Pallaval Veera Bramhachari *Editor*

Understanding the Microbiome Interactions in Agriculture and the Environment

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Understanding the Microbiome Interactions in Agriculture and the Environment

Editor
Pallaval Veera Bramhachari
Department of Biotechnology
Krishna University
Machilipatnam, Andhra Pradesh, India

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Editor and Contributors

About the Editor

Pallaval Veera Bramhachari is currently a Head and Senior Faculty member of the Department of Biotechnology at Krishna University, Machilipatnam, India. He has earlier served as a Postdoctoral research scientist at the Bacterial Pathogenesis Laboratory, Queensland Institute of Medical Research (QIMR-Berghofoer Research Center), Brisbane, Australia, and a DBT Postdoctoral fellow at the Department of Microbiology and Cell Biology, Indian Institute of Science (IISc), Bangalore. He completed his Ph.D. in Microbiology from Goa University, India. His major research interests are the investigation of the applied research in microbiology and cell biology including the biochemical mechanism of bacterial-biofilm formations, extracellular microbial polysaccharides, and the structure-function relationship of bacterial biosurfactants (glycolipids and rhamnolipids), pathogenic and virulence characteristics of bacteria, basic and translational cancer research. He has published more than 140 research articles in Scopus-indexed journals, authored and coauthored 7 international books and invited book chapters in prestigious peer-reviewed international edited volumes and presented 50 abstracts at various national and international conferences. He has served on the editorial board and as reviewer for several national and international journals. He is a member of numerous international scientific societies and organizations, most importantly, the Indian Science Congress and Society of Biological Chemists, India. He completed two major research projects from SERB, DST NRDMS, Govt of India.

He was awarded a Travel Scholarship from QIMR-2007, Australia, for attending the 4th Indo-Australian Biotechnology Conference in Brisbane, Australia, and was awarded with a young scientist travel fellowship (2007) from the DST, Govt. of India, for attending XVII Lancefield International Symposium at Porto Heli, Greece-2008. He was conferred with various prestigious awards, notably Science Education Research Board (SERB), Government of India-Young Scientist award (2011) with a research project and was nominated as Associate Fellow of Andhra Pradesh Academy of Sciences (APAS)-2016, MASTER TRAINER: Andhra Pradesh English Communications Skills Project. British Council & APSCHE 2017, Andhra Pradesh State Best Scientist award-2017, and Dr. V. Ramalingaswamy Memorial award for Biomedical Sciences-2019. He also obtained two Indian patents in 2017. He has more than 13 years of teaching and research experience at the university level.

Contributors

Chandra Sekhar Akila Molecular Genetics and Functional Genomics Laboratory, Department of Biotechnology, Yogi Vemana University, Kadapa, Andhra Pradesh, India

Anusha Department of Biotechnology, Krishna University, Machilipatnam, Andhra Pradesh, India

Yaser A. Arafath Department of Microbiology, School of Life Sciences, Pondicherry University, Puducherry, India

Emmanuel Atiatorme Department of Science and Environment, University of Education, Winneba, Ghana

Chanda V. Berde Department of Marine Microbiology, School of School of Earth, Ocean and Atmospheric Sciences (SEOAS), Goa University, Taleigao Plateau, Goa, India

Vikrant B. Berde Department of Zoology, Arts, Commerce and Science College, Lanja, Maharashtra, India

Siva Bolupalli Plant Molecular Biology Laboratory, Department of Botany, Yogi Vemana University, Kadapa, Andhra Pradesh, India

Mangrove Microbiomes: Biodiversity, Ecological Significance, and Potential Role in the Amelioration of Metal Stress

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Chanda V. Berde, Asha Giriyan, Vikrant B. Berde,
and Pallaval Veera Bramhachari

Abstract

The mangrove ecosystem through a rich productive ecosystem with a great diversity of flora and fauna both macro and micro is under the threat of severe pollution stress due to anthropogenic interference. Continuous input of pollutants is a major threat to this ecosystem affecting the indigenous microbial community playing a major role in the biogeochemical reactions and contributing to the richness of the biome. Being exposed to inputs from riverine sources which in turn receive huge amounts of pollutants in the form of industrial effluent discharge, agricultural runoff, domestic waste, sewage, etc., the major components in these discharges are pesticides, excessive inorganic compounds, high organic content, and metals. These pollutants especially the heavy metals tend to sink, have low solubility in water, and accumulate in the mangrove sediments, which act as the sinks for the heavy metals. Sediment contamination thus ultimately diminishes the mangrove ecosystem. Exposure to the pollutants especially heavy

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Chanda V. Berde, Asha Giriyan, Vikrant B. Berde and Pallaval Veera Bramhachari contributed equally with all other contributors.

C. V. Berde (✉)
Marine Microbiology, School of Earth, Ocean and Atmospheric Sciences (SEOAS), Goa University, Taleigao Plateau, Goa, India
e-mail: chanda.berde@unigoa.ac.in

A. Giriyan
Coastal Ecology and Marine Resource Center, The Energy and Resource Institute (TERI), Tiswadi, Goa, India

V. B. Berde
Department of Zoology, Arts, Commerce and Science College, Lanja, Maharashtra, India

P. V. Bramhachari
Department of Biotechnology, Krishna University, Machilipatnam, Andhra Pradesh, India

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metals results in changes in the microbial communities with the prevalence of metal-tolerant species. This chapter uncovers the ecological aspects of mangrove sediments focusing on the metal-tolerant microbiome and its role in the maintenance of the biome.

Keywords

Microbiome · Metal tolerance · Mangroves · Sediments · Pollution · Ecosystem balance

4.1 Introduction

Mangroves are wetland ecosystems with fine-grained sediment. The mangrove ecosystems function as habitats and breeding sites for a variety of fishes; mangroves are a source of timber and other plant products; they serve as carbon sinks and play role in atmospheric green gas removal by sequestering the organic contents in the water and sediments. This buried detritus in the anoxic sediments make up the coastal blue carbon (Twilley et al. 1992; Chmura et al. 2003; MacFarlane and Burchett 2002; Walters et al. 2008; Nellemann et al. 2009). The mangrove ecosystem has been identified as one of the most productive ecosystems having a very high net productivity as compared to other ecosystems (Donato et al. 2011).

During the last two decades, about 35% of mangroves globally have been known to be polluted with heavy metals (Feller et al. 2010; Gopalakrishnan et al. 2020). Accumulation of trace metals in the sediments occurs because of their lower water solubility and thus gets easily absorbed and retained in sediments, making the sediments an ultimate sink (Yu et al. 2008; Alvarez et al. 2011). The presence of heavy metals affects the microbial population, and the toxic effects are ultimately seen to reflect in the increased greenhouse emissions and carbon cycling (Nath et al. 2013; Usman et al. 2013). Though mangrove ecosystems are rich in organic matter, they are however deficient in nutrients like nitrogen and phosphorous (Vazquez et al. 2000). Despite this, they are regarded as a highly productive ecosystem because the microbiome present in the sediments is very active and productive that is responsible for nutrient cycling in the ecosystem through various geochemical processes.

The microorganisms, namely bacteria, archaea, fungi, viruses, and protists, make up the mangrove microbiome. To study the role of the microorganisms in the biogeochemical changes taking play in the mangrove sediments and correlate these with the environmental processes, hypothesis-driven studies are the need of the day. Which will help to understand the mangrove interactions at various levels and the contributions of microflora thus coming out with approaches for the protection and rehabilitation of mangrove forests? This thus calls for an urgent need to study the microbiomes of the mangrove sediments, including fungi, archaea, viruses, and protists, apart from bacteria, and understand their contribution to the ecosystem and overall environment functioning. Even though the mangrove ecosystem is greatly beneficial to man and the environment, its importance is neglected and it suffers from anthropogenic pressures.

4.2 Ecological Assessment of Sediments of Mangrove Ecosystems

Most mangrove ecosystems have human settlements in close proximities which are a source of contamination, especially the industrial discharge into the mangroves (Alongi 2002; Kong et al. 2015; Ren et al. 2015). Mangrove ecosystems are highly influenced by these humanoid activities leading to accumulation of the pollutants especially heavy metals and recalcitrant compounds (Bodin et al. 2013). Another factor leading to the contaminants reaching the sediments is the weaker winds along the coast and hence slower water movements which cause the pollutants to sink in (Cai et al. 2009). Contamination of the sediments thus deteriorates the quality of the aquatic system. Sediment Quality Guidelines are used to determine the contamination levels in sediments for monitoring and quality management (US EPA (United States Environmental Protection Agency) n.d.; Bakan and Özkoc 2007).

4.2.1 Heavy Metal Pollution

Numerous studies have been carried out worldwide on the degradation and pollution of mangroves with trace metals, especially heavy metals (Defew et al. 2005; Fernandes et al. 2012a; Bodin et al. 2013; Usman et al. 2013; Fernández-Cadena et al. 2014; Li et al. 2016). Heavy metals in low concentrations are required for growth and are toxic at higher concentrations. The metabolism of the organisms is affected leading to changes in growth patterns as well as reproduction and ultimately causing an imbalance in the food chains (Wright and Welbourn 2002). The organisms growing in heavy metal contaminated systems accumulate the metals in their body, and humans are the final link in the food chain (Stewart 1999; Mwevura et al. 2002; Wang et al. 2015; Yin et al. 2016).

Marine sediment composition and structure impact the accumulation of heavy metals in the sediments. The presence of clays, mud, and sands leads to the formation of complexes and these interactions make the heavy metals sink in the sediments (Nobi et al. 2010; Gao and Chen 2012). In a study carried out along the Saudi Arabian sea, the presence of heavy metals was assessed and showed a high concentration of Cr followed by Cu and Ni while other metals like Pb, Cd were at a lower concentration but enough to cause damaging effects on the biota of the sediments as well as waters of the mangrove econiches (Bouillon et al. 2003). Another study on the Saudi coast of the Arabian Gulf also gave similar results when the heavy metal concentration was analyzed, with chromium being the dominant metal in the surface sediments. The authors point out that dredging, landfilling, oil pollution, reclamation, sewage disposal, etc. are the sources of the pollution

(Youssef et al. 2015; Almasoud et al. 2015; El-Sorogy et al. 2016; Almahasheer 2018). Reports by Al-Kahtany et al. (2018) and Almahasheer (2019) assessed the heavy metal concentrations in Tarut island mangroves. Similar studies carried out in the Zhangjiangkou Mangrove National Nature Reserve of China assessed sediments for the presence of heavy metal concentrations of Cu, Cd, Pb, Cr, Zn, As, and Hg along with studies of its effects on the biotic components for studying ecological risk assessment and environmental management (Wang et al. 2016).

4.2.2 Assessment of Other Parameters

The mangrove sediment is rich in organic matter content which is majorly contributed by the plant litter from the canopy above (Alongi 2002; Asaeda and Kalibbala 2009; Wang and Sousa 2009). According to reports, the highest organic carbon accumulation occurs in the mangrove forests, i.e., up to 26 Tg/year (Breithaupt et al. 2012).

The organic content of mangrove sediment was found to vary from organic matter in surface layers which receive fresh plant litter. The elemental ratio of C:N was observed to be 20–30 as against the ratio of 10 required for the growth of microorganisms (Kristensen et al. 1995; Twilley et al. 1997; Wafar et al. 1997). Thus, a rapid initial drop in carbon and increase in nitrogen is required for the degradation of litter in the initial stages. Thus, it is observed that mangrove soils are deficient in dissolved inorganic nitrogen or DIN acting as its sinks from the surroundings (Alongi 1996; Rivera-Monroy and Twilley 1996). However, mangrove sediments remain nutrient-deficient, particularly in nitrogen and phosphorus (Holguin 1992; Vazquez et al. 2000; Skov and Hartnoll 2002).

The microbiota present in the sediment degrades and utilizes the organic matter present which contains mostly tannins, polyphenols, cellulose, lignin, and lignocellulose (Lee 1998). Numerous analyses carried out in India show high organic contents of up to 37% dry weight and C: N ratios reaching 27.3 (Bouillon et al. 2003). The organic carbon stocks, which are of mangrove origin, are thus very high. This organic matter found deposited in the sediments of the mangroves is indeed a source of carbon and nitrogen to the microbiota. An increase in seawater levels has resulted in the saltwater intrusion of estuarine regions. Changes in the ionic composition are also observed due to the inflow of land wash-offs adding loads of nitrates, from agricultural sources. These nitrates may be lost to the atmosphere upon conversion to nitrous oxide (Maier et al. 2000).

4.3 Mangrove Sediment Microbiome and Its Ecological Role

The 91% biomass of the mangrove microbiome consists of bacteria and fungi, while the remaining 9% comprises algae and protozoa. Most of the bacteria and fungi are attached to particles in sediment and process the energy flow and nutrients in the ecosystem. The microbiome of the mangrove ecosystem is responsible for carrying out all facets of biogeochemical cycling, including the transformation and degradation of pollutants. However, heavy metals being toxic even at very low concentrations, the microbiome gets affected and dominance of resistant microbiota is observed. The heavy metal sensitivity is more pronounced in the microbiome as compared to macro flora and fauna in the same environment (Zhou et al. 2013). Sediment microbiome studies carried out by Zhang et al. (2019) indicated the prevalence of prokaryotic alpha diversity in mangrove sediments. This biome harbors other prokaryotic groups also mostly belonging *Gammaproteobacteria*, *Deltaproteobacteria*, *Chloroflexi*, and *Euryarchaeota*.

In intertidal zones, the sediment microbiome is responsible for detritus decomposition and nutrient cycling (Campbell 2008). The microbiome is composed of nonrandom networks of bacteria, archaea, and fungi connected by positive, negative, and neutral relationships (Sul et al. 2013). While the active role of bacteria driving carbon fluxes is defined in mangrove sediment (Holguin et al. 2001), the role of fungi, in particular, is poorly understood, and the interactions of the different components are undescribed with many potential relationships in mangrove sediment. For example, fungi can promote habitat sharing with bacteria and vice versa (De Boer et al. 2005), and the relationship between methanogenic archaeal species and sulfate-reducing bacteria is well known in methane-rich sediments (Plugge et al. 2011).

Based on the functionality of the microorganisms present in the mangrove sediment, the microbiome composition is as below.

4.3.1 Nitrogen Fixers

In mangrove soils, diazotrophs play a major role as nitrogen fixers. The concentration of soluble nitrogen is seen to influence the scale at which the diazotrophic bacteria will carry out nitrogen fixation in the mangrove ecosystem. Due to the presence of higher soluble nitrogen concentrations as well as a lack of adequate carbon sources, nitrogen fixation rates were low (van der Valk and Attiwill 1984; Mann and Steinke 1989). Bacterial strains identified as the following genera *Azospirillum*, *Azotobacter*, *Rhizobium*, *Clostridium*, and *Klebsiella* have been characterized and shown to carry out nitrogen fixation in the mangrove ecosystems. These microorganisms along with nitrogen fixation carry out nitrogen reduction forming ammonia and thus it contributes to the overall balancing of nitrogen content in the mangrove ecosystems (Fernandes et al. 2012b).

4.3.2 Phosphate Solubilizers

Phosphate-solubilizing bacteria have the potential to convert insoluble phosphates to organic available forms. They play a vital role as suppliers of phosphorus to the mangrove plants. Conversion of inorganic phosphates to organic phosphates is favored in the mangrove sediments as the conditions are anoxic. In sediments close to the plant roots, the conditions are oxic and allow bacteria to grow and bring about phosphate solubilization. Some of the phosphate-solubilizing bacteria isolated from mangrove sediments were identified as *Bacillus atrophaeus*, *B. amyloliquefaciens*, *B. licheniformis*, *Chryseomonas luteola*, *Enterobacter aerogenes*, *E. asburiae*, *E. taylorae, Kluyvera cryocrescens*, *Paenibacillus macerans*, *Pseudomonas stutzeri, Vibrio proteolyticus,* and *Xanthobacter agilis* (Vazquez et al. 2000). Bacteria identified as genus *Chryseomonas, Kluyvera,* and *Xanthobacter*, with phosphate-solubilizing potential have been reported by Vazquez et al. (2000), from the mangrove sediments of Mexico.

4.3.3 Sulfate Reducers

The mangrove sediments harbor sulfate-reducing bacteria that carry out the degradation of organic matter under anaerobic environments prevailing in the sediments (Nedwell et al. 1994; Sherman et al. 1998). Sulfate reduction by these anaerobic bacteria accounts for the availability of soluble iron and phosphorus as well as for the emission of carbon dioxide from the sediments (Kristensen et al. 1991). Thus, the mineralization of sulfur, the production of soluble iron in the form of FeS_2 and soluble phosphorus, is making these minerals available to the microbiome for its growth and metabolism. Apart from these roles, sulfate-reducing bacteria are also found to play a role as nitrogen fixers as seen in plant-associated as well as plant-unassociated sediments in mangroves of Florida (Zuberer and Silver 1978). Bacterial groups were more abundant in these mangrove sediments in the rhizospheres of *R. mangle* and *A. germinans* mangroves (Zuberer and Silver 1978).

In the studies carried out in Goa (India), spore-forming sulfate-reducing bacteria were found associated with mangroves (Saxena et al. 1988). Eight species of sulfate-reducing bacteria belonging to four different genera were identified from mangroves of Goa, namely *Desulfovibrio desulfuricans, Desulfovibrio desulfuricans aestuarii, Desulfovibrio salexigens, Desulfovibrio sapovorans, Desulfotomaculum orientis, Desulfotomaculum acetoxidans, Desulfosarcina variabilis,* and *Desulfococcus multivorans* (Loka Bharathi et al. 1991).

4.3.4 Methanogens

Studies on the Indian mangrove sediments showed a large variation in the methanogenic populations which were due to abiotic factors of the water and sediments (Mohanraju and Natarajan 1992) as well as biotic factors mainly the presence of sulfate-reducing bacteria (Ramamurthy et al. 1990). Methanogenic bacterial strains produce methane in the anoxic conditions of the sediment such as the methanogenic bacterium, *Methanoccoides methylutens* (Marty 1985; Mohanraju et al. 1997). This methane diffuses to the aerobic sediment layers and gets oxidized by aerobic methanotrophs. There are reports of anoxic oxidation of methane in hypersaline microbial mats (Conrad et al. 1995). Metagenomic studies showed the presence of CH4-oxidizing genes from uncultured methanotrophs *Methylosarcina, Methylomonas,* and *Methylobacter* in mangrove soils (Lüke and Frenzel 2011). Mangrove ecosystems receiving high organic inputs due to anthropogenic activities show higher methane emissions indicative of higher methanogenic activities in the mangrove sediments (Giani et al. 1996; Strangmann et al. 1999). The presence of type I or type II methanotrophs in the mangrove sediments depends on the NaCl concentration and the alkalinity of the sediments (Bowman 2015a; Shiau et al. 2018; Ho et al. 2018). The type I methanotrophs *Methylomonas* and *Methylobacter* are mostly influenced by the pH of the saline ecosystems (Bowman 2015a, b; Shiau et al. 2017) and are responsible for the reduced methane emissions from these ecosystems.

4.3.5 Photosynthetic Anoxygenic Bacteria

Some research workers on mangrove sediments in India have reported purple sulfur and purple nonsulfur bacteria (families Chromatiaceae and Rhodospirillaceae) (Vethanayagam and Krishnamurthy 1995; Vethanayagam 1991). Dhevendaran (1984) and Chandrika et al. (1990) have reported the predominance of bacteria belonging to genera *Beggiatoa, Chloronema, Chromatium, Leucothiobacteria*, and *Thiopedia,* including some brown *Chlorobiaceae* species during studies carried out in mangrove regions of Cochin. A large proportion of the anaerobic microbiota was found to consist of phototrophic sulfur bacteria. While studies in Florida reported *Chromatium* species to be most abundant in the sediment samples (Zuberer and Silver 1978).

4.3.6 Viruses

This group of mangrove sediment microbiome is not studied much and remains highly uncharacterized. Most of the information available on mangrove soil viruses based on phylogenetic analyses does show the presence of diverse groups of viruses. These viral groups are postulated to bring about complex polysaccharide recycling and thus participate in global carbon cycling. Thus activities of the viral community in the sediment affect biogeochemical cycles through the organic carbon discharge as well as the release of nutrients from hosts. The viral auxiliary metabolic genes (AMGs) are responsible for driving biogeochemical cycles in the sediments microorganisms (Zhang et al. 2014; Anantharaman et al. 2014; Roux et al. 2016; York 2017). The prime role of the viruses in controlling the bacterial populations also affects the microbiome composition.

4.4 Characterizing Metal-Tolerant Microbiomes in Mangrove Ecosystem

The impact of climate change on the mangrove microbiome is a challenge. During the last two decades, around 35% of the world's mangrove ecosystem has been reportedly polluted with heavy metals (Feller et al. 2010; Gopalakrishnan et al. 2020). Mangrove ecosystems are vulnerable to various anthropogenic stresses that contain high levels of heavy metals (Zhang et al. 2014). Continuous exposure to heavy metals has drastic effects on mangrove ecosystems as the carbon cycling is disturbed. This is because of the toxicity of the inflowing heavy metals to the mangrove microbiota (Usman et al. 2013; Nath et al. 2013). Though mangrove ecosystems are organic matter rich, nitrogen and phosphorous deficiency are however relevant (Vazquez et al. 2000). Despite this, they are regarded as highly productive ecosystems because the microbiome present in the sediments is very active and productive that is responsible for nutrient cycling in the ecosystem through various geochemical processes. Most of the sediment bacteria and fungi process the energy flow and nutrients in the ecosystem. Though microorganisms drive vital biogeochemical processes, in the mangrove ecosystem, they are more sensitive to heavy metals than the higher level of organisms in the same environment (Zhou et al. 2013).

Natural benthic communities of the mangrove ecosystem are stable as long as there are external anthropogenic disturbances such as sewage disposal, oil spills, and exposure to high heavy metals loads from discharges from mining rejects and industrial wastes. Any disruption in sediments causes a shift of the microbial community leading to disturbed nutrient cycles with reduced nutrient availability and leaching of toxic microbial by-products, thereby affecting the ecosystem health.

An environment that is enriched with heavy metals places a great selective pressure on the microflora exposed, leading to the development of a specific microbiome that is resistant to different heavy metals. To defend or protect them from metal toxicity, the development of adaption and resistance is observed in microbes by sophisticated mechanisms. Heavy metal resistant microbiome comprises of metal resistome, the resistant microbiota. Metals are also of importance for respiration as well as other biological functions involved in carbon and nitrogen cycling (Andreote et al. 2012; Ragavan et al. 2016; Kandasamy 2000).

At present, most of the research work carried out on mangrove microbial communities and their characterization were focused on a temporal and spatial range that is important for the foundational understanding of the microbiome in this ecosystem. However, there is also a need to have more advanced technological research that would help to establish a link between mangrove microbe and the health of its ecosystems. The complexity of microbial communities and the technical constraints to identify and measure diversity has hampered our understanding of the functioning and microbial diversity. Since most of the microbes are unculturable, their abundance and diversity studies are not assessable by a conventional culture-based method. With the recent advances in next-generation sequencing (NGS) technology, few studies are being reported to understand the diversity and functional genomics of microbiomes. A broad picture of the microbial life in the mangrove ecosystem is still not satisfactorily presented. Comparative microbiome studies of the distinct mangroves using metagenomics will considerably help to a better understanding of the mangrove microbial community structure and its dynamics.

Using NGS, studies have revealed the effect of heavy metal contamination on the microbiome in some ecosystems (Feller et al. 2010; Andreote et al. 2012), However, the knowledge regarding microbiome changes with the influence of heavy metal presence is very specific, and little is known about the core resistant microbiome and its role in the contaminated ecosystem. The taxonomical studies on mangrove soil sediments from Sundarban revealed the dominance of *Acidobacteria, Actinobacteria, Bacteroidetes, Cyanobacteria, Firmicutes, Fusobacteria, Nitrospirae,* and *Planctomycetes* based on NGS metagenomic analysis (Das et al. 2018). While in Mai Po Ramsar Wetland in Hong Kong, SAR and China studies revealed *Actinobacteria, Acidobacteria, Nitrospirae*, and *Verrucomicrobia* in inner mangrove sediments, whereas Proteobacteria and Deferribacteria were detected in outer mangrove sediments (Gopalakrishnan et al. 2020). In comparing the mangrove sediment microbiomes of India and Brazil, the richness of bacteria was observed, while the Red Sea mangrove samples showed an abundance of archaea (Usman et al. 2013; Alzubaidy et al. 2016). These differences in microbial diversity could be attributed to mangrove species, geographical location, physicochemical parameters influencing the mangrove sediments, and anthropogenic activities which influence the community compositions.

Feng et al. (2017) reported *Acidobacteria, Actinobacteria, Bacteroidetes, Chloroflexi, Desulfobacterota, Gemmatimonadetes, Myxococcota, Nitrospirae,* and *Proteobacteria* were the dominant phyla found persistently in environments polluted with heavy metals. Firmicute and Proteobacteria were ubiquitously present bacterial groups in these environments. Proteobacteria contains taxa having extensive metabolic properties, thus enabling it to colonize a range of habitats, and thus have been reported to be a predominant heavy metal-resistant phylum in many polluted environments (Zhao et al. 2019; Li et al. 2020). As they have strong adaption and tolerance, this is also confirmed by culturing methods (Gopalakrishnan et al. 2020). A literature survey carried out by Hao et al. (2021) on heavy metal-resistant bacteria from different ecosystems revealed that more than 66% of isolates are Proteobacteria, dominated by Gammaproteobacteria (52.84%) followed by *Acidobacteria*. Metagenomic studies revealed archaea to be the second most frequently found phyla in metal-contaminated mangrove ecosystems. Other major phyla found in heavy metal polluted sites are *Chloroflexi* and *Nitrospirae*, mostly involved in nitrogen cycling (Ganguli et al. 2017; Liu et al. 2018). Figure 4.1 shows the distribution of various microbial phyla in the mangrove rhizosphere.

In general, laboratory-based experiments reveal that short-term or long-term exposure to heavy metals reduces the diversity of microorganisms. The presence of a low concentration of essential metals such as copper and zinc is required for the growth of a wide range of bacteria, which eventually results in increased microbial diversity. The constant diversity indicates the strong resilience and the capacity of

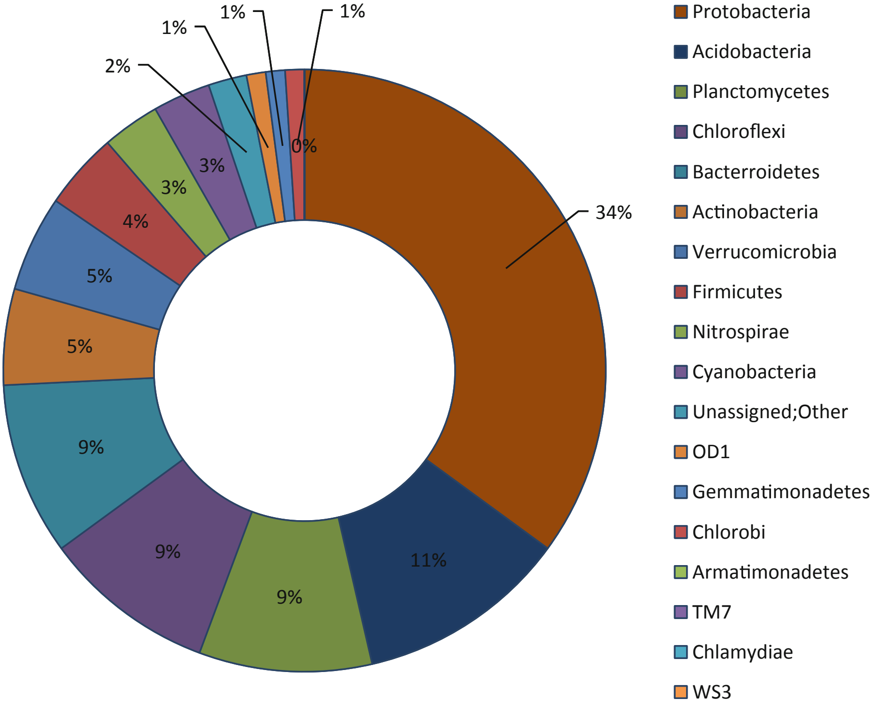

Fig. 4.1 Distribution of various microbial phylum in the mangrove rhizosphere

the microbial community to acquire resistance through horizontal gene transfer, without influencing microbial diversity (Lopez et al. 2017; Song et al. 2018).

4.5 Comparison of Microbiomes Across Diverse and Distinct Mangrove Ecosystems

Mangrove wetlands are influenced by both marine and terrestrial environments which cause gradients in salinity and organic matter in the sediments and fluctuating environmental conditions determine the microbiome in ecosystems differing significantly from others. Also, microbial diversity is influenced by mangrove species. Alzubaidy et al. (2016) reported Bacteroidetes dominance in the rhizosphere of *Avicennia* and in sediments without vegetation, *Actinobacteria* was predominant.

The heavy metal gradients can influence the microbial diversity by decreasing, increasing, or remaining constant. Mostly a decrease in the diversity is observed in studies following a severe heavy metal contamination exposure. Strong selection of microbiome occurs due to heavy metals purging sensitive taxa, leading to the enrichment of the resistant taxa but subsequently resulting in a decrease in diversity. Exposure to a low concentration of essential metals will result in a proliferation of a wide range of bacterial groups and thus an increase in the microbial diversity of that habitat.

Several studies on the phylogenetic diversity in mangroves are located across regions such as Brazil, China, and the Red Sea mangroves of Saudi Arabia (Alzubaidy et al. 2016). Ghosh et al. (2010) reported a predominance of Proteobacteria in the mangrove areas of Sundarbans. However, in some other regions of tropical mangrove swamps, metagenomic results revealed, Deltaproteobacteria (43.88%) as the major class, followed by Alphaproteobacteria and Gammaproteobacteria dominance of *Desulfococus* spp., which is attributed to their involvement in the sulfur cycle.

Reports show that methane fluxes are largely contributed by activities of methanogens and methanotrophic communities especially in the wetlands (Cai et al. 2016; Das et al. 2018; Sierocinski et al. 2018; Yu et al. 2020). Methane production is carried out by methanogens which are placed in Euryarchaeota phylum in the archaea domain, and methane oxidation is carried out by methanotrophic communities (Deng et al. 2016), including two main groups of Gammaproteobacteria, e.g., *Methylococcaceae* and Alphaproteobacteria, e.g., *Methylocystaceae* (Yu et al. 2020). Many studies have reported the relative abundance of methanogenic communities is promoted by the presence of heavy metals (Feng et al. 2017; Giannopoulos et al. 2019). Some studies show the inhibition of carbon dioxide emissions due to heavy metal pollution thus impeding organic matter decomposition (Jaiswal and Pandey 2019; Enya et al. 2020). Overall, there seems to be a lack of understanding of the effects and long-term consequences of heavy metal pollution on the methane emission as well as carbon dioxide emissions from contaminated mangrove ecosystems.

The microbiome structure of the affected mangrove areas showed a different structure as compared to the microbiome structure of pristine areas, especially metal-contaminated mangrove ecosystems. These structural alterations were less evident in the high taxonomic groups. The observed prevalence of Proteobacteria, Bacteroidetes, Chloroflexi, and Firmicutes suggest these groups be members of the core microbiome of mangrove sediments in subtropical areas (Andreote et al. 2012; Dias et al. 2012). The Proteobacteria group is highly influenced by anthropogenically affected mangroves (Mendes and Tsai 2014).

4.6 Implications or Applications of Sediment Microbiome

Various methods used for the quantitative evaluation of heavy metal concentration help to understand the potential risk to an ecology of an ecosystem (Yuan et al. 2011). However, the application of sediment microbiota as indicators is preferable as these are sensitive environmental variation indicators. Various cultural characteristics of the microbial cells are responsible for this application which includes a large surface area to volume ratio due to their small sizes, the permeability of the cell membranes, and the ability to utilize the various nutrients available in the ecosystems (Billings and Ziegler 2008; Ikenaga et al. 2010; Troxler et al. 2012). The ability of the microbiome to overcome numerous stress conditions also makes them preferable indicators. Some studies related to this aspect have been reported for substrate quality (Bossio and Scow 1998; Morrissey et al. 2014a), flooding (Mentzer et al. 2006; Unger et al. 2009), temperature (Zogg et al. 1997), salinity (Morrissey et al. 2014b), pollution (Córdova-kreylos et al. 2006), etc.

In particular, prokaryotic populations are highly susceptible to heavy metal pollution than eukaryotes (Frossard et al. 2017; Rajapaksha et al. 2004) in terms of biomass, activity, and diversity. Thus, the microbiota is frequently considered as potential indicators of ecological changes like monitoring them for heavy metal pollution (Li et al. 2020). The mangrove ecosystem and in particular the microbiome of the sediment contribute toward remediation of this ecosystem from metal pollutants. The heavy metals are redistributed between the sediment and the water columns above, by the metal-tolerant microbiome. The microbial community is shifted toward the dominance of the resistant genera as a result of the heavy metal pollutants in the sediments. These could be used as indicator species of environmental stress and toxicity changes in the sediment and mangrove ecosystems as a whole. Studies indicative of sea-level rise stressors, for example, showed changes in microbial diversity within weeks' duration which shows the early warning signals from the microbiomes which are indeed very useful for immediate action plan implementation (Wright and Welbourn 2002). The quality of aquatic ecosystems can be monitored by using benthic organisms because of their features like their geographical distribution, fixed lifestyle, capturing ease, and the bioturbation promotion (Cantillo et al. 1997; Nordhaus et al. 2006; Wang et al. 2015; Yin et al. 2016).

4.7 Conclusions and Fture Perspectives

The process of carbon sequestration, as well as carbon storage, is much faster in the mangrove wetlands as compared to forests or any other ecosystems. Hence, the mangrove ecosystems are the most productive and are also referred to as the blue carbon sinks. Anthropogenic activities cause disturbances in the physicochemical parameters of the econiches thus influencing the microbiota. Trace element pollution in general and heavy metal pollution, in particular, have been the focus of several studies. It is the need of the day to understand the effects of heavy metal pollution on methane, the carbon dioxide released in the atmosphere, and ultimately the variations in the associated microbial communities. This knowledge is very important to evaluate their ecological consequences and global warming implications in mangrove wetlands. Microbial biodiversity depending upon its resistivity and the concentration of the polluting heavy metal, can decrease, increase, or remain the same. There is a reduction in microbial biodiversity observed in ecosystems receiving heavy metal contamination. Strong selection of microbiome occurs due to heavy metals purging sensitive taxa, or short-term, leading to the proliferation of a few specific resistant groups and resulting in a subsequent decrease in diversity.

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