

HANDBOOK OF AQUATIC MICROBIOLOGY

**Edited by PRAMOD KUMAR PANDEY,
SUMANTA KUMAR MALLIK, AND RAMESHORI YUMNAM**



Handbook of Aquatic Microbiology

This comprehensive handbook covers the different aspects of the aquatic environment, microbiology, and microbial applications. The world's aquatic environment is facing a serious threat due to inappropriate planning, implementation, and management. This book compiles effective strategies for managing the aquatic environment. It highlights the role of microorganisms as pollution indicators, in bioremediation, and as bio-control agents. The book also covers the impact of pollution on microorganisms, biofilms, cyanobacterial blooms, and the metagenomics approach to isolate microbes. This book is essential for students and researchers of microbiology, environmental sciences, and biotechnology.

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Pramod Kumar Pandey, Sumanta Kumar Mallik, and
Rameshori Yumnam



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*Dedicated
to
Dr. Panjab Singh
in recognition of his unwavering service to the pursuit of
knowledge and his remarkable impact on Indian agriculture*



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Contents

Foreword	x
Preface.....	xi
Contributors	xii
Chapter 1 Microbiomes of the Aquatic Environment.....	1
<i>Pragyan Dash, Ritesh Shantilal Tandel, and Raja Aadil Hussain Bhat</i>	
Chapter 2 Microbial Planktonic Communities	12
<i>Garima, Kishor Kunal, and Parvaiz Ahmad Ganie</i>	
Chapter 3 Climate Change: A Strong Driving Force for Cyanobacterial Bloom.....	28
<i>Snatashree Mohanty, Anirban Paul, and Pramoda Kumar Sahoo</i>	
Chapter 4 Benthic Microbial Community in the Aquatic Environment.....	40
<i>Pramod Kumar Pandey, Richa Pathak, Rameshori Yumnam, and Sumanta Kumar Mallik</i>	
Chapter 5 Sediment Microbiology in the Aquatic Environment	56
<i>Sumanta Kumar Mallik, Richa Pathak, and Neetu Shahi</i>	
Chapter 6 Biogeochemical Cycles and Their Significance in Nutrient Recycling	77
<i>Abhay Kumar Giri, Sumanta Kumar Mallik, Parvaiz Ahmad Ganie, and Suresh Chandra</i>	
Chapter 7 Probiotics in Aquaculture.....	90
<i>Suresh Chandra and Nupur Joshi</i>	
Chapter 8 Microbiome in Aquaponics: Emergent Roles and Potential Applications	100
<i>Rameshori Yumnam and Maibam Birla Singh</i>	
Chapter 9 Microbial Community of Biofloc	135
<i>M. Rajkumar</i>	
Chapter 10 Extremophiles in Aquatic Environments and Their Ecological Significance.....	141
<i>Sumanta Kumar Mallik, Richa Pathak, Satya Narayan Sahoo, and Neetu Shahi</i>	

Chapter 11	Algicidal Microbes in the Aquatic Environment	161
	<i>Kapil S. Sukhdhane and Pramod Kumar Pandey</i>	
Chapter 12	Microbial Indicators of Aquatic Pollution.....	171
	<i>Kundan Kumar, Saurav Kumar, Satya Prakash Shukla, and Rajive Kumar Bhrmchari</i>	
Chapter 13	Impact of Emerging Pollutants on Freshwater Microbes.....	183
	<i>Saurav Kumar, Pritam Sarkar, Tapas Paul, and Kundan Kumar</i>	
Chapter 14	Eutrophication in Freshwater and Its Microbial Implications.....	194
	<i>Debajit Sarma and Deepak Kumar</i>	
Chapter 15	Bacterial Biofilm in the Aquatic Environment and Its Impact	210
	<i>Pramod Kumar Pandey</i>	
Chapter 16	Microbial Remediation in an Aquatic Environment	228
	<i>Ritesh Shantilal Tandel, Sanjay Rathod, Raja Aadil Hussain Bhat, and Pragyan Dash</i>	
Chapter 17	Environmental DNA and Its Application in Microbial Biodiversity Assessment ...	239
	<i>Neetu Shahi, Bhupendra Singh, Aslah Mohamad, and Sumanta Kumar Mallik</i>	
Chapter 18	Metagenomic Approach to Unculturable Microbes of the Aquatic Environment	251
	<i>Mamta Singh</i>	
Chapter 19	Microalgal Remediation in the Aquatic Environment	260
	<i>V. Santhana Kumar, Dhruva Jyoti Sarkar, Soma Das Sarkar, and Basanta Kumar Das</i>	
Chapter 20	Role of Microorganisms as Biocontrol Agents in Aquatic Environments.....	271
	<i>Sumanta Kumar Mallik, Richa Pathak, Neetu Shahi, and Mohan Singh</i>	
Chapter 21	Thermophilic Microbial Enzymes from Hot Springs and Their Role in Bioprocessing	293
	<i>Amit Seth</i>	
Chapter 22	Overview of Microbial Toxins in the Aquatic Environment.....	303
	<i>Pramod Kumar Pandey, M. Junaid Sidiq, and Rameshori Yumnam</i>	

Chapter 23 Applications of Geospatial Technology in the Mapping of Aquatic Microbes and Risk Assessment.....	323
<i>Ganesan Kantharajan, R. Bharathi Rathinam, Arur Anand, Ayyathurai Kathirvelpandian, Ajey Kumar Pathak, and Uttam Kumar Sarkar</i>	
Chapter 24 Statistical Aspects of Aquatic Microbiology.....	333
<i>V. Ramasubramanian and H. Sanath Kumar</i>	
Index	351

Foreword



The world's aquatic ecosystems are vital to the health of our planet, sustaining a myriad of life forms and serving as a critical component of the Earth's biogeochemical cycles. As our understanding of these intricate environments deepens, so does our appreciation for the pivotal role played by microorganisms in shaping the dynamics of aquatic ecosystems. It is with great pleasure that I would like to introduce the *Handbook of Aquatic Microbiology* edited by Dr. Pramod Kumar Pandey and others. This comprehensive volume will serve as an indispensable guide to the multifaceted world of aquatic microbiology, offering a profound exploration of the microbial life that thrives

beneath the surface of our oceans, lakes, rivers, and other water bodies. The importance of this field cannot be overstated, as the microbial inhabitants of aquatic environments influence fundamental ecological processes, drive nutrient cycling, and impact water quality.

In this handbook, the editors and authors have come together to provide a treasure trove of knowledge, encompassing a wide range of topics related to aquatic microbiology. From pristine freshwater systems to the most extreme aquatic habitats, the diversity and adaptability of aquatic microorganisms are showcased in intricate detail. Readers will have knowledge of the latest advancements in research, gaining insights into the vital roles played by aquatic microorganisms in nutrient cycling, bioremediation, and the maintenance of ecosystem health. It serves as an essential reference not only for researchers and professionals in the field but also for academicians, students, and anyone with a passion for understanding and protecting our planet's aquatic treasures. As we confront the challenges posed by climate change, pollution, and the ever-increasing demands on our water resources, a deep understanding of aquatic microbiology has never been more critical. The *Handbook of Aquatic Microbiology* is a beacon of knowledge in this endeavour, providing a compass to navigate the intricate and awe-inspiring world of microorganisms that inhabit our waters.

I commend and congratulate the authors and editors for their dedication to advancing our understanding of aquatic microbiology, and I am confident that this volume will be a source of inspiration and guidance for all who seek to explore and safeguard our planet's aquatic ecosystems.

Anupam Mishra
28 October 2023

Preface

The aquatic realm, comprising the vast expanses of oceans, rivers, lakes, and wetlands, is an intricate and dynamic ecosystem teeming with life, much of which is hidden from the naked eye. Within these watery realms, an invisible world of microorganisms plays a pivotal role in shaping the very fabric of our planet. From the blue depths of the open ocean to the serene tranquillity of freshwater ponds, microbial life forms the foundation of aquatic ecosystems, impacting not only the health of these environments but also the global biogeochemical cycles that sustain life on Earth.

The *Handbook of Aquatic Microbiology* is a culmination of the tireless efforts of numerous scientists, researchers, and experts in the field, each driven by an insatiable curiosity to unravel the mysteries of aquatic microbiology. In this comprehensive volume, we delve into the microscopic wonders that inhabit our waters, examining their ecological significance, their contributions to biogeochemical processes, their role in shaping aquatic food webs, and their interactions with human activities.

This book is intended as a compendium of knowledge, a guide for both seasoned researchers and newcomers to the field. It presents a synthesis of the current state of aquatic microbiology, offering a multidisciplinary perspective that bridges the gap between the fundamental principles of microbiology and the complex, dynamic aquatic environments in which these microorganisms thrive. Throughout these pages, readers will find a wealth of information ranging from microbial physiology to the ecological consequences of microbial activities in aquatic ecosystems.

Our aim is to provide a valuable resource for scientists, educators, policymakers, and anyone with an interest in the intricate web of life that flourishes beneath the water's surface. By exploring the world of aquatic microbiology, we hope to inspire curiosity and foster a deeper appreciation for the crucial role that these tiny organisms play in sustaining life on Earth. As editors, we are indebted to the dedicated contributors who have shared their expertise and insights, making this handbook a reality. Their commitment to advancing our understanding of aquatic microbiology is evident in the wealth of knowledge presented within these pages. We also extend our gratitude to the reviewers whose meticulous scrutiny ensured the quality and accuracy of the content.

In closing, we invite you to embark on a journey into the unseen world of aquatic microbiology. We hope that this handbook will serve as a valuable reference and a source of inspiration for all those who seek to explore the fascinating realm of aquatic microorganisms.

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1 Microbiomes of the Aquatic Environment

*Pragyan Dash, Ritesh Shantilal Tandel,
and Raja Aadil Hussain Bhat*

1.1 INTRODUCTION

Freshwater and marine ecosystems are home to a complex and diverse array of microorganisms, including viruses, bacteria, fungi, and algae. These microorganisms play an important role in aquatic ecosystem by acting as decomposers, as producers, and in nutrient cycles. Microorganisms interact with one another and their surroundings to influence the health and function of aquatic ecosystems. The community of microorganisms and combined genetic material, inhabiting a particular environment is summarized in the term ‘microbiome.’ For a million years, the aquatic microbiome has shaped the microbiome of each aquatic plant and animal; however, the host-associated microbiome is not a direct reflection of the water’s microbial community. Aquatic animals are subjected to multiple environmental, nutritional, and genetical selection forces, which impact the coevolved alliances between microbiome and organism (Song et al., 2017).

The functions of aquatic ecosystems depend on interaction between microorganisms and aquatic animals. Bacterial strains competing for nutrients can form more diverse and stable communities (Ghoul and Mitri, 2016). Symbiotic associations between bacteria and algae can improve photosynthesis and primary production efficiency in aquatic environments (Zhou et al., 2018).

The distribution and abundance at higher trophic levels, such as fish and other aquatic creatures, can be affected by changes in the composition of the microbial community. This can also have significant effects on nutrient cycling and ecosystem function. Therefore, for efficient ecosystem management and conservation, a deeper comprehension of the function of microbial communities in aquatic ecosystems is necessary. Aquatic habitats are projected to see considerable changes in microbial community structure and function as global temperatures rise. These changes will have a significant impact on ecosystem services and human well-being. Monitoring these changes and developing targeted management strategies can mitigate the impacts of climate change on aquatic ecosystems. This chapter emphasizes the diversity of microbiomes in aquatic algae, vertebrates, and macrophytes, and their interaction in the aquatic environment (Figure 1.1).

1.2 ALGAE-ASSOCIATED MICROBIOME

Algae, the phytoplankton, are a diverse group of aquatic organisms that play significant roles in maintaining the ecological balance of aquatic ecosystems. Interactions between phytoplankton, microalgae, and their associated microorganisms can be influenced by the production and release of various chemical mediators (Cirri and Pohnert, 2019).

The chemical signals exchanged between algae and microorganisms are associated with their survival, functioning, and health. There are several compounds, such as orfamide A, oxylipins, amino acids, vibrioferrin, methylamine, s-containing osmolytes, auxin, and vitamins, which play a role as defense metabolites, nutrients, growth promoters, antibiotics, signaling molecules, in the binding and uptake of iron, demobilization and killing, as osmolytes, etc. (Cirri and Pohnert, 2019).

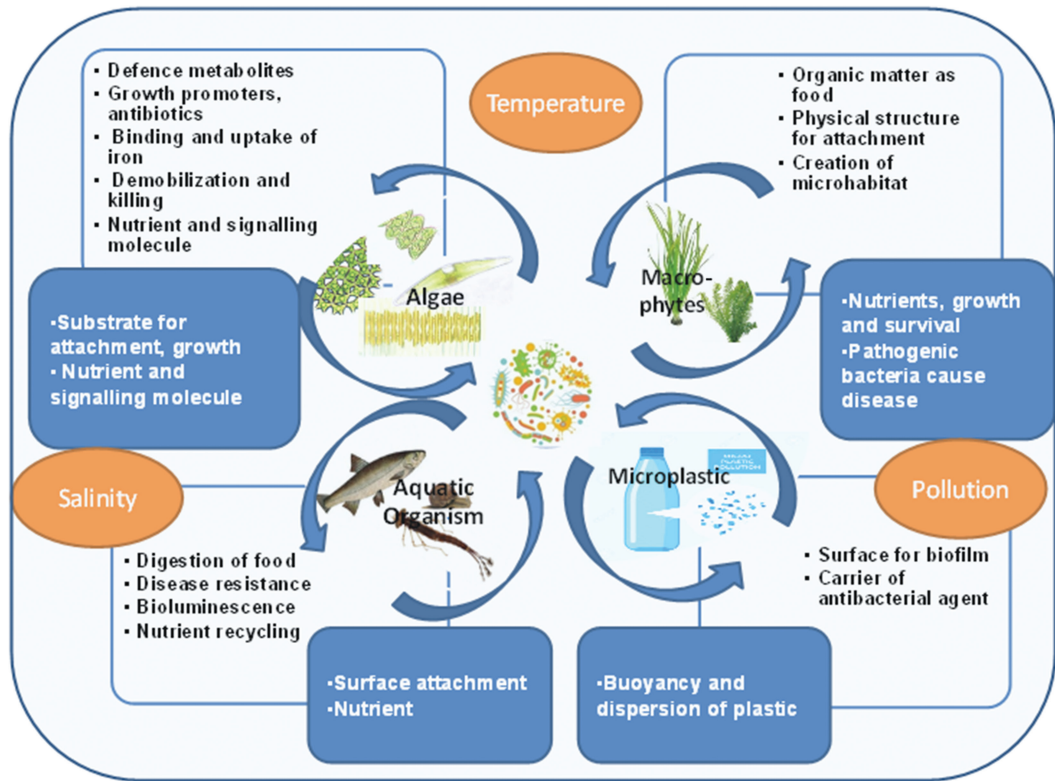


FIGURE 1.1 Interactions of microbiome in an aquatic ecosystem.

For example, nitrogen-fixing bacteria and methylamine-degrading bacteria release ammonia (NH_3), which increases nitrogen availability for microalgae. Tryptophan produced by microalgae serves as a precursor for the biosynthesis of auxins in bacteria and promotes mutualism (Amin et al., 2015). Bacteria from the *Roseobacter* clade (such as *Phaeobacter inhibens* and *Dinoroseobacter shibae*) can trade vitamins or vitamin precursors with algae that cannot synthesize them de novo (Croft et al., 2005; Wienhausen et al., 2017). In exchange for the amino acid tryptophan, *P. inhibens* and *Sulfitobacter* supply auxins and ammonium to diatoms and coccolithophores (Amin et al., 2015; Segev et al., 2016). *Ruegeria pomeroyi* can sense various sulfuric compounds released by microalgae and respond by producing auxins that support algal growth as well as quorum-sensing molecules that promote bacterial proliferation (Johnson et al., 2016; Durham et al., 2015).

Algicidal bacteria can even control the algal bloom by inducing the lysis of algal cells. A typical example is the bacterium *Pseudomonas protegens*, which surrounds the microalga *Chlamydomonas reinhardtii*. *P. protegens* deflagellates the alga and disrupts its Ca^{2+} homeostasis (Aiyar et al., 2017). Further, *P. inhibens* initially increases the coccolithophore's growth by releasing the growth-promoting indole-3-acetic acid (IAA), but later on, it triggers algal cell death by activation of pathways of oxidative stress.

Diatoms and most microalgae require inorganic nitrogen such as nitrate or ammonium, provided by cyanobacteria and nitrogen-fixing bacteria (Foster et al., 2011). Accordingly, the association of algae with nitrogen-fixing bacteria is seen in an ecosystem. Further, other bacteria, like the α -proteobacterium *Donghicola*, can convert the organic nitrogen source methylamine to ammonia. The ammonia is readily taken up by the diatom *Phaeodactylum tricornerutum*, and in return, bacteria proliferate with the exudates of the diatom (Suleiman et al., 2016).

Microbiome composition and diversity can be influenced by factors such as water quality, nutrient availability, and habitat. Algae living in polluted water have a less diverse microbiome, dominated by potentially pathogenic bacteria, than algae living in clean water. Some algae, like *Navicula accomoda* and *Stigeoclonium tenue*, can comfortably live in the most heavily polluted zones, while some, like *Cocconeis* and *Chamaesiphon*, are reported to occur only in unpolluted parts of streams (Sen et al., 2013).

Algal-associated microbial populations can control an ecosystem's primary production, carbon sequestration, and nutrient cycling. Additionally, algae are a crucial part of aquaculture, and the microbiomes linked to algae can have a direct impact on the species used for aquaculture in terms of nutrient availability, water quality, and disease resistance.

1.3 AQUATIC ORGANISMS–ASSOCIATED MICROBIOME

Aquatic organisms, including fish, crustaceans, and other fauna, rely on their associated microbiomes for their physiology and health (Colston and Jackson, 2016; Sehnal et al., 2021). Microbiomes related to aquatic organisms are found in various organs, including the skin, gills, gut, and mucus. Skin and gill of fish are the critical site for microbial colonization and play a significant role in protecting fish from pathogenic microbes (Ross et al., 2019), while the gut microbiome contributes significantly to the digestion and nutrient utilization, immune function, health, and overall behavior and ecology of aquatic organisms.

The gut microbial community is broadly divided into allochthonous and autochthonous microbiota based on their interaction with the host. The allochthonous microbiota comprises microorganisms that pass through the lumen along with the food, while the autochthonous microbiota resides permanently in the fish gut without causing any harm to it (Rajeev et al., 2021).

Microorganisms found in the gut of fish and other aquatic organisms can break down complex carbohydrates, proteins, and lipids that are otherwise indigestible by the host (Ringø et al., 2016; Givens et al., 2015). For example, a study on Atlantic salmon (*Salmo salar*) indicated that the gut microbiome produced enzymes that facilitated the digestion of complex carbohydrates, such as cellulose and chitin (Ringø et al., 2016). Similarly, in zebrafish (*Danio rerio*), the microbiota stimulated fatty acid uptake and lipid droplet formation in the intestinal epithelium and liver (Carmody and Turnbaugh, 2012; Semova et al., 2012). The gut microbiome is also known to modulate the host's immune response by producing antimicrobial compounds and promoting the development of immune cells (Gómez and Balcázar, 2008). In Nile tilapia (*Oreochromis niloticus*), certain bacteria in the gut microbiome were reported to be associated with increased resistance to bacterial infections (Tan et al., 2019). Li et al. (2018) and Yao et al. (2021) also reported that the gut microbiome of shrimp (*Litopenaeus vannamei*) played a crucial role in regulating the expression of immune-related genes and protecting the host against viral infections. In addition to digestion and immune function, the microbiome can also influence the behavior and ecology of aquatic organisms (Sullam et al., 2012). In killifish (*Fundulus heteroclitus*), the gut microbiome influenced their reproductive success, with certain microbial communities associated with higher reproductive output (Lombardo et al., 2011; Scott et al., 2020).

Interaction between host physiology, gut architecture, and ecological and environmental factors determines the diversity of the gut microbiome (Ghanbari et al., 2015). Also, the gut microbiome shows a direct relationship when feeding habit changes from herbivore to omnivore to carnivore in finfish species (Givens, 2012; Larsen et al., 2014). As reported in many studies, the early colonization of gut microbiota starts from the egg stage, based on the binding glycoproteins on the egg surface (Larsen et al., 2014). Upon hatching, a bacterium linked with egg chorions first emerges as a colony in the gastrointestinal system. Following that, different kinds of gut microbiota begin to colonize when fish drink water and consume food from the environment (Hansen and Olafsen, 1999). A healthy fish has a more varied alpha gut microbiota than a sick fish, and this variation can be used as a diagnosis to manage fish health (Clarke et al., 2014). Moreover, varied and abundant populations of gut microbes improve fish defense and protection mechanisms (Johnson et al., 2008).

The microbiome composition and diversity of these organs can be influenced by various factors such as water quality, diet, and habitat. Larsen et al. (2014) found that fish living in polluted water had a less diverse microbiome than fish living in clean water. The study also found that potentially pathogenic bacteria dominated the microbiome of fish living in polluted water. Similarly, Ingerslev et al. (2014) found that the gut microbiome of rainbow trout (*Oncorhynchus mykiss*) fed on a plant-based diet was composed of *Leuconostoc*, *Weissella*, *Streptococcus*, etc. The gut microbiome composition of fish fed on an animal-based diet consisted of Bacteroidetes, Proteobacteria, and Actinobacteria, which was different from the fish fed with a plant-based diet. Also, the microbiome of fish from freshwater habitats differs from that of fish from marine habitat (Fan et al., 2019). Among freshwater fish microbiome species, *Acinetobacter*, *Aeromonas*, *Flavobacterium*, *Lactococcus*, and *Pseudomonas*, obligate anaerobes *Bacteroides*, *Clostridium*, and *Fusobacterium*, and members of the family *Enterobacteriaceae* persist, whereas in marine fish, *Aeromonas*, *Alcaligenes*, *Alteromonas*, *Carnobacterium*, *Flavobacterium*, *Micrococcus*, *Moraxella*, *Pseudomonas*, and *Vibrio* dominate (Gomez and Balcázar, 2008).

1.4 AQUATIC MACROPHYTES–ASSOCIATED MICROBIOME

Aquatic macrophytes are dominant primary producers in many freshwater and marine environments, providing essential ecosystem services such as nutrient cycling, sediment stabilization, and habitat provision. Aquatic macrophytes interact with the environmental microbiome through various pathways, including the provision of organic matter, changes in water quality, and creation of microhabitats. Aquatic macrophytes release organic matter, which acts as a food source for the microbial community, increasing their abundance and diversity. The composition of the microbiome can be altered due to the water quality, which includes increased nutrient availability and light penetration, with some taxa flourishing in nutrient-rich habitats and others in nutrient-poor environments (Bárta et al., 2021). Moreover, the creation of microhabitats by aquatic macrophytes, such as roots and leaves, can provide a physical structure for the attachment and growth of microbes, leading to the formation of specialized microbial communities.

Furthermore, the microbiome is shown to significantly impact the growth and health of aquatic macrophytes. Some bacteria can form a symbiotic relationship with aquatic macrophytes, providing essential nutrients and improving their growth and survival (Zhu et al., 2021). On the other hand, pathogenic microorganisms can cause diseases in aquatic macrophytes, leading to declines in their populations and altering the structure and function of the ecosystem (Saha and Weinberger, 2019).

1.5 MICROPLASTIC-ASSOCIATED MICROBIOME

The makeup of microbial communities on the surface of microplastics or nanoplastics in an aquatic environment, referred to as the ‘plastisphere,’ has been an interest of research for several decades (Amaral-Zettler et al., 2020). The ability of bacteria and fungi to digest plastic particles, as well as the interaction between the microbial community and microplastics, has piqued scientists’ interest in environmental biotechnology (Barros et al., 2021).

Microplastics provide a surface for microbial attachment, leading to the formation of biofilms. The microbial communities associated with microplastics in aquatic ecosystems are diverse and depend upon the attachment on different types of plastics and water bodies (Table 1.1). Biofilms of microplastic in ponds had higher relative abundances of the phyla Proteobacteria, Firmicutes, and Chloroflexi, while river biofilms of microplastic had higher relative abundances of the phylum Acidobacteria and family Nitrospiraceae, Nitrosomonadaceae, and lower relative abundances of Proteobacteria (Hoellein et al., 2014).

Microbiomes belonging to bacterial genera such as *Klebsiella*, *Pseudomonas*, and *Sphingomonas* can degrade plastic (Kelly et al., 2021). *Rhodococcus ruber* C208 can degrade polyethylene film by up to 8% within 30 days of incubation, which increases with mineral oil up to 50% (Hadar and Sivan

TABLE 1.1
Microorganisms Associated with Microplastics in an Aquatic Environment

Microorganism	Type of Microplastic	Source of Isolation	Reference
<i>Vibrio alginolyticus</i>	Polyethylene	Mangrove	Tan et al. (2022)
<i>Vibrio harveyi</i> , <i>Enterococcus faecalis</i>	Polyethylene	Seawater	Hchaichi et al. (2020)
<i>Vibrio parahaemolyticus</i>	Polyethylene, polystyrene, polypropylene	North/Baltic Sea	Kirstein et al. (2016)
<i>Pseudomonas monteilii</i> , <i>P. mendocina</i> , <i>P. syringae</i>	Polyvinyl chloride (PVC)	River water in controlled conditions	Wu et al. (2019)
<i>Bacillus cereus</i> and <i>Bacillus gothelii</i>	Polystyrene	Mangrove ecosystems	Auta et al. (2017)
<i>Acinetobacter</i>	Polypropylene	River	Mughini-Gras et al. (2021)
<i>Flavobacterium</i>	Polyethylene terephthalate (PET)	River	Mughini-Gras et al. (2021)
<i>Aspergillus</i> , <i>Cladosporium</i> , <i>Wallemia</i>	Polyethylene (PE), Polyamide (PA), polyurethane (PU), polypropylene (PP), polystyrene (PS), and cellulose acetate (CA)	Western South Atlantic and Antarctic Peninsula	Lacerda et al. (2020)
<i>Aspergillus niger</i> , <i>Penicillium</i> spp., <i>Rhizopus</i> spp., <i>Mucor</i> spp., <i>Aspergillus nidulans</i> , <i>Fusarium</i> spp., <i>Microsporium canis</i> , and <i>Aspergillus fumigatus</i>	Polypropylene, polyester, polyvinyl chloride	Estuary	Williams et al. (2021)

2004). Changes in microbial communities in microplastics can influence the biomass of plastics, as reported in polyethylene terephthalate (PET) and polyvinyl chloride (PVC), and hence, can affect the buoyancy and dispersion of plastics in water (Miao et al., 2021).

Due to their small size, microplastics are ingested by a wide range of aquatic organisms, including bacteria, zooplankton, and fish. Plastic debris has been found in fishes, shellfish, and mussels, which after consumption, can enter the human body through trophic transfer, biomagnification, and bioaccumulation (Giani et al., 2019; Hermabessiere et al., 2019). Microplastic intake can adversely affect the health of aquatic organisms, as microplastics are potential carriers for pathogenic bacteria, antimicrobials, and toxic compounds (Campanale et al., 2020).

1.6 IMPACT OF ENVIRONMENTAL FACTORS ON THE STRUCTURE AND FUNCTION OF THE AQUATIC MICROBIOME

The aquatic microbiome is particularly vulnerable to environmental stressors, i.e., pollutants and changes in water quality. In recent years, researchers have explored the impact of various environmental stressors on the microbiome in aquatic environments, including pollution, temperature, and nutrient availability.

1.6.1 TEMPERATURE

Temperature is a key factor that shapes the diversity and composition of aquatic microbial communities, and it has been shown to impact the metabolic rates of these organisms significantly.

As temperature increases, the microbial community structure shifts, with thermophilic bacteria becoming dominant (Chiriac et al., 2017). In a study on a eutrophic lake, temperature increase was associated with a decrease in the abundance of cyanobacteria and an increase in the abundance of other phytoplankton taxa (Paerl and Paul, 2012; O'Neil et al., 2012).

Temperature can also influence the diversity of the microbial community, affecting the competitive dynamics between various species. In research on a freshwater reservoir, warming was linked to increased dominance of a single bacterial taxon, which displaced other taxa and reduced total diversity (Wang et al., 2021). On the contrary, another report on the freshwater lake shows an increase in microbial diversity and a more significant number of rare and low-abundance species with increasing temperatures (Islam et al., 2019).

Temperature profoundly impacts how the microbial community functions by affecting microbial metabolic rates. Changes in community composition, such as a decrease in the abundance of cyanobacteria and a rise in the quantity of other phytoplankton species, were linked to changes in nutrient cycling rates, such as enhanced rates of nitrogen fixation and denitrification at higher temperatures (Paerl and Paul, 2012).

Temperature can also influence microbial community function by affecting interactions between various microbial populations. In one freshwater lake, warming was linked to a decrease in the population of bacteria that consume methane, resulting in higher methane emissions from the lake (Schulz and Conrad, 1996). Similarly, higher temperature in a coastal marine ecosystem was linked to a decrease in the abundance of microbial populations engaged in the breakdown of petroleum hydrocarbons, implying that rising temperature may limit the ability of these communities to respond to oil spills (Chong et al., 2018).

1.6.2 SALINITY

Many aquatic habitats, including estuaries, salt marshes, and hypersaline lakes, experience changes in salinity due to fluctuations in water flow, evaporation, and precipitation, which can significantly change the composition and diversity of the aquatic microbiome. In the Great Salt Lake in Utah, it was found that extreme halophilic bacteria prevail in the north arm, which has a salinity range from 20 to 30 ppt, whereas moderate halophiles prevail in the south arm at around 15–17 ppt (Baxter et al., 2005). A similar finding was also observed in the lakes of China; *Bacteroidetes*, *Cyanobacteria*, and *Alpha proteobacteria* were the dominant bacterial phyla in low saline lakes, whereas *Gamma proteobacteria* and *Euryarchaeota* were abundant in moderately saline lakes (50–250 ppt). The hypersaline lakes (>250 ppt) were dominated by extreme halophiles such as *Halorubrum*, *Halohasta*, and *Natronomonas* from *Euryarchaeota* (Banda et al., 2021). Changes in salinity are shown to be connected with changes in the abundance of pathogenic *Vibrio* bacteria in the Baltic Sea and shrimp farms in Vietnam (Baker-Austin et al., 2013).

1.6.3 POLLUTION

Pollution, due to anthropogenic activities such as agriculture, industry, and urbanization, can introduce a wide range of pollutants into aquatic environments. These include nutrients, heavy metals, and organic chemicals. Several reports have shown that pollution can seriously affect the composition and performance of the aquatic microbiome. For example, a study conducted in a polluted river in Northeastern China revealed that the pollution decreased the overall bacterial diversity. However, the community was dominated by opportunistic and pathogenic bacteria such as *Acinetobacter johnsonii*, *Clostridium cellulovorans*, and *Trichococcus pasteurii* (Zhao et al., 2014). This shift in microbial composition can significantly impact ecosystem functioning, including nutrient cycling and water quality. In addition to changes in microbial composition, pollution can also lead to changes in microbial metabolism. In an estuary of China polluted with polycyclic aromatic hydrocarbons (PAHs), the microbial community was dominated by proteobacteria containing genes encoding for

dehydrogenases, which are the key enzymes for pyrene degradation (Zhang et al., 2019). However, these adaptations can also negatively impact ecosystem functioning, such as releasing greenhouse gases.

Pollution in the form of eutrophication is also a threat to aquatic microbiomes, leading to algal blooms and oxygen depletion. Eutrophication can lead to changes in the composition of microbial communities, most notably a shift from an autotrophic to a heterotrophic population (Meyer-Reil and Köster, 2000; Andersson et al., 2006). Furthermore, increased nutrient availability can lead to increased abundance of harmful bacteria, such as *Vibrio* (Baker-Austin et al., 2013).

1.7 CONSERVATION AND MANAGEMENT IMPLICATIONS FOR THE ECOSYSTEM

Understanding the interactions between the aquatic microbiome and its environment has important implications for conserving and managing aquatic ecosystems. Management of water quality, such as temperature, pH, and salinity, including controlling the levels of pollutants, can help to protect the diversity and stability of the aquatic microbiome.

One of the critical challenges in managing aquatic ecosystems in a changing climate scenario is predicting how microbial communities will respond to temperature changes. Many factors can influence the sensitivity of microbial communities to temperature, including the specific microbial taxa present, the availability of nutrients and other resources, and the presence of other stressors, such as pollution or invasive species. As a result, it can be challenging to predict the exact nature and magnitude of the impacts of temperature on microbial community structure and function.

However, several strategies can be employed to manage and conserve aquatic ecosystems in a changing climate scenario. One approach is to monitor microbial community structure and function over time, using high-throughput sequencing and other molecular techniques to track changes in community composition and metabolic activity. These facts can be used to identify critical microbial taxa and processes that may be particularly sensitive to temperature changes and to develop targeted management strategies to mitigate the impacts of climate change on ecosystem function.

Developing bioremediation strategies, which utilize microorganisms to remove pollutants from aquatic environments, is another important consideration for conserving and managing aquatic ecosystems (Gao et al., 2018). Another approach is to manage other stressors that can exacerbate temperature impacts on aquatic microbial communities. For example, reducing nutrient pollution can help maintain the resilience of microbial communities to temperature changes by reducing the risk of harmful algal blooms and other negative impacts on ecosystem function. Similarly, reducing the impact of invasive species can help maintain the diversity and function of native microbial communities, which may be more resilient to temperature changes than introduced species.

1.8 CONCLUSION

Microbiomes can have beneficial and detrimental effects on aquatic organisms, and host genetics, environmental conditions, and the surrounding microbiome community can influence their composition and function. However, there are still many knowledge gaps and future research directions in aquatic microbiome research, including understanding the mechanisms underlying microbiome–host interactions, identifying key microbial taxa and functional genes involved in these interactions, and investigating the effects of anthropogenic activities on aquatic microbiomes.

The microbiome plays a crucial role in maintaining the health of aquatic ecosystems and is shaped by a complex interplay of physical, chemical, and biological factors. Despite this, the aquatic microbiome is vulnerable to disturbance from eutrophication and global warming. Further research is needed for proper understanding of the impact of these disturbances on the overall ecosystem

health. Ultimately, this type of study will help chart out the management and conservation strategies for protecting aquatic ecosystems and the microorganisms that inhabit them.

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Microbiomes of the Aquatic Environment

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Benthic Microbial Community in the Aquatic Environment

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Sediment Microbiology in the Aquatic Environment

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Microbiome in Aquaponics

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Microbial Community of Biofloc

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Algicidal Microbes in the Aquatic Environment

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Bacterial Biofilm in the Aquatic Environment and Its Impact

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Microbial Remediation in an Aquatic Environment

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Microalgal Remediation in the Aquatic Environment

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Role of Microorganisms as Biocontrol Agents in Aquatic Environments

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Statistical Aspects of Aquatic Microbiology

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