Microbes as Agents of Change for Sustainable Development

Editors:
Shiv Prasad
Govindaraj Kamalam Dinesh
Murugaiyan Sinduja
Sathya Velusamy
Ramesh Poornima
Sangilidurai Karthika

Bentham Books

Microbes and Microbiomes for Clean and Green Environment

(Volume 2)

Microbes as Agents of Change for Sustainable Development

Edited by

Shiv Prasad
&
Govindaraj Kamalam Dinesh
Division of Environment Science
ICAR-Indian Agricultural Research Institute
New Delhi-110012, India

Murugaiyan Sinduja
National Agro Foundation, Taramani, Chennai
Tamil Nadu, India

Sathya Velusamy
Tamil Nadu Pollution Control Board, Chennai
Tamil Nadu, India

Ramesh Poornima
&
Sangilidurai Karthika
Department of Environmental Sciences
Tamil Nadu Agricultural University, Coimbatore
India

Microbes and Microbiomes for Clean and Green Environment

(Volume 2)

Microbes as Agents of Change for Sustainable Development

Editors: Shiv Prasad, Govindaraj Kamalam Dinesh, Murugaiyan Sinduja,

Sathya Velusamy, Ramesh Poornima & Sangilidurai Karthika

ISBN (Online): 978-981-5322-34-7

ISBN (Print): 978-981-5322-35-4

ISBN (Paperback): 978-981-5322-36-1

First published in 2024.

BENTHAM SCIENCE PUBLISHERS LTD.

End User License Agreement (for non-institutional, personal use)

This is an agreement between you and Bentham Science Publishers Ltd. Please read this License Agreement carefully before using the ebook/echapter/ejournal (**"Work"**). Your use of the Work constitutes your agreement to the terms and conditions set forth in this License Agreement. If you do not agree to these terms and conditions then you should not use the Work.

Bentham Science Publishers agrees to grant you a non-exclusive, non-transferable limited license to use the Work subject to and in accordance with the following terms and conditions. This License Agreement is for non-library, personal use only. For a library / institutional / multi user license in respect of the Work, please contact: permission@benthamscience.net.

Usage Rules:

1. All rights reserved: The Work is the subject of copyright and Bentham Science Publishers either owns the Work (and the copyright in it) or is licensed to distribute the Work. You shall not copy, reproduce, modify, remove, delete, augment, add to, publish, transmit, sell, resell, create derivative works from, or in any way exploit the Work or make the Work available for others to do any of the same, in any form or by any means, in whole or in part, in each case without the prior written permission of Bentham Science Publishers, unless stated otherwise in this License Agreement.
2. You may download a copy of the Work on one occasion to one personal computer (including tablet, laptop, desktop, or other such devices). You may make one back-up copy of the Work to avoid losing it.
3. The unauthorised use or distribution of copyrighted or other proprietary content is illegal and could subject you to liability for substantial money damages. You will be liable for any damage resulting from your misuse of the Work or any violation of this License Agreement, including any infringement by you of copyrights or proprietary rights.

Disclaimer:

Bentham Science Publishers does not guarantee that the information in the Work is error-free, or warrant that it will meet your requirements or that access to the Work will be uninterrupted or error-free. The Work is provided "as is" without warranty of any kind, either express or implied or statutory, including, without limitation, implied warranties of merchantability and fitness for a particular purpose. The entire risk as to the results and performance of the Work is assumed by you. No responsibility is assumed by Bentham Science Publishers, its staff, editors and/or authors for any injury and/or damage to persons or property as a matter of products liability, negligence or otherwise, or from any use or operation of any methods, products instruction, advertisements or ideas contained in the Work.

Limitation of Liability:

In no event will Bentham Science Publishers, its staff, editors and/or authors, be liable for any damages, including, without limitation, special, incidental and/or consequential damages and/or damages for lost data and/or profits arising out of (whether directly or indirectly) the use or inability to use the Work. The entire liability of Bentham Science Publishers shall be limited to the amount actually paid by you for the Work.

General:

1. Any dispute or claim arising out of or in connection with this License Agreement or the Work (including non-contractual disputes or claims) will be governed by and construed in accordance with the laws of Singapore. Each party agrees that the courts of the state of Singapore shall have exclusive jurisdiction to settle any dispute or claim arising out of or in connection with this License Agreement or the Work (including non-contractual disputes or claims).
2. Your rights under this License Agreement will automatically terminate without notice and without the

Bentham Science Publishers Pte. Ltd.
80 Robinson Road #02-00
Singapore 068898
Singapore
Email: subscriptions@benthamscience.net

CONTENTS

PART 1 SIGNIFICANCE OF MICROBIOME IN NATURAL RESOURCE MANAGEMENT

PART 2 ROLE OF MICROBES IN THE PRODUCTION OF RENEWABLE ENERGY

PART 3 MICROBIOME IN MITIGATING GHG EMISSION AND CLIMATE CHANGE IMPACTS

PART 5 ROLE OF MICROBES IN SOCIO-ECONOMIC DEVELOPMENT

PREFACE

The book “Role of Microbes and Microbiomes in Ecosystem Restoration” focuses on basic to advanced techniques in various roles of microbes and microbiomes in the abatement and restoration of polluted ecosystems, climate change, production of renewable energy sources, and waste management. It covers ecosystem sustainability, the UN decade of ecosystem restoration, efficient utilization of microbes and microbiomes and their role in socio-economic development, and the current status of polluted and degraded ecosystems.

Stepping into an unusual era of concurrent buffer leads to a shifting global climate. At the beginning of the twenty-first century, one of the active concerns in the human ecological background is the destruction of ecology and ecosystems. Human actions have evolved a remarkable power to affect the ecosystem. To address this developing issue, the science of restoration ecology and its applied practices provide a potentially cost-effective, buoyant answer. The notion of restoration has emerged as the dominant subject in the global environmental context. One of the most important goals of the UN Convention on Biological Diversity from 2011 to 2020 is to restore at least 15% of the world's damaged ecosystems. World leaders adopted the “Bonn Challenge” in 2011, which is a global commitment to rehabilitate 150 million hectares of deforested and damaged land by 2020. Most significantly, in 2015, the UN formalized these worldwide pledges by endorsing the 2030 Sustainable Development Goals, one of which focuses on ecological restoration. Microbes are ubiquitous, providing many critical services to the ecosystem, such as sustainable plant productivity and a stable environment for human life. They help to keep atmospheric CO_2 and nitrogen levels stable, which are now reduced due to greenhouse gases and other hazardous pollutants. On a global scale, microbial organisms are extremely strong. Bacteria create approximately 50% of total oxygen, 75% of added nitrogen to the atmosphere, and 92% of nitrogen removal from the environment. As a result, this book covers the potential of bacteria and microbiomes in many ecosystems.

In Chapter 1, Prasad *et al.* provide an overview of the causes of ecosystem destruction, the need for ecosystem restoration, the significance of microbiome in biomining, restoration of farm and degraded land, control of heavy metals, production of renewable energy, crop growth, biofertilizer production, mitigation of greenhouse gases, and waste management. It also encompasses the role of molecular techniques in ecosystem restoration and the challenges involved in adopting microbiomes for ecosystem restoration.

Microbes are the crucial living elements of soils that contribute to the sustainability of ecosystems because of their capacity for stress tolerance, vast effective genetic pool, ability to survive in various conditions, and capacity for catabolism. However, various factors like soil conditions, geographical and climatic factors, and soil stressors (drought, submersion, pollutants, and salinity) may result in distinct microbial composition and characteristics, as well as its mechanism to support ecosystem restoration and defense against all of these stressors. Hence, Pooja *et al.*, in Chapter 2, deliver the vital edaphic (pH, temperature, oxygen, nutrients, and moisture), geographical, climatic (UV radiation, elevated CO_2, temperature, permafrost thaw), and abiotic factors (drought, submergence, salinity, pollutants) involved in the establishment of microbes and microbiome.

In Chapter 3, Sinduja *et al.* discuss the ecological role of microorganisms participating in biogeochemical cycles, hoping to delineate the role of microbes and microbiomes in biogeochemical cycles. Microorganisms play an essential role in moderating the Earth's biogeochemical cycles; nevertheless, despite our fast-increasing ability to investigate highly complex microbial communities and ecosystem processes, they remain unknown. Hence, this chapter covers the strategies for proper management of prevailing natural resources, considerations for management, its role in the biogeochemical cycle, and the influence of beneficial soil microbes, such as plant growth promoting rhizobacteria and cyanobacteria, on natural resource management, with special emphasis on the role of soil enzymes in nutrient cycling.

Bioleaching (microbial leaching) is being studied intensively for metal extraction since it is a cost-effective and environmentally benign technique. Bioleaching with acidophiles involves the production of ferric (Fe III) and sulfuric acid. Cyanogenic microorganisms, in particular, can extract metal(s) by creating hydrogen cyanide. Besides, bioremediation is one of the most effective approaches for reducing environmental contaminants since it restores the damaged site to its original state. Hence, Chapter 4 by Poornima *et al.* provides a baseline on bioleaching, its types, microbes involved in bioleaching, bioleaching pathways, and the role of microbes in the bioremediation of polluted habitats.

In recent years, microbial-assisted bioremediation has emerged as a promising and eco-friendly alternative for HM remediation. This approach utilizes microorganisms to transform, immobilize, or detoxify HMs, making them less harmful and more accessible for removal. Hence, Naik *et al.*, in Chapter 5, highlight the eco-friendly use of microorganisms, their mechanisms that contribute to the bioremediation of HMs, and their potential use in the future.

In Chapter 6, Sajish *et al.* present the basic principle of an MFC and the role of microbes in a microbial fuel cell, genetic engineering, biofilm engineering approaches, and electrode engineering approaches for increasing the overall efficiency of an MFC for its practical implementation. Microbial fuel cell, a type of BES, is a budding technology that exploits the potential of electroactive microorganisms for extracellular electron transfer to generate electricity. Hence, this chapter encompasses the history of MFC, bio-electrochemically active microorganisms, electroactive microbial genera in microbial fuel cells, factors affecting the development of anode biofilm, biofilm engineering, and the recent advances in strain improvement for improved MFC performance.

Energy crises resulting from the depletion of petroleum resources, hikes in the price of fossil fuel, and unpredictable climate change are some of the recent concerns that have provoked serious research on alternative energy sources that will be sustainable. In this regard, biofuels are a straightforward substitute for fossil fuels. Renewable feedstocks are suitable ingredients that sustainably produce biofuels using microbial-based bioconversion processes. Industrially important enzymes are capable of degrading long-chained biopolymers into short-chained monomeric sugars and fermenting them into energy-dense biomolecules. Hence, Chapter 7, authored by Oyelade *et al.*, comprehensively reviews how sustainable bioenergy production through microbes using feedstocks can provide clean and green energy that can consequently facilitate ecosystem restoration. Feedstocks are pivotal to this biotechnological process.

In recent decades, biofertilizers have gained popularity as a viable alternative to unsafe chemical fertilizers in pursuing sustainable agriculture. They have an essential role in enhancing crop output and preserving long-term soil fertility, both of which are critical for fulfilling global food demand. Therefore, Chavada *et al.*, in Chapter 8, deliver the various microbes involved in nitrogen fixing, phosphorus and potassium solubilizing and mobilizing, sulfur oxidizing, and zinc solubilizing. The role of arbuscular fungi and plant growth-promoting rhizobacteria in biofertilizer production is also discussed.

Knowingly or unknowingly, agricultural systems face stress and resource quality degradation and their depletion by the activities of humans. Abiotic stresses, such as nutrient deficiency, water logging, extreme cold, frost, heat, and drought, affect agricultural productivity. Similarly, biotic factors like insects, weeds, herbivores, pathogens, bacteria, viruses, fungi, parasites, algae, and other microbes also limit good-quality products. Thus, Vijayalakshmi *et al.* discuss the application of microbes and microbiomes in biotic and abiotic stress management in Chapter 9. This chapter especially discusses the adaptive mechanisms of salt tolerance in plants, tolerance to abiotic stress, the emerging microbiome in soil biota, and nanomaterials' efficacy on stress.

Microbes play a significant role as either generators or consumers of greenhouse gases such as carbon dioxide (CO_2), methane (CH_4), and nitrous oxide (N_2O) through various processes. Sethupathi *et al.*, in Chapter 10, discuss the role of microbes and microbiomes in the emission of major greenhouse gases like CO_2, CH_4, N_2O, and NH_3. The potential of the microbiome in mitigating these greenhouse gases is also delivered in this chapter.

Given that there is potential for warmth to boost the release of carbon dioxide from dirt to the atmosphere due to better microbial disintegration of dirt raw material, the impact of environmental change on the soil carbon sink remains uncertain. If forecasted climate modification situations are precise, this boost in soil carbon loss might significantly worsen the dirt carbon cycle responses. Therefore, Chapter 11 by Al-Jawhari introduces us to the soil CO2 balance, environmental effects, and the significance of the soil carbon cycle and microbial decomposers, carbon cycle in soil, ocean, and ecosystem restoration under climate change perspective.

The generation of wastewater increases multi-fold because of industries and the overexploitation of freshwater resources. Wastewater treatment is always linked with waste recovery and its optimum utilization, which broadens the amplitude of wastewater treatment, enhancing the quality of the byproducts and as an efficient alternative for non-potable purposes. Microbiomes are crucial in biological wastewater treatment methods such as activated sludge, anaerobic digestion, and bioelectrochemical systems. The microbial population's activity and resilience in the microbiome significantly impact the performance and stability of these activities. Suganthi *et al.* present the biological wastewater treatment, growth and kinetics, and different microbial community types, including bacteria and fungus, actinomycetes, algae, plants, and the range of microbial wastewater treatment in Chapter 12.

Solid waste disposal is a significant issue that worsens daily as more people move into cities. In Chapter 13, Velusamy *et al.* provide the status of solid waste management in India, sources and types of solid wastes, various conventional solid waste management techniques, and the role of microbes in solid waste management through composting and anaerobic digestion.

Microorganisms are pervasive and genuinely make up the “unseen majority” in the marine environment. Although marine isolates have been the subject of laboratory-based culture methods for more than ten years, we still do not completely understand the ecology of marine microorganisms. Thus, in Chapter 14, Poornachandhra *et al.* explore marine microbial diversity, its utilization in bioremediation, and understanding their role in ecosystem sustainability.

Mangroves and wetlands are critical intermediary ecosystems between terrestrial and marine environments. These ecosystems offer a wide range of invaluable ecological and economic services. However, under the influence of natural and anthropogenic threats, mangroves and wetlands face rapid degradation. Hence, Chapter 15 by Haghani *et al.* is dedicated to enlightening us regarding the most critical features of microbial groups, including archaea, bacteria, algae, and fungi in mangroves and wetlands. Moreover, the biochemical transformations brought about by wetlands' microbial groups and the degree of complexity in microbial interactions are explained.

Jerome *et al.*, in Chapter 16, articulate the significance of forest microbiomes in ecosystem restoration and sustainability. Generally, forest microorganisms are essential to how plants interact with the soil environment and are necessary to access critically limiting soil resources. This chapter focuses on the ecosystems below and above ground level of a forest microbiome, including the soil microorganisms, their importance, and the diverse interrelationships among soil microorganisms (parasitism, mutualism, commensalism).

Employing field-based monitoring and restoration assessment techniques, surveying microbes or microbial populations is challenging or impossible. In contrast, it is now possible to precisely and quickly describe and quantify these diverse and functional taxonomic groups by sequencing large quantities of environmental DNA or RNA utilizing genomic and, in particular, meta-omic technologies. Hence, Nagendran *et al.*, in Chapter 17, throw light on using meta-omics techniques to monitor and assess the outcomes of ecological restoration projects and to monitor and evaluate interactions between the various organisms that make up these networks, such as metabolic network mapping. An overview of functional gene editing with CRISPR/Cas technology to improve microbial bioremediation is also provided herewith.

Chapter 18 by Satpathy *et al.* provides details on metagenomic approaches like Multi-Locus Sequence Typing (MLST), MOTHUR, Quantitative Insight into Microbial Ecology (QIIME), and PHAge Communities From Contig Spectrum (PHACCS) in the restoration of the temperate and tropical ecosystem.

Soil microorganisms also play a fundamental role in ecosystem functioning and conserving plant diversity. Exploring voluminous beneficial microorganisms and promoting the reestablishing of those beneficial microbes in the soil will preserve Earth's diverse native plant populations. Hence, Prasad *et al.*, in Chapter 19, delve into fundamental and conventional techniques and approaches that can be employed to maintain soil microbial populations. Furthermore, the chapter investigates the possibility of creating protocols for regulatory or commercial objectives, emphasizing the significance of ecological restoration by using bioinoculants or microbial colonies in degraded sites.

In Chapter 20, Shivakumar *et al.* examine the application of molecular methods to ecosystem regeneration. The various available molecular methods and how they have been applied to monitor ecosystem health, identify microbial communities in ecosystems, and comprehend interactions between microbes and plants are discussed. The chapter also discusses the application of molecular methods to the restoration of ecosystems that have been damaged, including the use of plant-microbe interactions to promote plant development in contaminated soils.

The sustainable industrial revolution is the way forward to help humankind to prolong its existence on Earth. John *et al.* enlighten us with the role of the microbiome in a sustainable industrial production system. In Chapter 21, they disclose the energy sector's current status, microbes' role in organic and amino acid production, and the role of microalgae in sustainable agriculture.

The human microbiome plays a vital role in human development, immunity, and nutrition, where beneficial bacteria establish themselves as colonizers rather than destructive invaders. In Chapter 22, Pradyutha *et al.* introduce microbes' role in human and animal health security. The various human and animal diseases and the potential of microbiota, such as probiotics, in disease treatment are also discussed in this chapter.

Shiv Prasad & Govindaraj Kamalam Dinesh
Division of Environment Science, ICAR-Indian Agricultural
Research Institute, New Delhi-110012, India

Murugaiyan Sinduja
National Agro Foundation, Taramani
Chennai, Tamil Nadu, India

Sathya Velusamy
Tamil Nadu Pollution Control Board
Chennai, Tamil Nadu, India

&

Ramesh Poornima & Sangilidurai Karthika
Department of Environmental Sciences
Tamil Nadu Agricultural University
Coimbatore, India

List of Contributors

A. Manikandan	Institute of Ecology and Earth Sciences, University of Tartu, Tartu, Estonia
A. Ch. Pradyutha	Department of Microbiology, Raja Bahadur Venkata Rama Reddy Women's College, Narayanguda, Hyderabad, Telangana, India
B.N. Brunda	Division of Microbiology, Indian Agricultural Research Institute, New Delhi, India
Boopathi Gopalakrishnan	School of Atmospheric Stress Management, ICAR-National Institute of Abiotic Stress Management, Maharashtra, India
Chidambaram Poornachandhra	Department of Environmental Sciences, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India
C. Poornachandhra	Department of Environmental Sciences, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India
Chidamparam Poornachandhra	Department of Environmental Sciences, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India
Deepasri Mohan	Division of Environmental Sciences, Sher-e-Kashmir University of Agricultural Sciences & Technology of Jammu, Jammu and Kashmir, India
E. Akila	Department of Agricultural Engineering, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India
Govindaraj Kamalam Dinesh	Division of Environment Science, ICAR-Indian Agricultural Research Institute, New Delhi-110012, India Division of Environmental Sciences, Department of Soil Science and Agricultural Chemistry, SRM College of Agricultural Sciences, SRM Institute of Science and Technology, Baburayanpettai-603201, Chengalpattu, Tamil Nadu, India INTI International University, Persiaran Perdana BBN, Putra Nilai, 71800 Negeri Sembilan, Malaysia
Ganesan Karthikeyan	Department of Environmental Sciences, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India
Helen Mary Rose	Division of Environment Science, ICAR-IARI, New Delhi, India
Ihsan Flayyih Hasan AI-Jawhari	Department of Biology, College of Education for Pure Sciences, University of Thi-Qar, Iraq
Ihuma O. Jerome	Department of Biological Science, Faculty of Science and Technology, Bingham University, Karu Nasarawa State, Nigeria
J.O. Ihuma	Department of Biological Science, Faculty of Science and Technology, Bingham University, Karu Nasarawa State, Nigeria
J. Sampath	Department of Environmental Sciences, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India
Joseph Ezra John	Department of Environmental Sciences, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India
K. Mathiyarasi	Division of Environment Science, Indian Agriculture Research Institute, New Delhi, India

Karthika Ponnusamy	Department of Microbiology, College of Basic Science & Humanities, Chaudhary Charan Singh Haryana Agricultural University, Haryana, India
Kovilpillai Boomiraj	Climate Research Centre, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India
Kamyar Amirhosseini	Department of Soil Science, Faculty of Agriculture, College of Agriculture and Natural Resources, University of Tehran, Tehran, Iran
Murugaiyan Sinduja	National Agro Foundation, Taramani, Chennai, Tamil Nadu-600113, India
Murugesan Kokila	Division of Environment Science, ICAR-IARI, New Delhi, India
Muthusamy Shankar	Division of Plant Genetic Resources, ICAR-Indian Agricultural Research Institute, New Delhi, India
M. Sinduja	National Agro-foundation Research & Development Centre, Chennai, India
Muthusamy Shankar	Division of Plant Genetic Resources, ICAR-Indian Agricultural Research Institute, New Delhi, India
Malgwi T. Doris	Department of Community Medicine, Nnamdi Azikiwe University, Nnewi, Anambra State, Nigeria
Murugaiyan Sinduja	Department of Environmental Sciences, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India
O.V. Oyelade	Department of Physics, Faculty of Science and Technology, Bingham University, Karu Nasarawa State, Nigeria
P.M. Brindhavani	Adhiyamman College of Agriculture and Research, Krishnagiri, Tamil Nadu-635105, India
Periyasamy Dhevagi	Department of Environmental Sciences, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India
R. Kalpana	National Agro Foundation, Research & Development Centre, Anna University Taramani Campus, Taramani, Chennai, Tamil Nadu, India
Ragul Subramaniyan	Plant Variety Examination Research Associate (PVERA), Protection of Plant Varieties & Farmers' Rights Authority, New Delhi, India
Ramesh Poornima	Department of Environmental Sciences, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India
Ravi Raveena	Department of Environmental Sciences, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India
R. Kaveena	Swamy Vivekananda College of Pharmacy, Tiruchengode, India
R. Raveena	Department of Environmental Sciences, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India
Ravi Raveena	Department of Environmental Sciences, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India
Sathya Velusamy	Tamil Nadu Pollution Control Board, Chennai, Tamil Nadu, India
Sangilidurai Karthika	Department of Environmental Sciences, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India
Selvaraj Keerthana	Department of Environmental Sciences, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India

Sagia Sajish	Division of Microbiology, Indian Agricultural Research Institute, New Delhi, India
Sethupathi Nedumaran	Division of Environment Science, ICAR-IARI, New Delhi, India
Sudhakaran Mani	Department of Environmental Scienc, JKK Munirajah College of Agricultural Science, Namakkal, India
S. Akila	National Agro-foundation Research & Development Centre, Chennai, India
Senthamizh Selvi	Department of Agricultural Microbiology, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India
S. Chaitanya Kumari	Department of Microbiology, Bhavan's Vivekananda College of Science, Humanities & Commerce, Sainikpuri, Secunderabad, Telangana, India
Thangaraj Gokul Kannan	Department of Environmental Sciences, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India
T. Gokul Kannan	Department of Environmental Sciences, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India
Tayo I. Famojuro	Department of Pharmacognosy, Faculty of Pharmaceutical Sciences, Bingham University, Karu Nasarawa State, Nigeria
Zahra Haghani	Department of Soil Science, Faculty of Agriculture, College of Agriculture and Natural Resources, University of Tehran, Tehran, Iran

Significance of Microbiome in Natural Resource Management

CHAPTER 1

Role of Microbes and Microbiomes in Natural Resource Management and the Regulation of Biogeochemical Processes and Nutrient Cycling

Murugaiyan Sinduja[1,*], P.M. Brindhavani[2], Govindaraj Kamalam Dinesh[3,4,5], Joseph Ezra John[6], K. Mathiyarasi[7], Sathya Velusamy[8], R. Kalpana[9] and **Ragul Subramaniyan[10]**

[1] *National Agro Foundation, Taramani, Chennai, Tamil Nadu-600113, India*

[2] *Adhiyamman College of Agriculture and Research, Krishnagiri, Tamil Nadu-635105, India*

[3] *Division of Environment Science, ICAR-Indian Agricultural Research Institute, New Delhi-110012, India*

[4] *Division of Environmental Sciences, Department of Soil Science and Agricultural Chemistry, SRM College of Agricultural Sciences, SRM Institute of Science and Technology, Baburayanpettai-603201, Chengalpattu, Tamil Nadu, India*

[5] *INTI International University, Persiaran Perdana BBN, Putra Nilai, 71800 Negeri Sembilan, Malaysia*

[6] *Department of Environmental Sciences, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India*

[7] *Division of Environment Science, Indian Agriculture Research Institute, New Delhi, India*

[8] *Tamil Nadu Pollution Control Board, Chennai, Tamil Nadu, India*

[9] *National Agro Foundation, Research & Development Centre, Anna University Taramani Campus, Taramani, Chennai, Tamil Nadu, India*

[10] *Plant Variety Examination Research Associate (PVERA), Protection of Plant Varieties & Farmers' Rights Authority, New Delhi, India*

Abstract: Life on Earth is possible due to the vital elements and energy transformations referred as biogeochemical cycle. Microorganisms play an essential role in moderating the Earth's biogeochemical cycles; nevertheless, despite our fast-increasing ability to investigate highly complex microbial communities and ecosystem processes, they remain unknown. Microbes are crucial in nutrient cycling and energy transfers between ecosystems and the tropics, but research on their intricate functions is still restricted due to technological inabilities. A better understanding of microbial communities based on ecological principles may improve our ability to predict ecosystem process rates using environmental variables and microbial physiology. We

---

[*] **Corresponding author Murugaiyan Sinduja:** National Agro Foundation, Taramani, Chennai, Tamil Nadu-600113, India; E-mail: seethasinduja@gmail.com

Shiv Prasad, Govindaraj Kamalam Dinesh, Murugaiyan Sinduja, Sathya Velusamy, Ramesh Poornima & Sangilidurai Karthika (Eds.)

explored the ecological role of microorganisms participating in biogeochemical cycles, hoping to delineate the role of microbes and microbiomes in biogeochemical cycles. Insights into these aspects can help us mitigate the effects of climate change and other future uncertainties by regulating the microbial-dependent biogeochemical cycle.

Keywords: Environment, Biogeochemical cycling, Microorganisms, Climate change, Ecosystems.

INTRODUCTION

In natural resource management, microorganisms play a prominent role in the biogeochemical cycling of nutrients. Microbiomes have demonstrable effects on the chemical makeup of the biosphere and its surrounding atmosphere, and they are deservedly recognized for their capacity to fix carbon and nitrogen into organic matter. Acclimatization typically begins with a higher commitment to obtaining and mobilizing stored resources when some factors become restricted [1]. The biogeochemical cycling of nutrients relies heavily on microbes. They are lauded for their ability to fix carbon and nitrogen into organic matter, and microbial-driven processes have visibly altered the chemical composition of the biosphere and its surrounding atmosphere [2]. Because soil quality is constantly deteriorating, a healthy soil system is now the outcome of physical, chemical, and biological soil quality indicators that are connected in a complicated network. The interests of the community and the needs of farmers are balanced by healthy soils. By preventing toxic compounds from being released into the environment, squelching infections, and preserving environmental sustainability, soil organic matter (SOM) improves soil health and quality [3]. In order to produce food sustainably, it refers to interactions between internal and exterior soil components. Effective soil microorganisms are essential for the establishment of the soil-plan--microbe interaction because they stimulate numerous biological processes and different pools of carbon (C) and macro- and micronutrients. The soil system has an enormous variety of microorganisms [4].

This chapter emphasizes the role of microbes and microbiomes in natural resource management by regulating biogeochemical processes and nutrient cycling. Although global understanding of microbes and microbiome dynamics is quickly rising, research on rhizospheric complexes is restricted despite their relevance in regulating soil-plant systems. Microorganisms in the soil consume organic matter, including dead organisms, and play an essential role in organic matter breakdown and nutrient cycle [5]. The nutrients are released by the breakdown of the organic molecule, allowing plants to absorb nutrients from the soil *via* their roots. Biogeochemical cycles transport nutrients throughout the ecosystem [6]. An ecosystem's biotic (living) and abiotic (non-living) components can exchange chemical elements like carbon or nitrogen in a process known as a biogeochemical cycle [7]. The elements that move through an ecosystem's processes are not wasted; rather, they are recycled or saved in reservoirs (sometimes referred to as “sinks”), where they can be kept for a long time. These biogeochemical cycles transfer substances from one organism to another and from one region of the biosphere to another, including elements, chemical compounds, and other kinds of matter. Ecosystems have a variety of biogeochemical cycles as part of the overall system [8]. A great example of a molecule cycled within an ecosystem is water, which is constantly recycled through the water cycle. Water vapor rises into the atmosphere, cools, and then eventually returns to Earth as rain (or other types of precipitation). Cycling is typical of all significant aspects of life.

Microorganisms are crucial in the biogeochemical cycling of nutrients. Microorganisms are weak despite the elements' immutability and their vast capability for molecular alterations [9]. This paper discusses the effects of elemental limitation on microorganisms with an emphasis on certain genetic model systems and representative bacteria from the ocean ecosystem. Studies on the genome and proteome reveal evolutionary adaptations that enhance growth in response to ongoing or recurrent elemental constraints [10]. Changes in protein amino acid sequences that considerably lower cellular carbon, nitrogen, or sulfur requirements are among them. These modifications range from dramatic (such as eliminating a requirement for a hard-to-find component) to quite modest. Acclimatization typically begins with a stronger commitment to obtaining and mobilizing stored resources when some factors become restrictive. The cell turns to austerity tactics like elemental recycling and sparing if elemental limitation continues. Research in the fields of ecology, biological oceanography, biogeochemistry, molecular genetics, genomics, and microbial physiology has shed new light on these essential cellular features [11]. This chapter also highlights many research studies findings that are devoted to the conservation of natural resources, global food security, and sustainable agriculture [12].

NATURAL RESOURCE MANAGEMENT – NEED OF THE HOUR

Natural resources are the elixir for living organisms, as human life's existence is highly dependent on the ecosystem and the services it provides to humankind. These natural resources include air, water, land, minerals, flora, fauna, *etc* [13]. They provide the fundamental backing to life by providing goods for sustenance and consumption. Natural resource management (NRM) is the efficient and sustained usage of these valuable resources, which otherwise would lead to depletion or reduction in their existence [14]. Increased human population and scientific developments in the recent decade have led to increased interaction between humans and the environment, eventually leading to increased usage of

CHAPTER 2

Role of Microbes and Microbiomes in Bioleaching and Bioremediation for Polluted Ecosystem Restoration

Ramesh Poornima[1,*], **Chidambaram Poornachandhra**[1], **Ganesan Karthikeyan**[1], **Thangaraj Gokul Kannan**[1], **Sangilidurai Karthika**[1], **Selvaraj Keerthana**[1] and **Periyasamy Dhevagi**[1]

[1] *Department of Environmental Sciences, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India*

Abstract: In an environmental degradation era, improving microbial activity in sustainable mining and pollutant removal has become necessary for the green economy's future. Bioleaching (microbial leaching) is being studied intensively for metal extraction since it is a cost-effective and environmentally benign technique. Bioleaching with acidophiles involves the production of ferric (Fe III) and sulfuric acid. Cyanogenic microorganisms, in particular, can extract metal(s) by creating hydrogen cyanide. Furthermore, environmental degradation and its rehabilitation are serious issues worldwide. Hydrocarbons, pesticides, heavy metals, dyes, and other contaminants are the principal factors significantly degrading the environment. Residual pollutants might also be challenging to remove. Bioremediation is one of the most effective approaches for reducing environmental contaminants since it restores the damaged site to its original state. So yet, only a tiny number of microorganisms (culturable bacteria) have been used, leaving a vast amount of microbial diversity undiscovered. Various bioremediation approaches, such as chemotaxis, bioaugmentation, biostimulation, genetically engineered microbes, biofilm formation, and advanced omics, have been widely used to improve the microbe's metabolic activity, degradation potential of persistent pollutants and restoration of polluted habitats. Microorganisms contribute to the rehabilitation of polluted ecosystems by cleaning up trash in an ecologically friendly way and producing harmless products. This chapter addresses the critical processes in improving bioremediation and current breakthroughs in bioremediation, including bacteria and plants.

Keywords: Bioleaching, microbes, mechanism, bioremediation, heavy metals, organic pollutants.

---

[*] **Corresponding author Ramesh Poornima:** Department of Environmental Sciences, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India; E-mail: poornimaramesh93@gmail.com

Shiv Prasad, Govindaraj Kamalam Dinesh, Murugaiyan Sinduja, Sathya Velusamy, Ramesh Poornima & Sangilidurai Karthika (Eds.)

INTRODUCTION

Earth’s crust withholds minerals that contain naturally occurring metals in its sulphide, oxide, and carbonate form. The metal-containing minerals are known as “ore”. The desired metals were excavated from the ores and purified by a technique called “mineral processing”. Pyrometallurgy and hydrometallurgy are the most used conventional methods in mineral processing. The former method utilizes heat to provoke chemical reactions to extract metals from the ores, which involves high cost and emission of greenhouse gases during the process. Hydrometallurgy utilizes an enormous quantity of water, which is a rising concern in today’s scenario. Also, this method extracts only water-soluble metals, leaving behind the insoluble ones. Each method has its downsides, making researchers and scientists explore a more economical and eco-friendly way to leach the desired metals from their ores. This led them to discover the application of microorganisms in metal leaching. The conversion of insoluble metals to their soluble form with the help of microbes is termed “bioleaching”.

The parallel term “biomining” refers to using bacteria or fungi to mobilize the metals from their solid state. A bioleaching or biomining method involves using bacteria to change insoluble metal oxides and sulfides into solvent particles that can then be recovered with the help of hydrometallurgy. This combined process is called “biohydrometallurgy” [1]. This solubilization and mobilization of metals occur through different processes like oxidation, complexation, and acidification exhibited by microorganisms. These biotechnological processes involving the interaction between microorganisms and the ores are described by the term “biometallurgy”. Biomining is chiefly adapted for metals, such as cobalt, copper, uranium, gold, zinc, and nickel. All metals except uranium were extracted from insoluble sulfides, while uranium was from oxides [2].

The recent findings in the biometallurgy process could lead to more inventive options than conventional metal extraction techniques. Various microorganisms have now been documented to play an important role in the geochemical cycles involving the formation, sedimentation, and degradation of minerals. With the help of these microbes, pure metals can be separated from the metal-ore network. When these microbes are grown in the presence of minerals for a prolonged time, they develop resistance and produce bioreagents [3]. The genetic data from these microbes could be utilized to develop genetically engineered microbiomes for specific purposes. Unlike the chemical extraction method, bioleaching was utilized to extract metals from poor-quality ores and tailings for a long time at mechanical scales. They also encourage profitable metal recovery, even from metal-containing wastes [4]. The biotechnological processes by microorganisms in metal extraction can change uneconomical ore stores into economically viable resources.

Microbes are essential in the bioremediation of contaminated ecosystems due to their potential significance in biomining. Bioremediation is a technology that promotes natural environment restoration by eliminating contaminants and avoiding additional contamination. Bioremediation is more environmentally friendly and cost-effective than alternative remediation processes such as chemical and physical. Bioremediation can reduce pollutant toxicity, which uses the metabolic capacity of microorganisms to convert, mineralize, and immobilize hazardous compounds into less toxic forms. Microbes have yet to be shown to degrade some xenobiotic substances, such as strongly halogenated and nitrated aromatic compounds and a few insecticides [5]. The efficiency of microorganisms, on the other hand, is based on several factors, including concentration, the chemical type of pollutants, availability, and the physiological properties of the environment.

Consequently, the factors influencing microorganism degradation potential are nutritional needs or environmental circumstances. Furthermore, bioremediation is classified into two forms depending on removing harmful chemicals and their transportation methods: *in situ* and *ex situ*. Hence, the chapter unravels the potential role of microbes and microbiomes in biomining and bioremediation.

ROLE OF MICROBES IN BIOLEACHING

Bioleaching is a mineral and metal extraction technique from the parent ore utilizing biological procedures. This process depends on the interaction of microbes, unlike any conventional techniques which utilize ecologically harmful chemicals. Bioleaching can also be used to extract metals and minerals from low-grade ores. Microbes get energy for their growth from minerals, which is slower than the other methods. However, bioleaching is considered a green innovation that become considerably more essential in future years, as it is cost-effective [6]. Bioleaching is also called transforming solid/insoluble metal into water-soluble forms using microbes. For example, copper present as sulfide is oxidized by microbes to water-soluble copper sulfate while the remaining residue is disposed of. The microbiological oxidation of host minerals containing metal complexes of interest is depicted in bio-oxidation. Biohydrometallurgy encompasses bioleaching and biomining. Biohydrometallurgy is an interdisciplinary field combining elements of geoscience, biotechnology, mineralogy, microbiology, mining engineering, and hydrometallurgy. The treatment of metals and metal-containing materials by wet methods is referred to as hydrometallurgy, and it por-

Role of Microbes in the Production of Renewable Energy

CHAPTER 3

Role of Microbes and Microbiomes in Microbial Fuel Cells: A Novel Tool for a Clean and Green Environment

Sagia Sajish[1,*], **Karthika Ponnusamy**[2] and **B.N. Brunda**[1]

[1] *Division of Microbiology, Indian Agricultural Research Institute, New Delhi, India*

[2] *Department of Microbiology, College of Basic Science & Humanities, Chaudhary Charan Singh Haryana Agricultural University, Haryana, India*

Abstract: Over the recent decades, there has been a tremendous need to develop alternative, sustainable, clean, and renewable energy resources. This demand is attributed to the exhaustion of fossil fuel reserves and the associated economic risks, the impact of fossil fuel use on the environment, and the associated global warming. Bioelectrochemical systems (BES), which use biological entities to generate electricity, are promising alternative clean renewable energy. Microbial fuel cell (MFC), a type of BES, exploits the potential of electro-active microorganisms for extracellular electron transfer to generate electricity. In an MFC, microbes oxidize the organic substrates fed into the anode chamber into electrons, protons, and CO_2. The electrons flow through the connected external load/circuit towards the cathode, creating the potential difference across the electrode and subsequent current output. A terminal electron acceptor at the cathode accepts the electrons and protons. In addition to electricity generation, MFC has extended applications in wastewater treatment, heavy metal remediation, bioremediation of environmental pollutants, biosensors for monitoring the environment, *etc*. This chapter will help understand the basic principle of an MFC and the role of microbes in a microbial fuel cell, genetic engineering, biofilm engineering approaches, and electrode engineering approaches for increasing the overall efficiency of an MFC for its practical implementation.

Keywords: Bioelectrochemical systems, bioremediation, biosensors, climate change, electroactive microorganisms, microbial fuel cells, wastewater treatment.

INTRODUCTION

The depletion of fossil fuel reserves is considered to be the major driver of unsustainability, which puts us and our future generations at risk of environmental

---

[*] **Corresponding author Sagia Sajish:** Division of Microbiology, Indian Agricultural Research Institute, New Delhi, India; E-mail: sagiagri001@gmail.com

Shiv Prasad, Govindaraj Kamalam Dinesh, Murugaiyan Sinduja, Sathya Velusamy, Ramesh Poornima & Sangilidurai Karthika (Eds.)

and economic security. However, extraction and use of fossil fuels for energy pose environmental risks with higher greenhouse gas emissions and associated global warming. Therefore, the global energy crisis, exhaustion of fossil fuel reserves, global warming, and the associated climate change have necessitated the search for alternative, sustainable, clean, and renewable energy sources [1]. The quest for such a clean and renewable energy source has been augmented in recent decades with promising results. Research and developments have been made in renewable energy sources like solar energy, wind power, geothermal energy, conversion of biomass to energy, *etc*.

According to the Renewables 2022 report by the International Energy Agency (IEA), global renewable energy capacity is estimated to surge by 70% (2400 GW) between the 2022 and 2027 forecast period. This is an 85% increase from the last five years' rate, which is mainly attributed to fossil fuel reserves depletion and the global energy crisis, making renewable energy resources an economically/environmentally viable energy resource [2]. However, no such individual renewable energy can compete and replace the use of fossil fuels currently; the combination of these sources is an alternative area to be investigated [3]. One such promising technology is the bioelectrochemical system. The bioelectrochemical system combines biochemical pathways (biological metabolism) and electrochemical techniques to generate electricity.

Bioelectrochemical systems (BES) are of two types: Microbial fuel cells (MFC) and microbial electrolysis cells (MEC). In microbial fuel cells, electroactive microorganisms convert chemical energy stored in organic/inorganic substrates into electrical energy. In Microbial Electrolysis Cell, biomass produces hydrogen using an applied external potential. A classic MFC comprises an anode and a cathode isolated by a proton exchange membrane, which prevents oxygen diffusion from the cathode to the anode, allowing only protons (H^+) to pass through it. In an anodic chamber, the microbial consortia oxidize the substrates (e.g., Glucose) [4]. Microbial fuel cells from various sources can be used with complex substrates like lignocellulosic biomass [5] and wastewater [6].

Thus, MFC is a reliable technology for waste to electricity production and subsequent decrease in the total amount of carbon dioxide liberated into the atmosphere compared to fossil fuels. Apart from bioelectricity generation, microbial fuel cells are also used in wastewater treatment, bioremediation of pollutants, recovery of heavy metals, desalination process, as a biosensor, *etc*. The ability to use various substrates and ambient operating conditions makes it more promising than conventional wastewater treatment methods and bioremediation. This chapter signifies the role of microbial fuel cells as a clean, renewable, and sustainable energy source. Special emphasis has been given to the role of electroactive microorganisms in MFC and strategies for efficient biofilm development on the anode surface and future perspective.

MICROBIAL FUEL CELL - HISTORY AND FUNDAMENTALS

Luigi Galvani, who coined the term animal electricity by first discovering the movement of a dead frog's muscles upon the strike by an electrical pulse, is considered the first electrochemist [7]. The first successful fuel cell with a 5KW system (hydrogen-oxygen fuel cell) was developed in 1959 by Francis Bacon [8]. Since then, diverse types of fuel cells have been developed and are categorized according to the electrolyte used. Subsequently, all these developments paved the way for the development of Biological fuel cells (BFs), wherein biochemical pathways are used to perform redox reactions for electricity generation. Biological fuel cells are classified into two types- enzymatic fuel cells (EFCs) [9] and microbial fuel cells (MFCs) [4]. Enzymes are used in EFCs, and live microorganisms are used in MFCs. The electrochemical catalytic efficiency of enzymes is superior to that of microbes but is unstable and less durable in contrast to living microbes. The use of microorganisms (*Saccharomyces cerevisiae*) for the generation of electricity was first performed at the beginning of the twentieth century (1911) by M.C. Potter [10]. It was in 1931 when Branet Cohen constructed microbial fuel cells that produce 35 volts and 2mA current when connected in series [11]. The practical application of MFC was demonstrated by using a benthic MFC to power a meteorological buoy for remote monitoring [12].

Configuration of MFC

A typical microbial fuel cell (MFC) consists of an anodic and cathode chamber partitioned by a proton/cation exchange membrane. On the anode of MFC, the proliferating microorganisms use their metabolic pathways to tap the chemical energy stored in the organic substrates supplied in the anode chamber. The oxidation of organic matter in the anode generates electron proton and carbon dioxide. The electron produced in the anode flows through an external circuit connected to a resistor or a load towards the cathode, generating a potential difference across the electrodes. As an electron moves towards the cathode, by convention, current flows from the positive towards the negative terminal. A proton moves across the proton exchange membrane towards the cathode for each electron that moves through the circuit. Oxygen is commonly used as an oxidant in the cathode of MFC, which serves as the terminal electron acceptor for the incoming protons and electrons from the anode generating water. Metal oxidants like chromium, cadmium, and copper can also accept electrons [4].

Typically, MFCs operate as close systems wherein the anode is completely maintained in an anaerobic condition. Such a condition is made to sustain in the

CHAPTER 4

Sustainable Production of Bioenergy through Microbes for Ecosystem Restoration: A Clean and Green Energy Strategy

O.V. Oyelade[1,*], **J.O. Ihuma**[2], **Govindaraj Kamalam Dinesh**[3,4,5] and **Ravi Raveena**[6]

[1] *Department of Physics, Faculty of Science and Technology, Bingham University, Karu Nasarawa State, Nigeria*

[2] *Department of Biological Science, Faculty of Science and Technology, Bingham University, Karu Nasarawa State, Nigeria*

[3] *Division of Environment Science, ICAR-Indian Agricultural Research Institute, New Delhi-110012, India*

[4] *Division of Environmental Sciences, Department of Soil Science and Agricultural Chemistry, SRM College of Agricultural Sciences, SRM Institute of Science and Technology, Baburayanpettai-603201, Chengalpattu, Tamil Nadu, India*

[5] *INTI International University, Persiaran Perdana BBN, Putra Nilai, 71800 Negeri Sembilan, Malaysia*

[6] *Department of Environmental Sciences, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India*

Abstract: Energy crises resulting from the depletion of petroleum resources, hikes in the price of fossil fuel, and unpredictable climate change are some of the recent concerns that have provoked serious research on alternative energy sources that would be sustainable. This book chapter reviews how sustainable bioenergy production through microbes using feedstocks can provide clean and green energy that can consequently facilitate ecosystem restoration. Feedstocks are pivotal to this biotechnological process. Microbes are also equally very vital. Therefore, changing from fossil fuel to bioenergy resource options is essential. Energy transition can, therefore, create emerging opportunities in bioenergy rendering and bioeconomy that will result in the possible use of clean and green energy. In this regard, biofuels are a straightforward substitute for fossil fuels. Renewable feedstocks are suitable ingredients that sustainably produce biofuels using microbial-based bioconversion processes. Microorganisms can massively secrete industrially important enzymes capable of degrading long-chained biopolymers into short-chained monomeric sugars and fermenting them into energy-dense biomolecules. Microbes play a crucial role in

---

[*] **Corresponding author O.V. Oyelade:** Department of Physics, Faculty of Science and Technology, Bingham University, Karu Nasarawa State, Nigeria; E-mail: oyeladeov@binghamuni.edu.ng

Shiv Prasad, Govindaraj Kamalam Dinesh, Murugaiyan Sinduja, Sathya Velusamy, Ramesh Poornima & Sangilidurai Karthika (Eds.)

the sustainable generation of biofuels and bioenergy. Bioenergy research is, therefore, crucial for a nation's economic stability and energy security. Additionally, reducing greenhouse gas emissions while promoting the use of renewable energies and the creation of livelihoods aids in the worldwide effort. Anthropogenic activities are highly reduced, thereby enhancing ecosystem restoration.

Keywords: Biofuels, Bioenergy, Ecosystem, Feedstock, Energy, Microbes, Renewable.

INTRODUCTION

Global climate change and energy security are the two issues that affect all countries [1]. Energy consumption has surged as a result of rapid industrialization and accelerated population expansion globally [2]. The importance of generating renewable fuels as a substitute for conventional fossil fuels has become more crucial because of the significant decline in fossil fuel concentration and the growing global demand for energy. In order to address the escalating levels of greenhouse gases in the Earth's atmosphere, which have consequently led to substantial alterations in global climate patterns, these modifications can have disastrous effects, including temperature and sea level rise. Transportation and energy generation using fossil fuels account for twenty-five and fourteen percent of the total emissions of greenhouse gases, respectively [3]. For instance, because it is both economically viable and ecologically acceptable, bioenergy has the potential to both replace traditional fuels and relieve environmental concerns [4]. Resources from nature, such as vegetation, woody biomass, and other organic wastes, are used to create bioenergy.

It is now the most prevalent renewable energy, providing around twelve percent of the worldwide gross total consumption of energy. Bioenergy comes in many forms; solid biomass, sometimes referred to as solid biofuels, comprises wood (logs, chips, tree bark, and dust particles from wood shavings), crop residue (fruit peels, corn cobs, hay), solid waste materials (trash, rubbish, waste from food processing unit), and gaseous or liquid-biofuels (biogas and bioethanol), which can be used for industrial purposes, transportation fuels, cooking, heating, and electricity generation. One of the most common types of bioenergy is solid biomass. In many nations, particularly developing countries, it has traditionally been used for heating or cooking. Solid biofuels provide more than 80% of the energy needed in Africa, primarily for cooking, and 30% of Austria's overall energy needs for heating. Bioenergy has a promising future because only a fraction of its potential can be used at this point. Although biomass has been utilized for at least 30 years, it is still challenging to use responsibly [5].

Critical features to take into account for its effective use include

1. The raw materials' availability, quality, and cost

2. The technology for conversion

3. Sustainability, which includes land use modification, carbon dioxide exhaustion, and reforestation

The severe threat presented by the increased atmospheric deposition of greenhouse gases, which led to substantial climatic disruptions, can be lessened by using adaptive bacteria to develop sources of sustainable energy from feedstock and organic wastes. In line with Liao *et al*., due to the range of chemical reactions that different microbes are capable of, which allow for the production of biodiesel form a wide range of substrates, interest in using microorganisms to manufacture various biofuels has been gradually increasing in recent years [6].

Biofuel production is done using a variety of conversion techniques. Several microorganisms produce enzymes that are crucial to the synthesis of biofuels [7]. The microbial enzymes can more effectively break down feedstocks from different biomass materials and create various types of fuel sources like biodiesel and biogas. The organic waste materials from animals and plants are converted to biofuels by the microbial enzymes that use them as substrates. Biofuels are produced from the biomass of animals and feedstocks from crop residues, microbes, fungi, and algae through biological and chemical processes. It is possible to convert biological biomass employing a variety of microbial components, including extracellular enzymes [8]. These microorganisms serve as source materials and produce enzymes appropriate for converting biomass [9, 10]. Examples of biomass-to-biofuel conversion include the bacterial conversion of sugars into ethanol and plant-derived substrates by cellulolytic microorganisms. Methane can be utilized to make methanol, and microalgae and cyanobacteria can photosynthesize atmospheric carbon dioxide into biofuels [6]. When used in bio electrochemical techniques for the synthesis of biohydrogen and bioelectricity, *Geobacter sulfurreducens* and *Shewanella oneidensis* demonstrate particular “molecular machinery” that promotes the movement of ions from bacterial exterior membranes to surfaces that are conductive [11, 12].

BIOENERGY AS AN EMERGING OPPORTUNITY

Sunlight energy is converted to bioenergy in plants, which produce fuels or power that can replace nonrenewable energy sources. With appropriate planning and management, bioenergy can aid in the fight against global warming while providing various economic and environmental benefits to rural areas [13].

Microbiome in Mitigating Ghg Emission and Climate Change Impacts

CHAPTER 5

Role of Microbes and Microbiomes in GHG Emissions and Mitigation in Agricultural Ecosystem Restoration

Sethupathi Nedumaran[1,*], **Deepasri Mohan**[2], **Helen Mary Rose**[1], **Murugesan Kokila**[1], **Muthusamy Shankar**[3], **Selvaraj Keerthana**[4], **Ravi Raveena**[4], **Kovilpillai Boomiraj**[5] and **Sudhakaran Mani**[6]

[1] *Division of Environment Science, ICAR-IARI, New Delhi, India*

[2] *Division of Environmental Sciences, Sher-e-Kashmir University of Agricultural Sciences & Technology of Jammu, Jammu and Kashmir, India*

[3] *Division of Plant Genetic Resources, ICAR-Indian Agricultural Research Institute, New Delhi, India*

[4] *Department of Environmental Sciences, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India*

[5] *Climate Research Centre, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India*

[6] *Department of Environmental Science, JKK Munirajah College of Agricultural Science, Namakkal, India*

Abstract: Microbes are crucial for the survival of life on Earth as they affect the major biogeochemical cycles that make our planet congenial for life, providing essential elements like carbon and nitrogen in required forms and quantities. Microbes also play a significant role as either generators or consumers of greenhouse gases, such as carbon dioxide (CO_2), methane (CH_4), and nitrous oxide (N_2O), through various processes in our environment. The distribution of these chemicals on the Earth and in the atmosphere is severely reliant on the equilibrium of these microbial progressions. The consumption of GHGs by microbes is facilitated through their use as substrates in processes like photo/chemoautotrophy, methanotrophy, and nitrous oxide reduction. The CO_2 emitted from the organic matter decomposition and terrestrial respiration is subsequently subjected to photosynthetic fixation partially and is mitigated through carbon sequestration into soil and biomass. The biogenic release of methane through the biological anaerobic decomposition of organic materials by methanogens constitutes an important source of atmospheric CH_4 while methanotrophs, through CH_4 oxidation, facilitate methane emission mitigation. The microbial nitrification-denitrification processes are the significant source of N_2O emission, while the N_2O-reducing bacteria are responsible for decreasing N_2O emissions *via* nitrous oxide reduc-

---

[*] **Corresponding author Sethupathi Nedumaran:** Division of Environment Science, ICAR-IARI, New Delhi, India; E-mail: sethumartha@gmail.com

Shiv Prasad, Govindaraj Kamalam Dinesh, Murugaiyan Sinduja, Sathya Velusamy, Ramesh Poornima & Sangilidurai Karthika (Eds.)

tion enzymatic processes. The complexity of the interactions between these microbes with neighboring biotic and bacterial variables in order to regulate Earth's greenhouse gas emissions is a factor that affects their activity. Hence, interdisciplinary approaches, including microbial ecology, environmental genomics, soil and plant sciences, *etc*., should be concentrated on mitigating greenhouse gases.

Keywords: Climate change, CO_2, GHG, Microbes, Mitigation, Microbiomes.

INTRODUCTION

Climate change and global warming are extensively recognized as serious contemporary global issues for humanity. These global environmental issues are caused by increased anthropogenic emission of greenhouse gases (GHGs) in the atmosphere, which exerts a warming effect due to the enhanced greenhouse effect. The greenhouse effect refers to the traps of solar radiation in Earth's atmosphere, facilitated by the existence of greenhouse gases (GHGs) that include carbon dioxide (CO_2), water vapor, methane (CH_4), and nitrous oxide (N_2O) that let incoming solar radiation to pass through, but then absorb the heat sent from the surface of the Earth, thus increasing temperature across the world. It is evident from the IPCC's sixth assessment report (AR6) that the cumulative anthropogenic CO_2 emissions have warmed Earth's ecosystems unequivocally [1]. Other threats due to GHGs are briefly listed in Table **1**. In various sectors, numerous indirect and direct sources involve the emission of GHGs in the atmospheric environment. The energy sector, which produces electricity and heat, is considered a significant emission source, while agriculture, forests, and other land uses, industrial and transport sectors are other sources of GHG contribution to the environment.

Table 1. Impact of greenhouse gases in the atmosphere.

Brief threats	References
Continuous increase in the Earth's surface temperature	[2]
Melting of glaciers (21% of Himalayan glaciers were lost in the past 40 years)	[3]
Radiation exposure	[4]
Changes in the atmospheric composition	[4]
Sea level rise	[5]
Violation of the agricultural system	[5]
Increased flood risk	[6]

Microorganisms play prominent roles in the carbon and nutrient cycle, agriculture, and the global food web, and their role in climate change needs consideration [7]. Microbial processes and their diversity in different ecosystems have significant roles related to global fluxes of GHGs and climate change. They are involved in both the emission and consumption of greenhouse gases (GHG), *viz.* carbon dioxide (CO_2), methane (CH_4), and nitrous oxide (N_2O) that are responsible for 98% of increased warming conditions [8, 9], which are ultimately the cause for climate change. Microbes play a vital role either as producers or users of these GHGs in the environment, as they can recycle or transform indispensable elements such as carbon and nitrogen [10]. Microbes consume these GHGs as resources for their growth through photo/ chemoautotrophy (algae, cyanobacteria, nitrifiers), methanotrophy (methane oxidizers), and nitrous oxide reduction (denitrifiers). Photosynthetic microbes consume CO_2 from the atmosphere, while the heterotrophs break down organic matter to release GHGs. The net carbon flux in different ecosystems is determined by the balance between microbes that depends on temperature and other climatic factors [11] since they also store and emit carbon into the atmosphere in massive quantities [12].

ROLE OF MICROBES AND MICROBIOMES IN GHG EMISSIONS

The greenhouse gases such as CO_2, $CH_{4,}$ and N_2O are produced mainly by microbial processes as their essential by-products [13]. In soil, the microbes play a significant role in the C-N cycle by decomposing organic materials and releasing CO_2 back into the atmosphere, accounting for 25% of the CO_2 naturally released into the atmosphere through microbial respiration, a primary channel for carbon efflux from ecosystems. Similarly, methanogenic microbes are known to produce the greenhouse gas CH_4 (Non-fossil) , which has 27.9 as per AR6 WG I report times more global warming potential than CO_2. The primary cause of nitrous oxide emissions in the soil is by the bacteria through nitrification and denitrification under aerobic and anoxic environments. N_2O has a 273 as per AR6 WG I times greater global warming potential than CO_2, contributing to around 19% of the overall global warming effect. Globally, naturally vegetated soils are estimated to generate 6.6 Tg of N_2O per year and 3.8 Tg of nitrous oxide per year in the Earth's atmosphere [14].

Role of Microbes and Microbiomes in CO_2 Emissions

Approximately 4.1 petagrams of carbon are added to the atmosphere as CO_2 per year, which has been predicted to rise dramatically by 2100 [15]. The atmospheric carbon amounts produced by microbial decomposition in the soil are around 7.5-9 folds of the annual anthropogenic emissions worldwide. The terrestrial environment is tightly linked with atmospheric CO_2 concentrations, such as carbon sequestration into the soil as biomass, emissions from respiration, and decomposition of organic matter subjected to partial photosynthetic fixation (Fig.

CHAPTER 6

Role of Carbon in Microbiomes for Ecosystem Restoration

Ihsan Flayyih Hasan AI-Jawhari[1,*]

[1] *Department of Biology, College of Education for Pure Sciences, University of Thi-Qar, Iraq*

Abstract: The most significant threat to civilization is climate change. Carbon dioxide (CO2), methane (CH4), and nitrous oxide (N_2O) are the three predominant greenhouse gases generated and utilized by microbes. Certain bacteria can induce diseases in humans, animals, and plants, exacerbating climate change. When conditions allow, microbes that utilize light- or chemoautotrophic activities (such as cyanobacteria and algae) and methanotrophic processes (which oxidize CH4) and those that reduce N_2O can also metabolize these three gases (denitrifies). The production or consumption of these gases by bacteria is contingent upon their environment and interactions, which humans frequently modify. At times, we can manipulate environmental variables to enhance the microbial degradation of these gasses. According to a recent Intergovernmental Panel on Climate Change (IPCC) study, 3.3 billion individuals globally are subjected to environmental change. At the same time, unsustainable growth patterns exacerbate ecological and human vulnerability to environmental hazards. As individuals, societal change agents, and microbiologists with expertise, we may assist in identifying methods to reverse the prevailing tendency. This chapter argues that understanding both the direct and indirect effects of climate change on microorganisms is essential to evaluate their potential positive and negative impacts on land-atmosphere carbon exchange and global warming. Furthermore, we suggest that this encompasses examining the complex interactions and feedback mechanisms that emerge during communication among microorganisms, plants, and their physical environment within the climate change framework. Furthermore, the influence of further global changes may exacerbate the effects of the environment on soil bacteria.

Keywords: Algae, climate, cyanobacteria, global warming, habitat, microorganisms.

INTRODUCTION

Environmental change is a significant therapeutic and political challenge of the twenty-first century. The release of the IPCC's Fifth Assessment Report (AR5)

---

[*] **Corresponding author Ihsan Flayyih Hasan AI-Jawhari:** Department of Biology, College of Education for Pure Sciences, University of Thi-Qar, Iraq; E-mail: dr.ihsan_2012@yahoo.com

Shiv Prasad, Govindaraj Kamalam Dinesh, Murugaiyan Sinduja, Sathya Velusamy, Ramesh Poornima & Sangilidurai Karthika (Eds.)

and the Special Report on Global Warming of 1.5 °C (SR1.5), encompassing data on over 12,000 species globally, has led to new studies revealing changes consistent with climate change. Two-thirds of springtime phenological events have advanced due to regional temperature changes, and approximately fifty percent of species have shifted their ranges to higher latitudes or altitudes, based on an analysis of over 4,000 species globally (with very high confidence). The distribution of species is changing, and international varieties, particularly those in northern latitudes, are more adept at adapting to environmental changes than indigenous species, potentially leading to the emergence of new invasive species due to anthropogenic increases in greenhouse gases [1]. The most significant challenge is understanding the biological mechanisms governing carbon exchanges among terrestrial, marine, and atmospheric systems and their responses to climate change through climate-ecosystem interactions that may amplify or mitigate local and global environmental adjustments [2]. Earthbound ecological communities are crucial in climatic circumstances as they emit and absorb greenhouse gases like carbon dioxide, methane, and nitrous oxide while sequestering significant amounts of carbon in live plants and soils [3]. The sink activity of terrestrial ecosystems is influenced by various interrelated factors, including anthropogenic and natural disturbances [4], agricultural land use [5], nitrogen enrichment [6], sulfur deposition [7], and fluctuations in atmospheric ozone concentration [8].

The potential for increased temperatures to enhance the release of carbon dioxide from soil to the atmosphere due to improved microbial decomposition of organic matter renders the effect of climate change on the soil carbon sink a significant area of uncertainty. If projected climate change scenarios are accurate, this increase in soil carbon loss could significantly exacerbate the responses of the soil carbon cycle [9]. The balance between photosynthesis and respiration fundamentally determines the carbon content of ecosystem carbon budgets due to climate change, encompassing both autotrophic respiration and heterotrophic soil microbial respiration. Although our comprehension of the assimilatory component of the carbon cycle, specifically photosynthesis and its response to environmental changes, is well established, significant gaps remain in our knowledge regarding soil respiration reactions [10, 11]. Numerous factors influence soil respiration, including complex interactions and feedbacks among climate, plants, symbionts, and free-living heterotrophic soil microorganisms. This results in a lack of understanding regarding soil respiration and its sensitivity to climate change [12]. All organisms rely on the Earth's provision of essential materials. Reutilizing these elements is essential to prevent depletion, as the Earth is a closed system with a finite supply of crucial components, including hydrogen (H), oxygen (O), carbon (C), nitrogen (N), sulfur (S), and phosphorus (P). Decomposing and transforming deceased organic matter into forms that other creatures can utilize mostly rely on bacteria. The principal microbial enzyme systems are believed to drive the Earth's biogeochemical cycles [13]. The combination of photosynthesis and respiration governs the terrestrial carbon cycle in equilibrium [14]. Photosynthesizing plants and chemoautotrophic microbes, which convert atmospheric CO_2 into organic matter, are the primary "carbon-fixing" autotrophic organisms that transfer carbon from the atmosphere to the soil (Fig. **1**). Subsequently, various unique processes responsible for the respiration of both autotrophic and heterotrophic organisms release fixed carbon back into the environment [10].

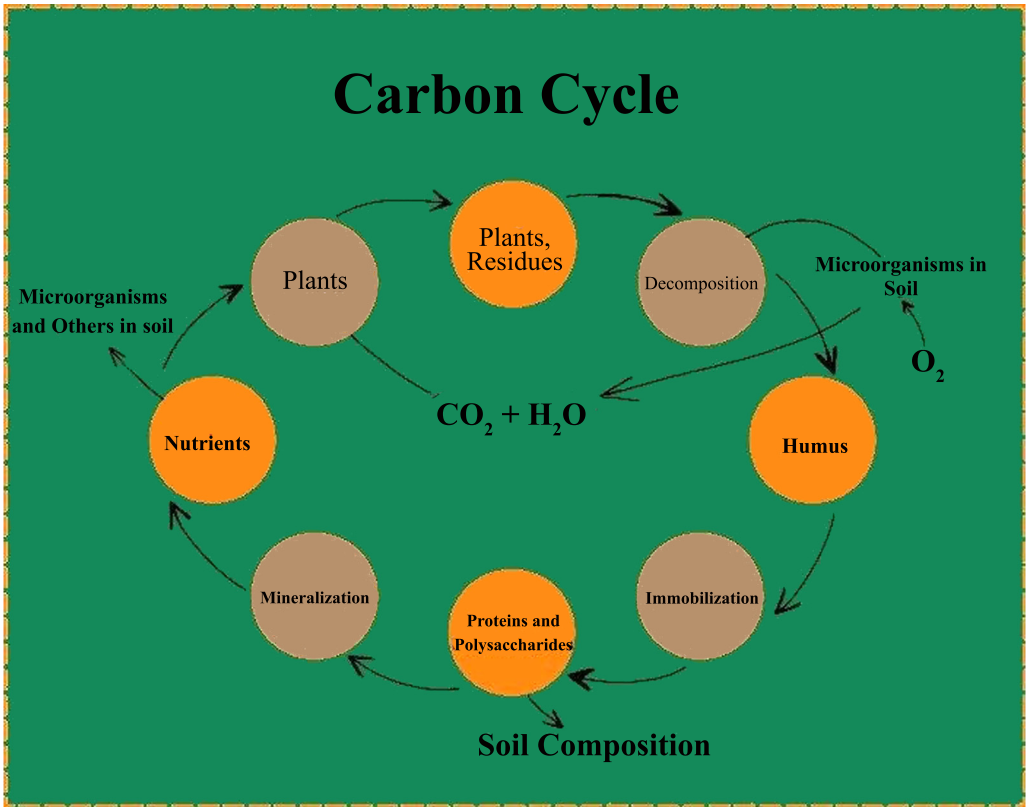


Fig. (1). Carbon cycle in the terrestrial ecosystem.

The "natural carbon-consuming" heterotrophic microorganisms utilize carbon derived from plant, animal, or microbial sources as a substrate for metabolism, sequestering a portion of the carbon in their biomass while releasing the remaining carbon as metabolites or CO_2 back into the environment, which is encompassed in the reverse process [15]. Since numerous soils globally are oxic and unsaturated, carbon dioxide is the primary source of respiration. A study [16] indicates that hydrogenotrophic archaea in peatlands and rice fields reduce CO_2

Importance of Microbiome in Ecosystem Sustainability

CHAPTER 7

Marine Microbes and Microbiomes: Role and Importance in Ecosystem Sustainability

C. Poornachandhra[1,*], **M. Sinduja**[2], **S. Akila**[2], **A. Manikandan**[3], **J. Sampath**[1], **R. Kaveena**[5], **T. Gokul Kannan**[1] and **Muthusamy Shankar**[4]

[1] *Department of Environmental Sciences, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India*

[2] *National Agro-foundation Research & Development Centre, Chennai, India*

[3] *Institute of Ecology and Earth Sciences, University of Tartu, Tartu, Estonia*

[4] *Division of Plant Genetic Resources, ICAR-Indian Agricultural Research Institute, New Delhi, India*

[5] *Swamy Vivekananda College of Pharmacy, Tiruchengode, India*

Abstract: Marine environments are among the most unfavorable due to salinity, pH, sea surface temperature, wind patterns, ocean currents, and precipitation regimes. Due to the frequent changes in environmental conditions, the microorganisms that live there are better suited to adjusting to unfavorable conditions, which is why they have complex characteristic qualities of adaptation. Consequently, by forming biofilms and producing extracellular polymeric substances, the microorganisms isolated from marine habitats are intended to be better exploited in the bioremediation of soils and water bodies contaminated with toxic pollutants. Many marine bacteria have also been reported to produce bioactive compounds, which found their use in many biotechnological applications. This chapter explores marine microbial diversity, its utilization in bioremediation, and understanding their role in ecosystem sustainability.

Keywords: Ecosystem sustainability, Microbial diversity, Microbiomes, Nutrient cycling, Pharmaceuticals, Remediation.

INTRODUCTION

Marine planktonic microbes dominate ocean biogeochemical processes and biomass. Although several environmental factors have been demonstrated to impact microbial communities, there is disagreement regarding how these factors affect microbial communities [1]. Quantifying the relative contributions of enviro-

---

[*] **Corresponding author C. Poornachandhra:** Department of Environmental Sciences, Tamil Nadu Agricultural University,Coimbatore, Tamil Nadu, India; E-mail: poorna155c@gmail.com

Shiv Prasad, Govindaraj Kamalam Dinesh, Murugaiyan Sinduja, Sathya Velusamy, Ramesh Poornima & Sangilidurai Karthika (Eds.)

nmental factors in creating microbial community structure is necessary for predicting how ecosystems react to environmental changes, such as climate change [2]. In this chapter, we concentrate on how environmental selection affects oceanic microbiomes. Stochastic effects make it difficult to find key variables through observational sampling [3], geographical variations in populations, behaviors, and ecological divergence among closely related microbes [4]. Despite these difficulties, it is generally accepted that bacterio-plankton reacts to environmental factors such as temperature and salinity, as well as the abundance of resources such as nutrients and interactions with other organisms [5]. The term "biological diversity" refers to the diversity of all living things, including those belonging to species and ecological complexes [6]. The tropical Indo-Western Pacific region, which encompasses waters along the coasts of Asia, Southeast Africa, Northern Australia, and the Pacific Islands, has the highest overall marine diversity [7].

However, the rate of extinction for biodiversity on Earth is worrying. Therefore, mapping and quantifying marine biodiversity at all structural levels should be done using a method based on ecological and evolutionary processes [8]. The paradigms pertaining to biodiversity patterns in terrestrial systems may not be applicable to marine conditions since marine systems differ from terrestrial systems in many ways [9]. The ability of terrestrial ecosystems to connect their three-dimensional space to either permanent or semi-permanent physical structures fundamentally sets them apart from marine ecosystems. The world Ocean has a 312,000 km long coastline and a volume of 1.46 x 10^9 km^3 with an average depth of 4000 m [10] and is the planet's largest ecosystem. Despite the fact that humans have exploited it for a variety of reasons for millennia, most studies on biological diversity focus on terrestrial systems, and our understanding of marine biodiversity is much less advanced than that of land [11]. Microorganisms are pervasive and genuinely make up the "unseen majority" in the marine environment. Although marine isolates have been the subject of laboratory-based culture methods for more than ten years, we still do not completely understand the ecology of marine microorganisms. Marine microbes have been studied for a few decades, and new discoveries of previously undiscovered groups like SAR11 and pico autotrophs like *Prochlorococcus* have significantly increased the diversity of marine microbes.

However, the significance of microbial taxonomy, an experimentally complex and labor-intensive process, becomes apparent from sparse and dispersed knowledge about the number of species. When the variety of biological life is measured by the number of species known for each group, the diversity of microorganisms is vastly understated. In comparison to plants and animals, the idea of bacterial species is not only more typological and less evolutionary, but it is also much broader and inclusive. To comprehend the phylogenetic perspective, the mechanism of degradation, and the creation of novel treatment strategies, it is thus essential to study diversity at the genetic level. In terms of microbial genomics, the first two decoded microbial genomes were *Mycoplasma genitalium* and *Haemophilus influenzae*. However, a decade ago, microbial genome sequencing could not gain traction. Today, however, each microbial DNA is sequenced on an individual basis. The entire collection of genes an organism can access is contained in its genome. Exploring microbial diversity is undoubtedly an important and fascinating topic. Additionally, knowledge of the diversity of marine microbes aids in the isolation and identification of novel and promising microbes with high selectivity for resistant substances.

PRESENT STATUS OF MICROBIAL BIODIVERSITY

Approximately 3.5 billion years have passed since the beginning of modern microorganisms' evolutionary history, which has primarily taken place in marine environments. The first division of living things into two very different categories are eukaryotes, which have a nuclear membrane, and prokaryotes, which do not include bacteria, the 'first and simplest division of living beings. The “Five Kingdoms” of life animals, plants, fungi, protists (Protozoa), and monera (Bacteria) were, however, highlighted by taxonomists of the 20th century. The “urkingdoms” or “domains” consist of Bacteria (eubacteria), Archaea (archaebacteria), and Eucarya (eukaryotes) based on the 16S or 18S rRNA composition. These three domains overlap in the water regarding size spectra, physiological traits, metabolic patterns, and ecological roles. Prokaryotes typically have a loosely arranged DNA called the nucleoid and rigid cell wall, including archaea and bacteria. Although there may be considered over 40 divisions of bacteria, the 16S rRNA gene sequences used to infer the division-level diversity of the bacterial domain revealed 36 divisions. Cultivated strains of several described divisions, which were the first to be defined phylogenetically, provide good representations of these divisions.

Marine Microbial Diversity

The world Ocean has a 312,000 km long coastline and a volume of 1.46 x 10^9 km^3 with an average depth of 4000 m [10] and is the planet's largest ecosystem. The ocean substantially impacts global climate due to its enormous size and volume. Microorganisms play a significant role in our conceptions of life and can be found anywhere in nature. Most of the biomass found in the oceans is made up of microorganisms. The various evolution in the marine microbial ecology is shown in Fig. (**1**). Microorganisms are so numerous that they are thought to account for between 55 and 86% of the planet's prokaryotic biomass or 3.55×10^{29} cells. In

CHAPTER 8

Microbiomes in Mangroves and Wetlands: Their Role and Importance in Ecosystem Sustainability

Zahra Haghani[1] and **Kamyar Amirhosseini**[1,*]

[1] *Department of Soil Science, Faculty of Agriculture, College of Agriculture and Natural Resources, University of Tehran, Tehran, Iran*

Abstract: Mangroves and wetlands are critical intermediary ecosystems between terrestrial and marine environments. These ecosystems offer a wide range of invaluable ecological and economic services. However, under the influence of natural and anthropogenic threats, mangroves and wetlands face rapid degradation. Microbes and microbiomes are integral components of a mangrove, playing key roles in the stability of the ecosystem. The present chapter compiles a comprehensive review of the classification and the role of microorganisms in the sustainability of mangrove and wetland ecosystems. The chapter discusses the most critical features of microbial groups, including archaea, bacteria, algae, and fungi in mangroves and wetlands. Bacterial groups under discussion consist of sulfur-related bacteria, nitrogen-related bacteria, phosphate-solubilizing bacteria, and photosynthetic bacteria. A separate section is dedicated to periphytic communities encompassing a microhabitat involving various prokaryotic and eukaryotic microorganisms. Moreover, biochemical transformations brought about by wetlands' microbial groups are explained. In addition, the following chapter emphasizes the degree of complexity in microbial interactions and draws attention to how alterations to these interactions ultimately impact ecosystems' health status. Furthermore, the role of wetland microorganisms in processes, such as detoxification, bioremediation, methanogenesis, carbon sequestration, nutrient cycling and transformations, and primary production is articulated.

Keywords: Biodiversity beneficial microorganisms, Ecosystem services, Mangrove restoration, Microbial processes, Wetland microbiology, Wetland ecology.

INTRODUCTION

Comprehensively, flooded and submerged habitats have tremendous ecologic and economic value, including but not limited to flood storage, drought prevention,

---

[*] **Corresponding author Kamyar Amirhosseini:** Department of Soil Science, Faculty of Agriculture, College of Agriculture and Natural Resources, University of Tehran, Tehran, Iran; E-mail: amirhosseini.k@ut.ac.ir

Shiv Prasad, Govindaraj Kamalam Dinesh, Murugaiyan Sinduja, Sathya Velusamy, Ramesh Poornima & Sangilidurai Karthika (Eds.)

water purification, biodiversity preservation, climate change mitigation, nutrient accumulation, and fishery [1]. In particular, mangroves and wetlands are biologically-diverse and highly productive hotspots that offer a wide array of vital ecosystem services. Indeed, diverse biological communities that commonly thrive in estuaries play critical roles in realizing these services [2]. Despite their ecologic and economic importance, mangroves and wetlands face rapid degradation, and their overall decline approximates 50%. Natural environmental changes, anthropogenic activities, and the synergistic combination of the two threaten these ecosystems globally and are regarded as the primary agents driving ecological deterioration and wetland degradation [3]. Accordingly, studying the biological systems that are integral to such ecosystems proves helpful in implementing effective restoration programs that maintain or enhance mangroves' and wetlands' health and sustainability.

Characteristics of mangroves and wetlands have been adequately described in limnological sciences. Based on physiochemical limnology studies, such ecosystems are characterized by low oxygen levels with oxygen in-flow and out-flow controlled by molecular diffusion [4]. Soils of wetlands are saturated with water and possess low aeration porosity. The diffusion process is 10,000 times slower in an aqueous medium than in gas-filled pores [4]. Consequently, anaerobic condition prevails in the wetland ecosystem. This condition has essential consequences on oxidation-reduction reactions.

Furthermore, all forms of life comprising bacteria, fungi, cyanobacteria, microalgae, macroalgae, and fungus-like protists have been reported in these ecosystems [5]. In particular, microorganisms contribute to organic matter turnover by generating detritus by degrading mangrove organic residues of plant and animal origins [6]. A slow rate of organic matter oxidation commonly accompanies the anaerobic condition of the wetland environment. Therefore, such ecosystems are typically rich in organic matter [4]. Although some wetlands and mangroves may suffer nutrient deficiencies [7], nutrient regeneration from decomposing mangrove detritus and nutrient transformations by microbial activity establish an efficient nutrient recycling system in these habitats [8].

Bogland microbiomes and their processes are integral to ecosystem sustainability and restoration. As the basis of wetland ecosystems, the soil is a crucial indicator of the changes in wetland ecological characteristics. In wetlands research, especially mangrove restoration, soil physicochemical properties and soil enzymes are key soil attributes that are often regularly altered with the number of wetland restoration years [9]. In such ecosystems, free-living bacteria, fungi, and yeasts have been reported to play a significant role in the formation of detritus [10]. Bacteria perform various activities such as photosynthesis, nitrogen fixation, methanogenesis, carbon sequestration, and regulation of nutrient and energy flow [11]. Fungi species synthesize a wide array of enzymes catalyzing various biochemical processes [12]. Despite the wealth of systematic information, little knowledge of their role in bioremediation, restoration, and sustainability exists. Accordingly, ecological restoration of degraded wetlands is necessary for achieving ecological balance and food security. Despite numerous studies on biogeography, botany, zoology, ichthyology, environmental pollution, and the economic impact of mangroves, little is known about the diversity and activities of microbes in mangroves and wetlands [8].

The present chapter presents a comprehensive assessment of the microbial biodiversity of submerged habitats. Additionally, the following chapter explains the principal mechanisms involved in the nutrient-recycling system of microbiomes. It aims to highlight the critical roles of various microbes and microbiomes in ecosystem restoration and sustainability of mangroves and wetlands.

MANGROVE AND WETLAND MICROBIOMES

Mangroves and wetlands encompass unique physicochemical properties whose intertwining culminates in an ecology of considerable complexity. As remarked earlier, mangroves and wetlands are characterized by specific properties, including low oxygen levels, high organic matter content, and salinity, among which anoxic conditions and accumulation of carbon compounds appear to be the most influential characteristics impacting microbiomes (Table **1**). With undeniable importance as intermediary ecosystems between terrestrial and marine environments, mangroves and wetlands are hospitable hosts to many biological species ranging from unicellular microorganisms to macroscopic members of the Plantae kingdom. The scrupulous interplay among the living and non-living components of mangroves and wetlands is the key determinant of such ecosystems' health and sustainability. Table **1** outlines some of the most critical properties of wetland ecosystems and their impact on microbial communities.

Table 1. Critical properties of wetland ecosystems and their impact on the microbiomes.

Properties	Impact on Microbiome
pH	Alters microbial community composition and activity.
Temperature	Regulates bacterial community diversity and function.
Geographic gradients	Influences global distribution of microbes across habitats.
Soil Particle Size	Impacts soil bacterial community structure in wetlands.
Redox Potential	Regulates the abundance and species diversity of microbial communities along with their biochemical functions.

CHAPTER 9

Forest Microbiomes: Their Role and Importance in Ecosystem Sustainability and Restoration

Ihuma O. Jerome[1,*], **Malgwi T. Doris**[2], **Tayo I. Famojuro**[3], **R. Raveena**[4] and **Govindaraj Kamalam Dinesh**[5,6,7]

[1] *Department of Biological Science, Faculty of Science and Technology, Bingham University, Karu Nasarawa State, Nigeria*

[2] *Department of Community Medicine, Nnamdi Azikiwe University, Nnewi, Anambra State, Nigeria*

[3] *Department of Pharmacognosy, Faculty of Pharmaceutical Sciences, Bingham University, Karu Nasarawa State, Nigeria*

[4] *Department of Environmental Sciences, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India*

[5] *Division of Environment Science, ICAR-Indian Agricultural Research Institute, New Delhi-110012, India*

[6] *Division of Environmental Sciences, Department of Soil Science and Agricultural Chemistry, SRM College of Agricultural Sciences, SRM Institute of Science and Technology, Baburayanpettai-603201, Chengalpattu, Tamil Nadu, India*

[7] *INTI International University, Persiaran Perdana BBN, Putra Nilai, 71800 Negeri Sembilan, Malaysia*

Abstract: A forest is a large area of land covered with big trees of different species, approximately covering one-third of the Earth's surface. Forest ecosystems are more than what can be seen physically (aboveground); below the ground level, they are extraordinarily diverse and have unique communities of microbiomes with a large population of bacteria and fungi species. These microorganisms are essential to how plants interact with the soil environment and are necessary to access critically limiting soil resources. This book chapter focuses on the ecosystems below and above ground level of a forest microbiome, including the soil microorganisms, their importance, and the diverse interrelationships among soil microorganisms (parasitism, mutualism, commensalism). The aboveground part of a plant is known as the phyllosphere, harboring diverse microorganisms, such as viruses, bacteria, filamentous fungi, yeast, algae, and rarely protozoa and nematodes with a role in disease resistance that is critical to plant health and development. The rhizosphere is the soil region immediately adjacent to and affected by plant roots where plants, soil, microorganisms, nutrients,

---

[*] **Corresponding author Ihuma, O. Jerome:** Department of Biological Science, Faculty of Science and Technology, Bingham University, Karu Nasarawa State, Nigeria;
E-mail: jeromeihuma@binghamuni.edu.ng

Shiv Prasad, Govindaraj Kamalam Dinesh, Murugaiyan Sinduja, Sathya Velusamy, Ramesh Poornima & Sangilidurai Karthika (Eds.)

and water meet and interact. In this region, plants and microbes coordinate and show a symbiotic relationship by fulfilling each other's nutrient requirements, roles, and functions. The endosphere is the plant interior and is colonized by endophytes, and their functions range from mutualism to pathogenicity. Archaebacteria, anaerobic bacteria, aerobic prokaryotes, fungi, and viruses exist as forest biomes. Examples of fungi include *Trichoderma harzianum and* obligate parasites *Puccinia striiformis*and*Gremmeniella abietina.* Plants, fungal endophytes, mycoviruses, and the environment all participate in a four-way interactive system.

Keywords: Abiotic, Archaea, Association, Biotic, Bacteria, Endosphere, Ecosystem, Forest, Forest microbiomes, Fungi, Hubs, Microorganisms, Microbial communities, Rhizosphere, Trees, Rree pest, Plants, Phyllosphere, Soil, Virus.

INTRODUCTION

Forest, in its simplest definition, is a large area of land dominated by trees (mostly comprised of different species) and associated fauna that inhabits a specific land area. According to expert estimations, approximately thirty percent of the surface of the planet is covered with forests. According to Pan and co-workers [1], forests are the predominant terrestrial ecosystem and are evenly distributed on the surface of the Earth. Forests cover a total land area of approximately 4 billion hectares, which is estimated to be 31% of the world's total area [2].

Nearly 80% of the Earth's plant biomass comprises forests, with a 75% gross primary production. The forest biomes are composed of tropical forests, temperate forests, and boreal forests, with a net direct annual output estimated at 21.9 gigatonnes, 8.1 gigatonnes, and 2.6 gigatonnes, respectively [1], and they have significant economic as well as ecological value. Forest ecosystems are more than what can be seen physically – they do not only comprise the plants and animals aboveground. Diverse and complex fungi and bacteria communities inhabit the Earth's surface underground. To get access to these scarce soil nutrients, plants rely on fungal and bacterial interactions with their soil environment.

A forest ecosystem is, therefore, a place that provides natural habitat to millions of microorganisms. It can be classified into three common types: tropical, boreal, and temperate. Forest ecosystems play essential roles in the environment by balancing the climate of the planet Earth, providing oxygen, maintaining the balance of carbon dioxide in the atmosphere and biogeochemical cycles, and preventing soil erosion. This is the general description of a forest aboveground; however, diverse fungi and bacteria communities (microbiomes) exist and cohabit below the ground level. These soil microorganisms are equally necessary for interdependence cycles.

Forest microbiomes are microbial organisms closely associated with tree species in a forest ecological community. Microbiota and microbiome are used interchangeably, describing the assembly of tree-associated microorganisms and the relationships between groups. The existence of these organisms is essential to the interaction between soil and plant environment and is required to access soil resources. The subterranean stratum of the organism establishes interconnected systems amongst trees, facilitating the exchange of nutrients and providing mutual support in the face of adverse conditions [3]. In addition, the existence of microorganisms in the soil plays a vital function in aiding the conversion of nutrients within forest ecosystems, therefore contributing to the overall stability and long-term viability of these ecosystems. These microbes enhance energy transformation processes and facilitate interactions between the many components of the ecosystem, both above and below the surface of the ground.

Soil microorganisms are essential to forest ecosystems as they are vital in nutrient transformations. Forest ecosystems depend on these nutrient transformations and interactions between above and underground components for stability and sustainable development that drive forest ecosystem processes [4].

IMPORTANCE OF SOIL ORGANISMS

Soil organisms are of importance in many ways and are outlined below:

- Accountable for cycling of K, P, C, N, and other nutrients in the soil.
- Increase and strengthen soil structure
- Replace and decompose organic materials
- Support soil health and quality
- Enhance soil penetrability and soil aeration

FOREST ECOSYSTEM

As described earlier, a forest ecosystem provides a natural habitat to millions of plants, animals, fungi (Unicellular and multi-cellular), and microbial species. It can be classified into three general types: temperate, tropical, and boreal [1]. This division is a result of the climatic condition of a particular locality. The three types of forest ecosystems are:

- Temperate Forest
- Tropical Forest
- Boreal Forest

Role of Microbes in Socio-Economic Development

CHAPTER 10

Microbiomes in Promoting a Sustainable Industrial Production System

Joseph Ezra John[1], Boopathi Gopalakrishnan[2], Senthamizh Selvi[3], Murugaiyan Sinduja[1], Chidamparam Poornachandhra[1,*], Ravi Raveena[1] and **E. Akila[4]**

[1] *Department of Environmental Sciences, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India*

[2] *School of Atmospheric Stress Management, ICAR-National Institute of Abiotic Stress Management, Maharashtra, India*

[3] *Department of Agricultural Microbiology, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India*

[4] *Department of Agricultural Engineering, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India*

Abstract: The sustainable industrial revolution is the way forward to help humankind prolong its existence on Earth. The first step could be facilitating the natural process under a controlled environment to produce the desired products instead of chemicals. The industrial sectors, especially food and pharmaceuticals, depend on microbes for most of their production. Biocontrol, enzyme, and fuel production have been explored in recent years. Microbial production systems encompass the metabolites produced by bacteria, fungi, or viruses that facilitate industrial processes. These secondary metabolites have been noted to pose implications in many fields, including agriculture. After the advent of modern genetic engineering techniques, the utilization of microbiota in various activities is increasing due to their simplicity and cost-effectiveness. The gene mounting and biotechnological tolls have aided in manipulating these microbes' secondary metabolites, thereby improving productivity. Furthermore, multi-disciplinary and comprehensive approaches directed towards improving microbial production are described in this chapter.

Keywords: Bioproducts, Bioenzymes, Biofertilizers, Microbiomes, Pharmaceuticals, Sustainability.

---

[*] **Corresponding author Chidamparam Poornachandhra:** Department of Environmental Sciences, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India; E-mail: poorna155c@gmail.com

Shiv Prasad, Govindaraj Kamalam Dinesh, Murugaiyan Sinduja, Sathya Velusamy, Ramesh Poornima &
Sangilidurai Karthika (Eds.)

INTRODUCTION

Global ecosystems are under much stress due to industrialization and population growth. Urbanization frequently occurs on previously farmed land, and to increase food production, farmers frequently intensify their practices and use agrochemicals, which comprise a wide range of structurally different chemicals. Although the Green Revolution and the development of industries in the countries improved people's lives and boosted the world economy, environmental quality was generally degraded due to industrial waste's detrimental effects on the soil, water, and atmosphere. This affects the soil fertility in addition to the heavy metal contamination from industries. Toxic contaminants from polluted areas are now being reduced using techniques including recycling, disposal in a landfill, burning of wastes, and pyrolysis. Nevertheless, these techniques harm the ecosystem and produce intermediary chemical compounds that are much more poisonous and difficult to remediate. Microbes are widely used in food processing, food additives, alcoholic and non-alcoholic beverages, biofuels, metabolites, biofertilizers, chemicals, enzymes, bioactive molecules, vaccines, antibiotics, medicines, and other commercial products. A list of algal species involved in the production of essential products is presented in Table **1**.

Table 1. List of algal species involved in the production of important products.

S. No.	Algal Species	Products	Uses
1.	*Spirulina platensis*	Phycocyanins	Nutraceuticals, cosmetics
2.	*Chlorella vulgaris*	Ascorbic acid	Food supplement
3.	*Haematococcus pluvialis*	Carotenoids, astaxanthin	Nutraceuticals, pharmaceuticals, additives
4.	*Odontella aurita*	Fatty acids	Pharmaceuticals, cosmetics, baby food
5.	*Porphyridium cruentum*	Polysaccharides	Pharmaceuticals, cosmetics
6.	*Dunaliella salina*	Carotenoids	Nutraceuticals, food supplements, feed
7.	*Spirulina platensis, Dunaliella salina, Haematococcus pluvialis*	Phycobiliproteins	Pigments, cosmetics, vitamins
8.	*Chlorella minutissima* *Schizochytrium* sp.	PUFAs	Nutraceuticals, food supplement
9.	*Euglena gracilis* *Euglena gracilisa* *Prototheca moriformis*	Vitamins (Biotin, α-tocopherol and Vitamin C)	Nutrition

(Table 1) cont.....

S. No.	Algal Species	Products	Uses
10.	*Nostoc, Hapalosiphon*	Indole-3-acetic acid, or 3-methyl indole	Plant growth and development
11.	*Nostoc muscorum, Hapalosiphon fontinalis*	Vitamin B12	
12.	*Tolypothrix tenuis*		
13.	*Cylindrospermum* sp.		

Research on green technology is now being done to replace dangerous toxic pollutants. Microbes and microbial products in this field hold promise for ensuring food security in a dynamic environment and decomposing dangerous pollutants [1]. Using microbiological methods, agriculture can be developed sustainably. These microbes can enhance crop plants' access to nutrients through several mechanisms, enhancing plant growth. This chapter addresses the critical mechanisms that microbes could use to support environmental management and environmentally sound industrial production systems. In addition, the examples of effective applications of microorganisms for healthier, cleaner ecosystems without compromising crop yield or industrialization are shown in the sections below. These bioproducts and enzymes play essential roles in the food, bioenergy, cosmetics, and pharmaceutical industries. Traditionally, the glucose that is mainly hydrolyzed from food grain starch is used to make biofuels like bioethanol. Consequently, producing biofuels from molasses rather than glucose is a tactic to conserve food resources. However, some valuable products made by molasses-derived microorganisms have significant uses in food processing, preservation, safety, and nutrition.

NEED FOR MICROBES IN THE INDUSTRIAL PRODUCTION SYSTEM

Ecological connections bind nearly all living things and microorganisms together. There are many ways in which microorganisms are advantageous to people, and they also significantly impact both human welfare and the ecosystem. They also play a vital role in industrial production processes. They are employed in the energy sector to make fuels, chemicals, and energy, in the pharmaceutical sector to make insulin, antibiotics, and probiotics, in the food sector to make food and process it, and in the agricultural sector to make biofertilizers and biocontrol agents.

Energy Industry

In a significant part of energy conversion, microorganisms can convert waste biomass to bioenergy. It is used to create fuels that can be burned, including butanol, ethanol, hydrogen, methane gas, lipids, and others. Using certain bacteria

CHAPTER 11

Role of Microbes and Microbiomes in Human and Animal Health Security

A. Ch. Pradyutha[1,*] and **S. Chaitanya Kumari**[2]

[1] *Department of Microbiology, Raja Bahadur Venkata Rama Reddy Women's College, Narayanguda, Hyderabad, Telangana, India*

[2] *Department of Microbiology, Bhavan's Vivekananda College of Science, Humanities & Commerce, Sainikpuri, Secunderabad, Telangana, India*

Abstract: Most of the various categories of bacteria and fungi that comprise the human microbiota are primarily incapable of causing diseases. Human beings and animal microbiomes can influence their health and homeostasis through the synthesis of necessary nutrients and vitamins, metabolism of drugs, guarding against pathogenic microbes, additional production of bile acids from the host, immune response, vulnerability to illness, and consistent behavior change. Animal species harbor distinctive microbiomes and possess greater complexity compared to the human microbiome. Living organisms are somewhat exposed to microbes in the newborn stage, at the time of delivery from the birth passage or vagina, and through breastfeeding. The kind of microbes the infant carries relies exclusively on the species seen in the mother. Further, changes in the microbiota of animals and humans depend on exposure to the environment and type of diet. This change can help benefit the health of the host or put one at a more significant chance for disease. This transformation of the microbiome in earlier life holds possible health importance to developing the immune system, influencing health effects including gastroenteritis, asthma, hay fever (allergic rhinitis), and chronic illnesses like diabetes. In addition to the genes of the family, surroundings, medication use, and diet greatly determine what microbiota is present in animals and humans. All of these aspects construct a particular microbiome from individual to individual. An adult living being is colonized by multiple species of bacteria. The total biomass of these microorganisms is typically estimated at around 0.2 kg in adults. The microbiomes present in human and animal bodies serve several functions. They contribute to the breakdown of food, allowing for the digestion of complex carbohydrates, fiber, and other substances that our bodies cannot process alone. Additionally, these microbiomes produce essential nutrients that are made available to us. They also play a vital role in neutralizing toxins or harmful compounds, promoting detoxification, and safeguarding our well-being. Using microorganisms in therapies is one of the clinical revolutions in the 21st century. Numerous research studies have revealed the crucial functions of microbes and microbiomes in human and animal health security.

---

[*] **Corresponding author A. Ch. Pradyutha:** Department of Microbiology, Raja Bahadur Venkata Rama Reddy Women's College, Narayanguda, Hyderabad, Telangana, India; E-mail: pradyutha.g@gmail.com

Shiv Prasad, Govindaraj Kamalam Dinesh, Murugaiyan Sinduja, Sathya Velusamy, Ramesh Poornima & Sangilidurai Karthika (Eds.)

Keywords: Allergic rhinitis, Diseases, Gastroenteritis, Immune system, Microbiome, Toxins.

INTRODUCTION

Within the depths of the human and animal body resides a formidable and enigmatic kingdom of microorganisms [1]. Bacteria, fungi, viruses, and their intricate interactions, metabolites, and genetic components coexist on or within the human and animal body, collectively referred to as microbiomes [2]. These countless microbial communities thrive in various regions, forging a complex and diverse microbiome crucial for maintaining individual well-being. Disruptions in this delicate balance can lead to a host of ailments, including autoimmune conditions, cardiovascular disorders, and even cancers [3]. Consequently, analyzing the human and animal microbiome is paramount in understanding health. Microbiome research has witnessed an unprecedented surge in recent decades, captivating the attention of both the scientific community and the general public [4]. This burgeoning field of study has kindled profound curiosity and fascination among scientists and individuals alike. An all-encompassing investigation is currently underway to categorize and unravel the functional roles of the human microbiome, cementing its status as an indispensable powerhouse in the realm of health and disease [5].

The human microbiome plays a vital role in human development, immunity, and nutrition, where beneficial bacteria establish themselves as colonizers rather than destructive invaders. For example, vaginal Lactobacilli produce lactic acid, maintaining a low pH to protect against pathogen growth. Disorders in the microbiome have been linked to autoimmune conditions such as diabetes, rheumatoid arthritis, muscular dystrophy, multiple sclerosis, and fibromyalgia. Intriguingly, research suggests that these autoimmune diseases may be transmitted not through DNA inheritance but by inheriting the family's microbiome. The human microbiome also exhibits significant effects such as preventing pathogen invasion by inducing competition for resources and space, boosting the host's immune response, producing pathogen-harming antibiotics (Colicins), synthesizing essential vitamins like K and B, and occasionally becoming pathogenic when host defenses weaken. Additionally, the ubiquitous presence of the human microbiome and its resemblance to certain pathogens can sometimes lead to diagnostic confusion.

Recognizing the immense importance of the human microbiome, the National Institutes of Health (NIH) launched the Human Microbiome Project (HMP) in 2008. This ambitious five-year initiative, with a budget of around $115-$150 million, aimed to map the microbial composition of healthy individuals using genome sequencing techniques. On June 13, 2012, the HMP investigators established a reference database and identified the range of normal microbiome variation in humans. The NIH continues to support the Human Microbiome Project, funding research to catalog the diverse bacteria that inhabit humans and investigate correlations between microbiome changes and human health. The objectives of the HMP encompass the comprehensive characterization of the human microbiome, including its composition, diversity, function, and gene sequencing, as well as exploring the association between infections and microbiome modifications. The project also focuses on developing new computational methods and devices, establishing a resource repository, and addressing the ethical, legal, and social implications of human microbiome research.

This chapter aims to provide an overview of the significant role of microbes and microbiomes in ensuring the security of human and animal health, shedding light on their profound impact on various aspects of well-being.

OUTLINE OF HUMAN AND ANIMAL MICROBIOME (NORMAL FLORA)

The human body harbors a diverse array of microorganisms known as normal flora, which peacefully coexist without causing disease [6]. In a fascinating revelation, it has been discovered that our bodies are inhabited by over 10 times more microbial cells, totaling nearly 100 trillion cells, than human cells [7]. Astonishingly, despite their abundance, the collective weight of the microbiome is approximately 200 grams. These microbiomes constitute intricate ecological communities consisting of symbiotic organisms, commensals, and potentially pathogenic microorganisms that reside in various regions of our bodies. Among these regions, the gut is home to the most prominent microbial residents, while the skin and genitals also host significant populations. What is truly remarkable is that these microorganisms, along with their genetic material, establish their presence within us from the moment of birth and persist throughout our entire lives [8].

Microbes begin to populate the human body from the moment of birth. Newborns acquire microorganisms through various means, primarily from their mothers, during the delivery process. This transmission occurs either through a passage through the birth canal or by coming into contact with the mother's skin during a cesarean procedure. Among the crucial bacteria involved in this microbial transfer is Lactobacilli, a resident flora naturally inhabiting the mother's vagina. These beneficial bacteria colonize the baby's gut, playing a vital role in enhancing the digestion of lactose sugar found in milk [9]. What makes each person's microbiome truly unique is the fact that no two individuals share the exact same

SUBJECT INDEX

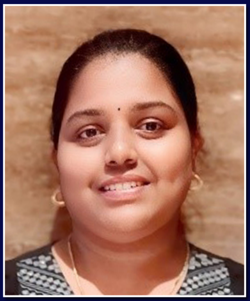
Shiv Prasad, Govindaraj Kamalam Dinesh, Murugaiyan Sinduja, Sathya Velusamy, Ramesh Poornima & Sangilidurai Karthika (Eds.)

Shiv Prasad

Shiv Prasad is a principal scientist (ARS) with 26 years of experience in agricultural research and teaching. He holds Ph.D. from ICAR-Indian Agricultural Research Institute, New Delhi, India. He has contributed significantly to biomass waste recycling, screening, and evaluation of fungal, bacterial, and yeast strains for saccharification and ethanol fermentation, monitoring and impact assessment of greenhouse gases, air pollution, heavy metals, and their effect on agriculture. He has published over 167 research and review articles, 4 books, and 35 chapters. His research works have been extensively cited more than 7735 times with an H-index of 36 and i10-index of 70. He has been honoured with several prestigious awards, including the National Dr. Rajendra Prasad Award (ICAR), International Award (Elsevier) for best papers in the past 30 years, distinguished researcher award in ecology, and editor in many prestigious journals.

Govindaraj Kamalam Dinesh

Govindaraj Kamalam Dinesh is an assistant professor of environmental sciences at SRM Institute of Science and Technology, holds Ph.D. from ICAR-Indian Agricultural Research Institute, New Delhi. He is a young advantage fellow (Institute of Biosciences, USA) and research fellow (INTI International University, Malaysia). With more than 25 peer-reviewed papers, 14 book chapters, and more than 70 popular articles, he serves as a subject expert for Tamil Nadu Public Libraries' Book Selection Committee, Government of Tamil Nadu. He has working experience as a journalist and editorial member in a top magazine and journals. His goal is to bridge the gap between science and society, creating an inclusive and dialogic learning environment.



Murugaiyan Sinduja

Murugaiyan Sinduja is a technical executive at National Agro Foundation. She was awarded doctoral degree from Tamil Nadu Agricultural University. She is a distinguished environmentalist specializing in heavy metal remediation. With more than 30 research publications and more than 10 book chapters. She has mentored more than 100 internship students from various colleges and participated in over 20 conferences, earning multiple awards. She is a certified lead auditor for FSSC 22000 Version 6, which contributed to the development of the quality system of all industries worldwide.

Sathya Velusamy

Sathya Velusamy is an environmental scientist at Tamil Nadu Pollution Control Board with masters and doctorate in environmental sciences from Tamil Nadu Agricultural University. She is with lot of aspiration towards research and her research arena intrigued towards bioremediation and phytoremediation which gave her an identity in the field of environmental pollution and remediation. She has received a grant from DST -SERB funded scheme under the Early Career Research Award. She also has excellence in the field of organic agriculture, soil health enhancement and development of sustainable technologies for remediation of contaminated sites. She is involved actively in the study of "Soil Quality Mapping across Industrial Areas of Tamil Nadu using Geospatial Tools".

Ramesh Poornima

Ramesh Poornima is an assistant professor of environmental sciences at Vanavarayar Institute of Agriculture, Pollachi, Tamil Nadu. She holds a Ph.D. in environmental sciences from Tamil Nadu Agricultural University (TNAU), specializing in mitigating ozone stress on rice cultivars. Her research focuses on environmental sustainability, including bioremediation, composting, and the effects of microplastics on agriculture. She has worked as a senior research fellow on projects funded by ISRO and TNPL, contributing to studies on industrial effluent irrigation and environmental impact assessments. She has published extensively in the international journals and has guided student research in composting technology. She is well known for her practical expertise in environmental science, and has received awards for her research and presentations. She actively participates in national and international conferences, making significant contributions to the field of climate-resilient agriculture.

Sangilidurai Karthika

Sangilidurai Karthika is an environmental researcher with Ph.D. in environmental sciences from Tamil Nadu Agricultural University. She has received the Commonwealth Split-site Ph.D. Scholarship and the Department of Science and Technology—Student Junior Research Fellowship. Her publications are extensive, and she excels in microplastics analysis, risk assessment, and ecotoxicological studies. Her broad experience in environmental quality parameters, including soil, water, and wastewater, makes her a distinguished scientist.