colonize the plant roots and few can affect microbial colonization. For example: *Pseudomonas putida* residing in rhizophere region secretes benzoxazinoids to establish successful connection with host plants and increase the growth of oxalabacteraceae plant members by making nitrogen available to thrive under stressful conditions [60,61]. Galactoside secretions were utilized by *S. meliloti* [62]. Interestingly few exudates like Isothiocyanates (ITC) and glucosinolates secretions affect rhizomicrobial growth species namely *Pseudomonas syringae*, *Sphingomonas suberifaciens* and *Fusarium oxysporum* [66]. The plant genotype decides complexity and specificity nature of root exudates which attracts specific beneficial microbes' interaction. Fatty acid secretion increased *Bacillus flexus* colonies in *Limonium sinense* (halophyte) plant [64]. Secreted amino acids help in chemotaxic movement of *Pseudomonas protegens* [65]. *Arthrobacter protophormiae* (SA3) and *Dietzia natronolimnaea* (STR1) improve wheat plants to withstand high salt and low water stress by triggering IAA and ET signalling pathways [67]. During cold stress, rhizobacteria like *Funneliformis mosseae* and *Paraburkholderia graminis* lowered ROS generation in tomato plants [68]. Likewise, *Trichoderma asperellum* induced phytohormone production in cucumber plants that make plants tolerant to saline conditions [69]. Certain rhizobacteria named *Bacillus methylotrophicus, Bacillus licheniformis*, and *Bacillus aryabhattai* increase wheat plant capacity to heat stress by reduced RO generation [70]. *Bradyrhizobium japonicum* (mycorrhizae) activates nod factor that tends to enhance root surface area, root length and lateral root hair number in *Arabidopsis thaliana* [71]. *Caulobacter*, *Serratia*, *Flavobacterium*, *Chromobacterium* and *Methylobacterium* mitigated abiotic stress response in *Psoralea corylifolia* and *Triticum aestivum* plants [78]. *Funneliformis mosseae* increased secondary metabolites, reduce oxidative stress and enzyme activity along with increasing fresh and dry weights. AM fungus inoculation on soybean plants improved salt tolerance ability by targeting StNHX1 gene (Na^+ /H^+ antiporter gene) [73]. *Nicotiana benthamiana* produce capsidiol induce defense response by activating ethylene signalling pathway towards *Phytophthora infestans* [79]. *Mesorhizobium ciceri* was inoculated with *Bacillus* sp. and *Enterobacter aerogenes* increased root nodulation, nitrogen uptake, phosphorous and total protein in chickpea plants [80]. The RNA transcript analysis of *Arthrobacter endophyticus* and *Nocardiopsis alba* revealed carotenoid, glycerolipid, phenylalanine production upon salt stress by upregulating chlorophyll a, hydroxyproline rich glycoprotein, cytokinin dehydrogenase and K^+ uptake in *A. thaliana* [82]. An actinomycetes named *Streptomyces* sp. produced betalain, isoquinoline, alkaloid and zeatin under salt stress in *Solanum lycopersicum* cv. Jingpeng [83]. The mutation in disease causing gene (mpg1) in *M. grisea* abrupt appressoria structure and lowered infection symptoms on rice plants [105]. *Frankia* sp. produced cytosolic glutamine synthetase to metabolise soil nitrogen and promote *Datisca glomerata* plants growth [84]. The GC-MS analysis helps in secondary metabolites/ root exudates identification and the secretions were linked to functional aspects and variations in *A. thaliana* plant [29,33]. A proteomic study was performed wherein PR proteins (PR10) helps in the identification of *Sinorhizobium meliloti* colonization to improve *M. truncatula* plants roots architecture and the process is regulated by auxin production [23]. *Pseudomonas syringae* sprayed on *Arabidopsis* plants induce PR proteins and SA production [32]. RNA transcript analysis revealed that organic acids (fumaric acid) secreted by maize roots was helpful in *Bacillus amyloliquefaciens* biofilm formation [63]. Utilizing genomic and metabolomic techniques, it was possible to identify antifungal metabolites like surfactin, iturin fengycin, and rhizocticin-A produced from *Bacillus cabrialesii* and *Bacillus amyloliquefaciens* effective against spot blotch disease of *Triticum turgidum* [28,31]. The amino acids, phenol (alanine, arginine, asparagine) and coumarins (cinnamic, salicylic, syringic, ferulic, caffeic acids) play a diverse role in attraction, quorum sensing, symbiotic interaction, rhizomicrobial growth and virulence gene activation. Therefore, identification of root secretions helps in better understanding of root colonization process, secondary metabolite secretions, water and minerals transport, biochemical compounds synthesis, regulatory and stress responsive genes.

4. Saprophytic Microbial Interaction Can Be Beneficial or Parasitic in Rhizosphere

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Root exudates released by plants act as signalling molecules which can instigate both pathogenic and mutualistic interactions in rhizosphere. It has been documented that plant roots association helped microbes to establish connection with plants and strengthen plant defense [90]. The root exudates produce sugars (glucose, sucrose, galactose, fructose) and organic acids (malic, lactic, citric and oxalic acids) that serve as C-source which provide energy to increase microbial colonies number. Strigolactones increased plant root length and root hairs. Saprophytic microbes act as decomposers by converting complex organic into smaller simple molecules. They cycled N, P and other micronutrients to make available to plants [91,92]. The saprophytic fungi can act as growth promoters and enhancers of plant defense responses. For eg: *Streptomyces ganmycicus, Trichoderma, Gliocladium, Pseudomonas* and *Bacillus subtilis* reduced disease incidence in *Rhizoctonia solani* in Maize and Soybean plants [92]. Biocontrol agents reduced parasitic fungal infection in roots via antagonistic behaviour and induced ISR in host plants [95]. Beneficial microbes produce nod factors to form nodule in leguminous roots to fix nitrogen and convert into ammonia that can be absorbed by plants [93]. *R. leguminosarum* (nodule forming bacteria) deliver protection in faba bean plants against mosaic virus infection by decreasing H_2O_2, MDA contents (oxidative stress indicators) and increasing defense related enzymes [94]. Rhizospheric fungi (*T. harzianum*, *T. asperellum*, *Aspergillus tubingensis*, *Penicillium* sp., *T. funiculosus*) increased PAL, POX, Chitinase and β-Glucanase activity. The lignin and callose deposition in chilli plants with *C. capsici* infection impart resistance towards anthracnose disease. These rhizospheric fungal interactions can increase biochemical parameters like carbohydrates, amino acids, proteins, chlorophyll and chilli fruit yield [8]. Allelopathic plants produce defense chemicals that specifically act on weed plants and this defense strategy is dependent on plant roots secretions. The defense molecules composition, amount and their control mechanism are dependent on plant pathogen interaction [96]. Beneficial microbial diversity in rhizospheric region can be improved by physical methods like crop rotation and intercropping as the plant selects unique bacteria via producing root exudates which interact with plant roots to improve soil fertility and maximum crop yield [97]. AMF mycorrhizae increase phosphorous content via mutualistic association with plants by enzymatic breaking down of insoluble P into soluble form [95]. Thus, the presence of microbial soil flora depends on correct root architecture, root type and niche. The beneficial interactions improve soil health by increasing microbial colony, deep root penetration in soil, protection from soil erosion and adverse climatic factors.

If microbial interaction is incompatible then it will produce infection symptoms that reduce crop yield and resistance towards noxious pathogens. Some saprophytic microbes can be pathogenic/ opportunistic to cause plant diseases **[Figure 2]**. *Aspergillus* sp. and *Bacillus* sp. were plant growth promoters in cotton plants and *A. chevalieri*, *A. egyptiacus* were defense enhancer in *Vicia faba* plants [88,89]**.** It was observed that rhizomicrobial interaction deliver protection by producing chitinases, glucanases, myrosinases [92]. *Alternaria* sp., cause early blight, leaf spots, head rot, and black rot disease in plants. But in some plants, some of its species named *Alternaria* sp. A13 can act as plant growth promoter and improve secondary metabolite [cinnamic acid 4-hydroxylase and lithospermic acid B] contents [86,87]. The root fungi can be parasitic/ saprophytic depending on the presence/absence of host. There will be competition and interference between soil microbes with parasitic and beneficial nature. The type of interaction is decided by root structure, secretions, and living root activities. The mechanism by which microbes interact include vesicle transport, diffusion, and ion channels [91]. Developing variety by designing root architecture with higher root length and more lateral roots to have plasticity towards changing environment conditions. Biochar positively control rhizomicrobial activity and promote good yield [22]. Carbon derived from plant roots can be stored as soil organic matter which depends on the carbon input and decomposition rate. Root resident microbes help in the degradation of organic matter and remove pollutants to improve soil fertility and resilience [87]. Overall, root resident beneficial microbes act as inducers to deliver nutrients for plant growth, tolerance to abiotic stressors and serve as good pathogen inhibitors [98].

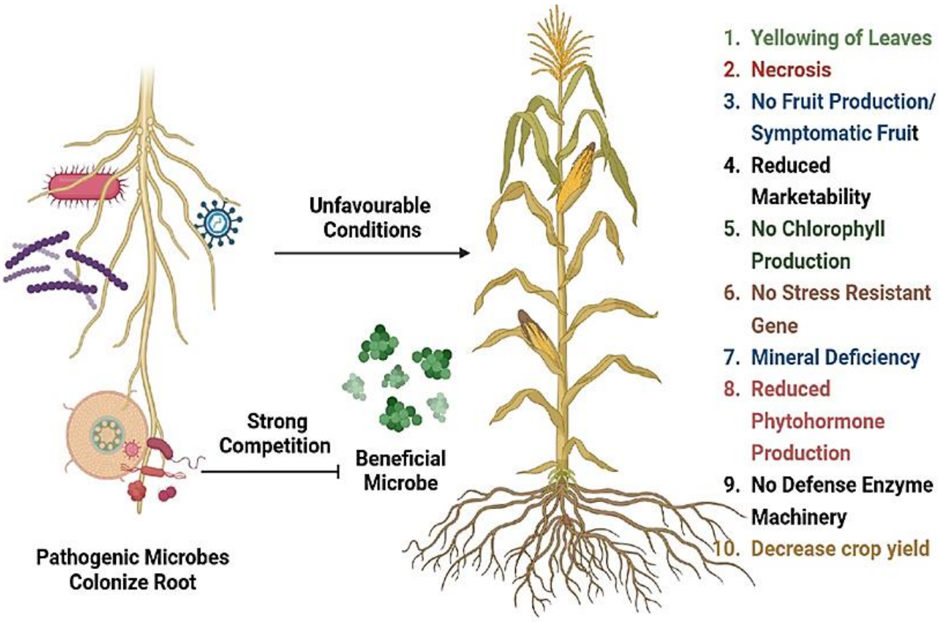

Figure 2. An overview of Pathogenic/ Parasitic mode of interaction in Plant Rhizobiome.

5. Conclusions

To achieve sustainable food production, root architecture has to designed in such a way that plants must have long root length, more root hairs and numbers. This could be achieved by artificially inoculating beneficial microflora in soil roots that help the plants to penetrate deeper in soil to absorb vital nutrients chiefly N, P, K and other micro, macronutrients which ultimately lead to higher crop yield. These rhizomicrobiota induce enzymes lignin and callose in roots to improve defensive system and prevent pathogen entry. The beneficial microflora competes naturally with parasitic pathogens for niche and food. The root secretions are dependent on plant species, soil nature and climatic conditions. The soil health can be maintained by increasing soil beneficial flora by adopting crop rotation and intercropping methods. Improving rhizobiome can increase beneficial microflora colony number that help plants to withstand drought, salinity and various stressed conditions. The pathogenicity is decided by low and high molecular weight compounds that play a vital role in plant interaction. Malnutrition and hunger problems are the major issues at present and will increase in more higher rate in the coming years. The main gateway to attain safe, sustainable food production is to develop broad range of rhizomicroformulation that can manage disease causing pathogens, infection symptoms, increase positive soil-root feedback mechanism, improve plants health and productivity. Using scientifically distinct but functionally similar useful strains could be good and promising tactic in near future to design definite disease standards and multi-targeted biocontrol methods.

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Abbreviations

The following abbreviations are used in this manuscript:

ACC	Aminocyclopropane-1-carboxylate deaminase
PGPR	Plant Growth Promoting Rhizobacteria
PGPF	Plant Growth Promoting Fungi
SOD	Superoxide Dismutase
POX/POD	Peroxidase
PAL	Phenylalanine lyase
PPO	Polyphenol Peroxidase
N, P, K	Nitrogen, Phosphorous, Potassium
ABA	Abscissic acid
SA	Salicylic acid
JA	Jasmonic acid
H2O2	Hydrogen peroxide
IAA	Indole-3-acetic acid
AHLs	Amino homoserine lactones
HCN	Hydrogen cyanide
CAT	Catalas
GA-	Gibberellic acid
PR	Pathogenesis related proteins
ET	Ethylene
MDA	Malondialdehyde
APX	Ascorbate peroxidase
GR	Glutathione reductase
GST	Glutathione-S-transferase
GPX	Gaucol peroxidase

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