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A Review-Enhancing Plant Resilience in Saline Environments with Core Microbial Mangrove Communities

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Abstract **Review Article**

Microorganisms are pivotal in delivering a wide range of direct and indirect benefits to plants, demonstrating superior efficacy compared to synthetic molecules. This review centres on the complex interactions within rhizophytic and endophytic communities, especially in challenging saline environments, leveraging 'Core Microbial Mangrove Communities (CMMC)'. Highlighting the importance of mangrove rejuvenation, the study examines how specific microbial taxa contribute to fostering long-term sustainable practices in these habitats and suggests that microbial communities exhibit rapid and positive responses to restoration efforts.

Keywords: Core Microbial Mangrove Communities (CMMC); Plant Growth Promoting Microorganisms (PGPMs); Plant-Microbial Interactions.

INTRODUCTION

Mangroves emerge as pivotal players in mitigating the impacts of tidal waves and cyclones, functioning as the principal defense against flooding and soil erosion. Valued between 90,000 to 140,000 US dollars annually, mangroves are recognized as invaluable natural resources, offering a plethora of ecosystem services such as habitat provision for diverse marine life, coastline stabilization, and significant contributions to the global carbon budget (Fig. 1) (Ferreira *et al.*, 2023). Central to the functionality of mangrove ecosystems are the microorganisms constituting the mangrove microbiome, including bacteria, archaea, fungi, and protists, which play pivotal roles in supporting these ecosystem services.

Understanding and harnessing the potential of the mangrove microbiome pose both significant goals and formidable challenges in efforts to protect, manage, and mitigate threats to mangroves. Microbes within mangrove sediments are crucial for nitrogen cycling through various processes such as fixation, denitrification, and ammonification, while those residing on roots and leaves surfaces facilitate nutrient availability, provide defense against pathogens, and initiate decay processes (Alishahi *et al.*, 2020). Urgent research is needed to elucidate the intricate interactions between microorganisms and mangroves to ensure the conservation and rehabilitation of these critical ecosystems, especially in light of impending Sustainable Development Goals (SDGs) and the Decade on Ecosystem Restoration.

Although restoration efforts employing strategies like out-planting and raised bed methods have yielded mixed outcomes, success rates have improved significantly with the inoculation of local microbial species (Zimmer *et al.*, 2022). However, our current understanding of mangrove microbial communities remains largely descriptive and limited in spatial and temporal scope, despite the recognized significance of dynamic factors such as air exposure, oxygen concentrations, salinity levels, and seasonal variations in rainfall on microbial community dynamics (Vincent and Owens, 2021). Additionally, while microbial processes in mangroves have demonstrated relevance to biogeochemical cycling and associated ecosystem services, a comprehensive understanding of these processes and their drivers is still nascent. Moving forward, restoration efforts should prioritize a deeper understanding of microbial community structure and function to ensure the success of conservation endeavours in mangrove ecosystems.

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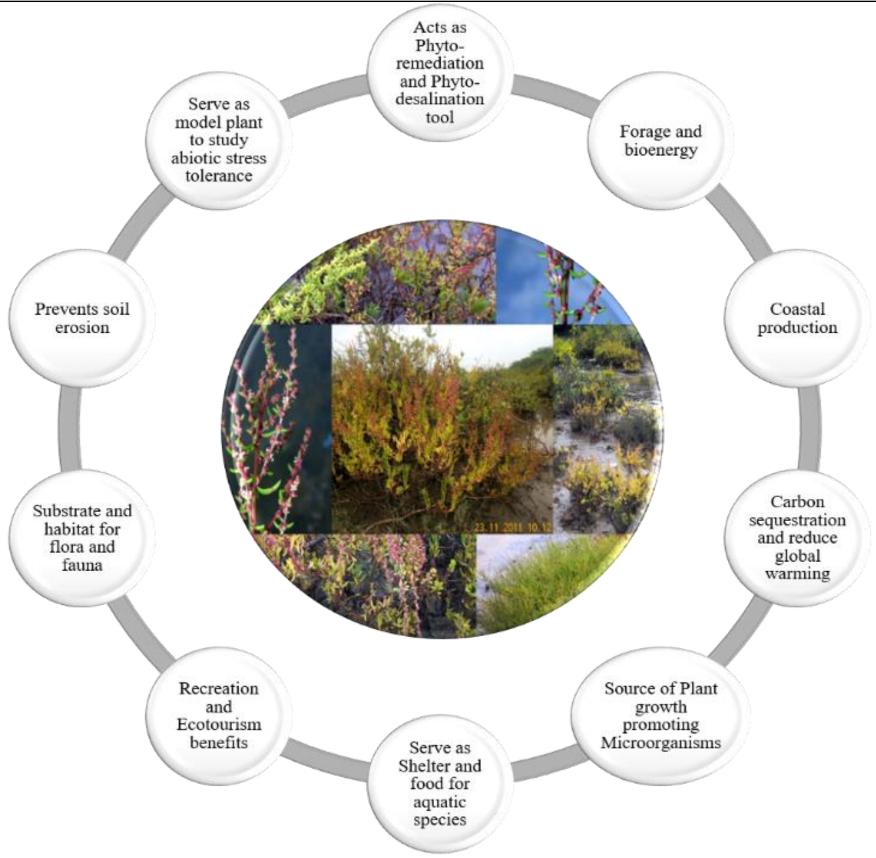

Figure 1: Outlines the multifaceted potential uses of coastal mangrove ecosystem

Coastal Marvels: Unraveling the Rhizosphere Dynamics in Mangroves and Halophytic Plants

In the intricate realm of soil microbiology, microbial communities navigate a complex and unpredictable environment shaped by a multitude of factors and dynamic interactions. Soil type, texture, climatic conditions, chemical fertilization, and the specific plant species inhabiting a given soil type all contribute to this intricate milieu. Within this environment, the rhizosphere emerges as a focal point where the interplay between microorganisms and plants unfolds. Defined as the soil volume surrounding and influenced by plant roots, the rhizosphere provides a conducive habitat for microorganisms, fostering their proliferation in greater numbers. This symbiotic relationship between plants and microorganisms in the rhizosphere is pivotal, as microorganisms supply plants with growth-promoting substances, establishing a mutually beneficial association (Goswami *et al.*, 2020). In natural soil environments, microbial growth is often limited by nutrient availability. However, root-secreted compounds, comprising approximately 17% of photosynthetic products, including organic acids, sugars, and amino acids, serve as a vital nutrient source for soil microbes. These compounds stimulate microbial growth and enhance extracellular enzyme activity, playing a crucial role in nutrient cycling and soil health (Chen *et al.*, 2019). Given the indispensable role of belowground microbes in facilitating aboveground physiological processes in plants, comprehending the composition and dynamics of microbial communities in the plant rhizosphere is imperative (Yamamoto *et al.*, 2020).

Table 1: List of rhizospheric core microbial communities associated with the coastal plants

Origin	**Taxonomic identification**	**Group**	**Part**	**Potential function**	**Reference**
Aeluropus littoralis	*Byssochlamys spectabilis* *Chaetomium globosum* *Cephalotheca foveolata* *Penicillium melinii* *Alternaria tenuissima* *Nigrospora chinensis*	Fungi	Root	Siderophore, HCN and ammonia production	Tarroum *et al.*, 2021
Arthrocnemum indicum	*Pseudomonas stutzeri* *Ochrobactrum anthropic*	Bacteria	Root	IAA production, N_2 fixation, phosphate solubilisation, and ACC deaminase activity	Sharma *et al.*, 2016

Origin	**Taxonomic identification**	**Group**	**Part**	**Potential function**	**Reference**
Arthrocnemum macrostachyum	*Microbulbifer rhizosphaerae* *Labrenzia salina*	Bacteria	Root	IAA, siderophore production, and phosphate solubilization	Camacho *et al.*, 2016;
Aster tripolium	*Bacillus cereus* *Bacillus pumilus*	Bacteria	Root	IAA, Ammonia, HCN, N_2 fixation, Nodulation, siderophore production, ACC deaminase activity and pathogen inhibition	Landwehr *et al.*,2002; Szymańska *et al.*, 2016
	Glomus geosporum	Fungi	Root	Reducing ethylene (ACC deaminase activity)	
Atriplex sp.	*Glomus geosporum* *Glomus caledonium*	Fungi	Root	Phosphate solubilisation, siderophore production and reducing ethylene activity	Landwehr *et al.*,2002
Avicennia marina	*Salinicola rhizosphaerae* *Idiomarina mangrovi* *Zunongwangia mangrove* *Pseudomonas maricaloris*	Bacteria	Root	ACC deaminase activity, mineral solublization and increase phosphatase	Bibi *et al.*, 2017; Chen *et al.*, 2019
Carex scabrifolia	*Gynuella sunshinyii*	Bacteria	Root	Not Defined	Chung *et al.*, 2015
Cyperus conglomeratus	*Microbulbifer celer*	Bacteria	Root	IAA production, Phosphate solubilisation, Nodulation and degrade hydrocarbons compounds	Bibi *et al.*,2017
Halocnemum strobilaceum	*Brevibacillus borstenlensis* *Halomonas sinaensis* *Pseudoalteromonas ruthenica* *Marinobacter daqiaonensis* *Aidingimonas halophila* *Chromohalobacter israelensis*	Bacteria	Root	N_2 fixation, IAA, GA production, ACC deaminase activity, osmoregulation and transport	Bibi *et al.*, 2017
Kandelia candel	*Erythrobacter mangrovi*	Bacteria	Root	Not Defined	Ye *et al.*, 2020
Salicornia bigelovii	*Rhizobium spp.* *Bacillus spp.* *Klebsiella pneumoniae*	Bacteria	Root	N_2 fixation, Antioxidant enzymes and photosynthetic pigments	Rueda-Puente *et al.*, 2010
Salicornia brachiata	*Brachybacterium saurashtrense* *Brevibacterium casei* *Zhinguelliuella somnathii* *Cronobacter sakazakii* *Rhizobium radiobacter* *Agrobacterium tumefaciens* *Halomonas sinaensis*	Bacteria	Root	N_2 fixation, IAA production, phosphate solubilization, ACC deaminase activity, osmoregulation, and transport	Jha *et al.*, 2015
Salicornia europaea	*Bacillus endophyticus* *Bacillus tequilensis* *Planococcus rifietoensis* *Variovorax paradoxus* *Arthrobacter agilis* *Pseudomonas pseudoalcaligenes*	Bacteria	Root	N_2 fixation, IAA production, proline accumulation, proteaseactivity, quorum quenching, and regulation of Na+ and K+ homeostasis	Yamamoto *et al.*, 2020
Salicornia ramosissima	*Pseudomonas oryzihabitans* *Psychrobacter faecalis* *Vibrio neocaledonicus* *Bacillus vietnamensis* *Bacillus infantis* *Bacillus australimaris* *Bacillus aryabhattai*	Bacteria	Root	N_2 fixation, IAA production, ACC deaminase Activity and Pathogen suppression	Ferreira *et al.*, 2021
Salsola imbricata	*Bordetella avium* *Nocardioides deserti* *Isoptericola salitolerans*	Bacteria	Root	IAA, HCN, Antagonistic activity	Bibi *et al.*, 2017

Origin	Taxonomic identification	Group	Part	Potential function	Reference
	Streptomyces phaeopurpureus				
Sesuvium portulacastrum	*Aeromonas hydrophila,* *Pseudomonas aeruginosa* *Corynebacterium xerosis* *Escherichia coli*	Bacteria	Root	EPS, biofilm formation, quorum quenching, Phosphatase enzyme activity, basal respiration and antioxidant	Anburaj *et al.*, 2012
Suaeda fruticosa	*Arthrobacter pascens* *Bacillus licheniformis* *Zhihengliuella flava*	Bacteria	Root	Increased plant biomass, Phosphate solubilisation, ABA, GA and siderophore production	Goswami and Deka, 2020

Mangroves and associated halophytic plants have been identified as significant reservoirs for plant growth-promoting rhizospheric microorganisms (PGPRMs), particularly under stressful conditions (Table 1). Certain PGPR strains, such as *Azotobacter, Bacillus, Enterobacter, Klebsiella,* and *Pseudomonas* isolated from root systems of *Arthrocnemum indicum, Aster tripolium, Avicennia marina, Kandelia candel, Salicornia sp, Sesuvium portulacastrum, Suaeda fruticosa* demonstrate the ability to enhance stress tolerance in plants by producing antioxidants that neutralize Reactive Oxygen Species (ROS) (Anburaj *et al.*, 2012; Jha *et al.*, 2015; Sharma *et al.*, 2016; Ye *et al.*, 2020). Additionally, a group of microbial communities known as Arbuscular Mycorrhizal Fungi (AMF) form mutualistic associations with approximately 80% of plant species, enhancing nutrient absorption and promoting the production of bioactive compounds. These fungi facilitate plant growth by improving water and nutrient uptake, thereby augmenting plant efficiency. Moreover, AMF exhibit beneficial effects in controlling foliar and root pathogens by activating induced systemic resistance (ISR) in host plants like *Atriplex sp, Aeluropus littoralis, Aster tripolium, Ceriops tagal* through various signaling pathways (Landwehr *et al.*, 2002; Szymańska *et al.*, 2016; Tarroum *et al.*, 2021). Among the prominent phyla, Glomeromycota have been extensively utilized as plant growth-promoting fungi (PGPFs), emphasizing their pivotal role in fostering plant growth and resilience.

Coastal Insights: Endophytes as Bio-Reservoirs of Plant-Derived Natural Products and Promoters of Host Health in Mangroves and Coastal Plants"

The challenge of maintaining optimal growth and biomass production in plants, particularly under abiotic stress conditions such as salinity, has long hindered productivity, resulting in diminished yields and stunted growth. Salinity stress disrupts various physiological and biochemical processes within plants, exacerbating the production of reactive oxygen species (ROS), ion toxicities, and osmotic imbalances, leading to water deficits. In this context, endophytes, a diverse group of microorganisms including bacteria, fungi, and actinomycetes, offer a promising avenue for enhancing plant resilience. These organisms form symbiotic relationships with plants, residing within their internal tissues without causing harm, and contribute significantly to plant health and growth through mechanisms such as phosphate solubilization, phytohormone synthesis, nitrogen fixation, and suppression of phytopathogens (Arora *et al.*, 2014; Szymanska *et al.*, 2016; Bibi *et al.*, 2017).

The influence of salinity on endophytic microbial communities in coastal plants presents a unique ecological dynamic, potentially impacting plant adaptation to adverse conditions, including elevated salinity levels commonly encountered for the above said. While these endophytes primarily originate from soil, the specific characteristics of saline soils and the geographical context of affected regions can shape the composition of endophytic communities associated with halophytes. Remarkably, despite seasonal variations, the interior nature of plant tissues provides a relatively stable environment for diverse endophytic communities compared to the fluctuating conditions of saline soils (Indira & Srinivasan, 2017; Mora-Ruiz *et al.*, 2018; Furtado *et al.*, 2019; Rush *et al.*, 2024). Meta-statistical analyses underscore the positive impact of endophytes, including bacteria, filamentous fungi, and yeast, in mitigating plant stress induced by drought, nitrogen deficiency, and salinity.

Table 2: List of endophytic core microbial communities associated with the coastal plants

Origin	Taxonomic identification	Group	Part	Potential function	Reference
Arthrocnemum macrostachyum	*Chromohalobacter canadensis* *Rudaea cellulosilytica* *Bradyrhizobium spp.* *Halomonas radicis*	Bacteria	Root	N_2 fixation, root nodulation, IAA production, phosphate solubilization, ACC deaminase activity, osmoregulation and transport	Mora-Ruiz *et al.*, 2018; Navarro-Torre *et al.*, 2020
	Staphylococcus equorum *Kushneria indalinina*		Stem		
Aster tripolium	*Serratia marcescens* *Thalaspirilla permensis*	Bacteria	Root	IAA production, N_2 fixation, phosphate solubilization,	Szymańska *et al.*, 2016

Origin	**Taxonomic identification**	**Group**	**Part**	**Potential function**	**Reference**
	Pseudomonas stutzeri			ACC deaminase activity pathogen suppression and phytohormone production	
Avicennia marina	*Erwinia toletana*	Bacteria	Root	Not Defined	Bibi *et al.*, 2017
	Leptosphaerulina chartarum *Phomopsis azadirachtae*	Fungi	Stem	Heavy metal absorption	
	Phyllosticta capitalensis	Fungi	Leaf	Not Defined	
Avicennia officinalis	*Fusarium oxysporum*	Fungi	Root	Siderophore, HCN and ammonia production	Ranganathan and Mahalingam, 2019; Apurva Sawant and Rodrigues, 2020
	Alternaria longipe		Stem		
	Aspergillus lavus *Aspergillus niger*		Leaf	Antioxidant, cytotoxic activity and heavy metal degradation	
Bassia dasyphylla	*Monosporascus ibericus*	Fungi	Root	Not Defined	Li *et al.*, 2020
Bruguiera gymnorhiza	*Fusarium striatum* *Xylaria feejeensis*	Fungi	Stem	Siderophore production	Ukwatta *et al.*, 2019
	Nigrospora sphaerica		Leaf		
Cakile maritima	*Enterobacter hormaechei* *Pseudomonas plecoglossicida*	Bacteria	Root	Pathogen suppression, antagonistic activity, and siderophore production	Christakis *et al.*, 2021
	Staphylococcus saprophyticus *Oceanobacillus picturae* *Bacillus altitudinis*	Bacteria	Leaf	ACC deaminase pathogen inhibition and mobilizes iron	
Ceriops tagal	*Colletotrichum gloeosporioides*	Fungi	Leaf	Antioxidant potency and Phosphorous transporter	Luo *et al.*, 2019
Chenopodium album	*Bacillus siamensis* *Staphylococcus succinus subsp. succinus* *Streptomyces griseoviridis*	Bacteria	Leaf	Carbon source, Sodium transporter, antioxidant and antagonistic activity	Gao *et al.*, 2021
Cressa cretica	*Bacillus cereus*	Bacteria	Leaf	Pathogen inhibition	Arora *et al.*, 2014
Cyperus conglomeratus	*Microbulbifer halophilus* *Bacillus cereus*	Bacteria	Root	IAA production, Phosphate solubilisation, Nodulation and degrade hydrocarbons compounds	Bibi *et al.*, 2017
Eragrostis minor	*Bipolaris prieskaensis*	Fungi	Root	Not Defined	Li *et al.*, 2020
	Preussia sp.2		Stem		
Excoecaria agallacha	*Aspergillus versicolor* *Cladosporium sp*	Fungi	Stem	GA production, antimicrobial and cytotoxic activity	Wang *et al.*, 2018
Glaux maritima	*Actinoplanes* *Marinomonas* *Rhizobium sp.*	Bacteria	Root	N_2 fixation, phosphate solubilization, IAA, siderophore, GA3 production, ACC deaminase activity and anti-fungi activity.	Yamamoto *et al.*, 2020
Halocnemum strobilaceum	*Bacillus licheniformis* *Marinobacter zhanjiangensis* *Bacillus pumilus* *Bacillus safensis*	Bacteria	Root	ABA, IAA, HCN production, phosphate solubilisation, antioxidant and antagonistic activity	Bibi *et al.*, 2017
Haloxylon ammodendron	*Parapedobacter deserti* *Sphingobacterium haloxyli*	Bacteria	Stem	Antioxidant and antagonistic activity	Gao *et al.*, 2021
	Bacillus swezeyi *Streptomyces setonii*		Leaf	Pathogen inhibition	

Origin	Taxonomic identification	Group	Part	Potential function	Reference
Ipomoea pes-caprae	*Alternaria alternate* *Cladosporium tenuissimum* *Fusarium oxysporum*	Fungi	Root, Stem	Siderophore, HCN and ammonia production and antimicrobial activity	Manasa *et al.*, 2020;
Kalidium foliatum	*Microbacterium halophytorum*	Bacteria	Leaf	Siderophore production	Li *et al.*, 2020
	Monosporascus ibericus	Fungi	Root		
	Alternaria eichhorniae		Stem		
Kandelia candel	*Pestalotiopsis humus / foedan*	Fungi	Stem	Pathogen resistance	Li *et al.*, 2020
	Phyllosticta capitalensis		Leaf		
Limonium sinense	*Serratia rubidaea* *Streptomyces pactum* *Glutamicibacter halophytocola* *Isoptericola dokdonensis* *Microbacterium paraoxydans*	Bacteria	Leaf	IAA, HCN and antagonistic activity	Qin *et al.*, 2018
Limonium tetragonum	*Fusarium oxysporum*	Fungi	Root	Gibberellin, IAA production and Pathogen resistance	Khalmuratova *et al.*, 2021
Lycium ruthenicum	*Streptomyces griseoaurantiacus*	Bacteria	Root, Stem	IAA, HCN and antagonistic activity	Liu *et al.*, 2019
	Kocuria rosea		Leaf		
Matthiola tricuspidata	*Micrococcus aloeverae*	Bacteria	Leaf	IAA, siderophore production, phosphate solubilization, and phytopathogen antagonistic activity	Christakis *et al.*, 2021
Phragmites australis	*Alternaria alternate* *Alternaria tenuissima* *Phoma macrostoma* *Peyronellaea glomerata*	Fungi	Root	Gibberellin, IAA production, Pathogen resistance	Salimi *et al.*, 2019; Khalmuratova *et al.*, 2021
	Radulidium subulatum		Stem		
Porteresia coarctata	*Penicillium chrysogenum*	Fungi	Leaf	Phosphatesolublization	Zhu *et al.*, 2018
Prosopis strombulifera	*Bacillus subtilis* *Achromobacter xylosoxidans* *Brevibacterium halotolerans* *Pseudomonas putida*	Bacteria	Root	Phytohormone production, protease and antioxidant activity	Sgroy *et al.*, 2009
Reaumuria songarica	*Sarocladium kiliense* *Aspergillus fumigatiaffinis*	Fungi	Root	Antimicrobial, cytotoxic and Phosphate solublization	Li *et al.*, 2020
Rhizophora apiculata	*Cladosporium cladosporioides* *Acremonium strictum*	Fungi	Leaf	Heavy metal absorption	Rukachaisiriku *et al.*, 2012
Rhizophora mucronata	*Dicyma pulvinata* *Myxotrichum chartarum*	Fungi	Root	Siderophore production	Hamzah *et al.*, 2018;
	Fusarium lateritium *Eurotium chevalier* *Fusarium napiforme*		Leaf		
Rosa rugosa	*Rhizobium halophytocola* *Haloferula luteola* *Martelella endophytica*	Bacteria	Root	Not Defined	Bibi *et al.*, 2017
Salicornia brachiata	*Bacillus cereus*	Bacteria	Leaf	pathogen inhibition	Arora *et al.*, 2014;
Salicornia europaea	*Microbacterium kitamiense* *Saccharospirillum*	Bacteria	Root	EPS, biofilm formation and detoxification	Furtado *et al.*, 2019; Yamamoto *et al.*, 2020

Origin	Taxonomic identification	Group	Part	Potential function	Reference
	Sulfurimonas				
	Kushneria *Curtobacterium flaccumfaciens*		Stem	Antioxidants, peptidoglycan biosynthesis, Seed germination, biocontrol agent	
	Paradendryphiella arenariae *Alternaria alternata* *Alternaria chlamydospora*	Fungi	Leaf	Production of natural cytotoxic /secondary metabolites	
Salicornia ramosissima	*Halomonas taeanensis* *Thalassospira lohafexi* *Providencia rettgeri* *Staphylococcus xylosus* *Brevibacterium casei*	Bacteria	Root	IAA production, phosphate solubilization and Pathogen suppression	Ferreira *et al.*, 2021
Salsola collina	*Streptomyces puniceus* *Bacillus swezeyi*	Bacteria	Stem	Antagonistic activity and Pathogen resistance	Gao *et al.*, 2021
	Alternaria alternate, *Alternaria franseriae*	Fungi	Stem		
Salsola imbricata	*Bacillus halosaccharovorans* *Agromyces indicus*	Bacteria	Leaf	Pathogen inhibition	Bibi *et al.*, 2017
Seriphidium santolinum	*Pezizomycotina sp.*	Fungi	Root	Not Defined	Li *et al.*, 2020
Sonneratia apetala	*Cladosporium cladosporioides* *Fusarium equiseti*	Fungi	Root	Phosphorous Solubilisation and Heavy metal absorption	Nurunnabi *et al.*, 2020
	Aspergillus niger		Leaf	Antioxidant, antimicrobial cytotoxic and Heavy metal degradation	
Spharanthus indicus	*Bacillus cereus*	Bacteria	Leaf	pathogen inhibition	Arora *et al.*, 2014
Suaeda acuminata	*Pseudomonas cedrina* *Pseudomonas psychrophila* *Stenotrophomonas maltophilia* *Staphylococcus warneri*	Bacteria	Root	Phytohormone production, Phosphatase enzyme activity, basal respiration, carbon availability and Pathogen suppression	Alishahi *et al.*, 2020; Li *et al.*, 2020
Suaeda australis	*Alternaria alternata* *Cladosporium sp.*	Fungi	Root	Gibberellin, IAA production and Pathogen resistance	Khalmuratova *et al.*, 2021
Suaeda fruticosa	*Bacillus megaterium* *Paenibacillus amylolyticus* *Pseudomonas putida* *Sanguibacter keddieii* *Lelliottia amnigena*	Bacteria	Root	EPS, biofilm formation, aquaporins, antioxidant activity and Heavy metal absorbtion	Alishahi *et al.*, 2020
Suaeda maritima	*Microbacterium oxydans* *Pseudomonas putida* *Arthrobacter luteolus* *Microbacterium saperdae* *Hoeflea suaedae* *Labrenzia suaedae* *Zhihengliuella flava*	Bacteria	Root	Phytohormone production ACC deaminase activity, Pathogen suppression, reduce ABA & salicylic acid	Indira & Srinivasan, 2017; Alishahi *et al.*, 2020; Khalmuratova *et al.*, 2021
	Alternaria alternata *Cladosporium sp.*	Fungi	Root	Gibberellin, IAA production, and Pathogen resistance	
Suaeda monica	*Alternaria alternata* *Aspergillus terreus*	Fungi	Leaf	Antimicrobial cytotoxic activity	Indira & Srinivasan, 2017
Suaeda nudiflora	*Bacillus cereus*	Bacteria	Leaf	pathogen inhibition	Arora *et al.*, 2014
Suaeda salsa	*Bacillus zhangzhouensis* *Bacillus suaedae*	Bacteria	Root	Increased plant biomass; gibberellic acid production,	

Origin	Taxonomic identification	Group	Part	Potential function	Reference
	Achromobacter piechaudii *Advenella kashmirensis* *Pseudomonas stutzeri* *Pseudomonas oryzihabitans* *Pseudomonas putida* *Pantoea agglomerans* *Paenalkalicoccus suaedae*			phosphate solubilization, ACC deaminase activity, aquaporins, colonization Stress response, chemotaxis, metabolism, and global regulation	Alishahi *et al.*, 2020; Xu *et al.*, 2022
	Alternaria alternata *Alternaria franseriae* *Alternaria eichhorniae*	Fungi	Stem		
Tetragonia tetragonioides	*Stenotrophomonas maltophilia*	Bacteria	Root	Phytohormone production GA production /regulation, Phosphatase enzyme activity, basal respiration, and carbon availability	Egamberdieva *et al.*, 2022
	Pseudomonas moraviensis *Bacillus amyloliquefaciens* *Curtobacterium plantarum*		Leaf	Seed germination, decreasing ethylene levels, pathogen resistance and Systemic colonization transporter	
Zygophyllum simplex	*Agromyces sp*	Bacteria	Root	Phosphate solublization, IAA and Siderophore production	Eida *et al.*, 2018
	Alternaria alternate *Penicillium chrysogenum*	Fungi			

Endophytic bacteria and fungi play pivotal roles in enhancing plant tolerance to stress by modulating ethylene levels, synthesized in response to various biotic and abiotic stressors (Janowsky *et al.*, 2019). Proteobacteria emerge as prominent endophytic bacteria in halophytic plants such as *Aster tripolium and Suaeda maritima*, while genera like *Pseudomonas* and *Bacillus* demonstrate plant growth promotion and biocontrol capabilities in various coastal species (Manasa *et al.*, 2020; Li *et al.*, 2020; Khalmuratova *et al.*, 2021). Furthermore, understanding the functional significance of endophytic fungi, particularly their role in nutrient uptake, stress tolerance, and production of bioactive compounds, is crucial for enhancing plant productivity and ecosystem resilience (Table 2). Recent research underscores the prevalence of Ascomycota fungi, particularly Pleosporaceae, in halophytes, with genera like *Aspergillus* and *Fusarium* contributing to stress alleviation, while *Bipolaris prieskaensis* and *Sarocladium kiliense* demonstrate host-specific associations and production of valuable bioactive metabolites (Apurva Sawant and Rodrigues, 2020; Li *et al.*, 2020; Egamberdieva *et al.*, 2022). These findings emphasize the multifaceted contributions of endophytic microbial communities to plant health, stress mitigation, and ecosystem function, underscoring their potential for sustainable restoration practices.

Core-Microbiome Mangroves: Exploring Co-Cultivation Strategies for Enhanced Metabolic Pathways

In coastal ecosystems, microbial communities engage in mutualistic relationships characterized by intricate metabolic interactions (Fig. 2). Bacteria utilize fungal exudates, while fungi influence bacterial activities, particularly through penetration into leaf tissues, facilitating the degradation of specific polymers into plant-assailable molecules. These metabolic pathways, pivotal for plant health and ecosystem functioning, are now the focal points of contemporary research efforts. The metabolic activities orchestrated by these microbial communities serve as functional indicators reflecting the unique characteristics of mangrove sediments. Dominant microbial players such as *Syntrophobacter, Sulfurovum, Nitrospira, and Anaerolinea* serve as linchpins in the intricate biogeochemical transformations of carbon, nitrogen, and sulfur within mangrove ecosystems (Eida *et al.*, 2018; *et al.*, 2018). Despite advancements in understanding these metabolic pathways, challenges persist, particularly in activating silent gene clusters that encode for specific metabolites. Co-cultivation strategies involving bacterial-fungal consortia and mutagenesis have shown promise in unlocking the biosynthetic potential of microbial strains, albeit with limited success. Addressing these challenges is critical for realizing the full potential of microbial communities in these contexts. Recent hypotheses have proposed parallel genetic origins for metabolites in both endophytes and plants, suggesting the existence of shared biosynthetic pathways. Endophytes, mirroring their host plants, independently biosynthesize secondary metabolites, offering a platform for genetic manipulation (Ranganathan and Mahalingam, 2019). Horizontal gene transfer, an evolutionary mechanism, further enhances the adaptive capabilities of endophytic microbes, presenting opportunities for novel trait acquisition. Harnessing these mechanisms holds immense potential for enhancing productivity and sustainability through innovative microbial interventions.

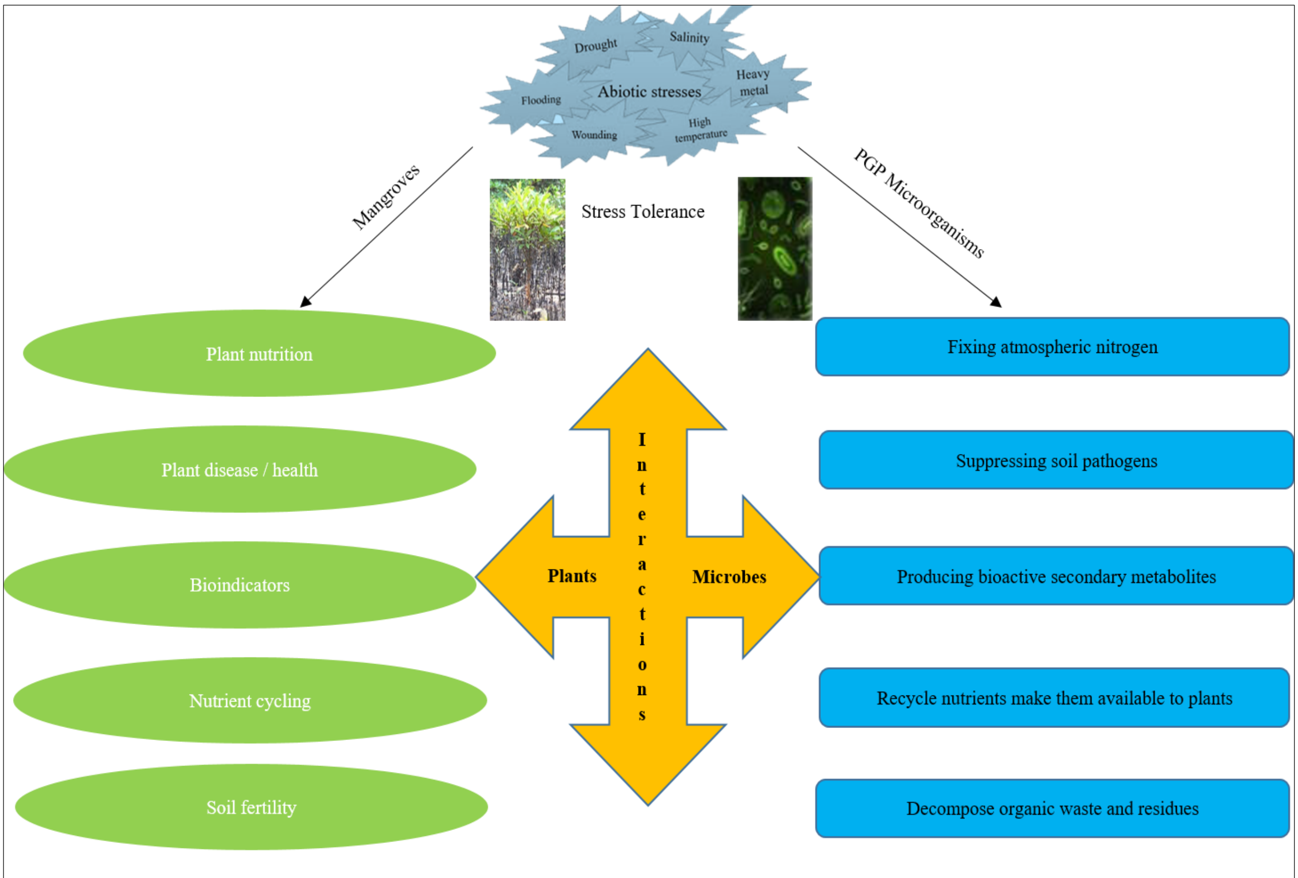

Figure 2 : comprehensive overview of the symbioses between mangrove plants and their associated microbial communities in coastal ecosystems.

Utilizing halotolerant beneficial microbes as inoculants represents a promising avenue for sustainable restoration practices. The diverse genera identified within mangroves associated halophytic endophytes, such as *Bacillus*, *Enterobacter*, and *Trichoderma*, underscore their potential for stress tolerance and growth promotion (Christakis *et al.*, 2021). The development of synthetic bio-inoculants, possessing attributes like non-pathogenicity, colonization ability, and culturability, offers avenues for tailored solutions. However, ensuring the efficacy of these inoculants over diverse environmental conditions necessitates long-term field trials and rigorous assessment under relevant geographical production scenarios. Hence, It's infer that the dynamic interactions between bacterial and fungal communities in coastal plants highlight their co-dependence engaging research into co-cultivation strategies, metabolic pathways, and microbial interactions will pave the way for harnessing the full potential of beneficial microbes, fostering sustainable practices for enhancing resilience, restoration and rehabilitation efforts.

CONCLUSION

The prevalence of microbial taxa within host species suggests a potential pivotal role for the core microbiome in upholding host biological functions, paralleled by the hypothesized significance of ubiquitous microbes in natural ecosystems' overall ecological dynamics. This prompts the hypothesis of a 'core mangrove microbiome' shared across species, yet despite this shared microbial foundation across regions and species, distinctions in microbial community composition persist, influenced by factors such as species, geography, and mangrove system structure. While research on mangrove bacterial communities is extensive, studies on fungi, archaea are relatively scarce, a gap further complicated by the intricate nature of mangrove ecosystems. With escalating interest in mangrove restoration, comprehending the microbial associations within these environments emerges as an increasingly critical aspect of conservation efforts, particularly with advancing insights into the integral roles microbes play in supporting and perpetuating host well-being. This study lays groundwork for forthcoming investigations into diversity and host ecology, potentially leading to discoveries crucial for bioremediation, herbivore resistance and ecological development. This descriptive work provides a foundation for future studies to understand the functional roles of plant-microbial interactions and community patterns.

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