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Ecological Functions and Microbial Diversity in Terrestrial and Aquatic Environments: New Approaches in Biotechnology and Bioinformatics for Environmental Monitoring and Management: A Mini Review

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Abstract

Microbial diversity and ecological roles in terrestrial and aquatic environments are considered to be fundamental pillars of maintaining biological balance and ecosystem sustainability. Investigating microbial communities using advanced biotechnology and bioinformatics approaches has enabled accurate analysis and effective management of environmental health. This review article provides a comprehensive analysis of the biodiversity of microorganisms, especially bacteria and fungi, and examines their effects on bioremediation processes, nutrient cycles, and maintaining ecological balance in soil and water. The use of advanced methods such as 16S rRNA gene sequencing and bioinformatics tools has enabled more precise identification of the structure, function, and dynamics of microbial communities down to the molecular level. These techniques play an important role in identifying key species, assessing the effects of pollution, and predicting the response of microbial communities to environmental changes. Research conducted between 2023 and 2025 has shown that the integration of biotechnology with bioinformatics offers new methods for environmental monitoring, improving soil and water quality, and sustainable management of pollutants. In addition to highlighting the importance of microbial diversity as environmental indicators, this study also addresses the challenges and opportunities in the development of biomonitoring technologies and bioinformatics modeling.

Key words: Microbial diversity, Soil, Water, Biotechnology, Bioinformatics, Environmental monitoring, Microbial ecology

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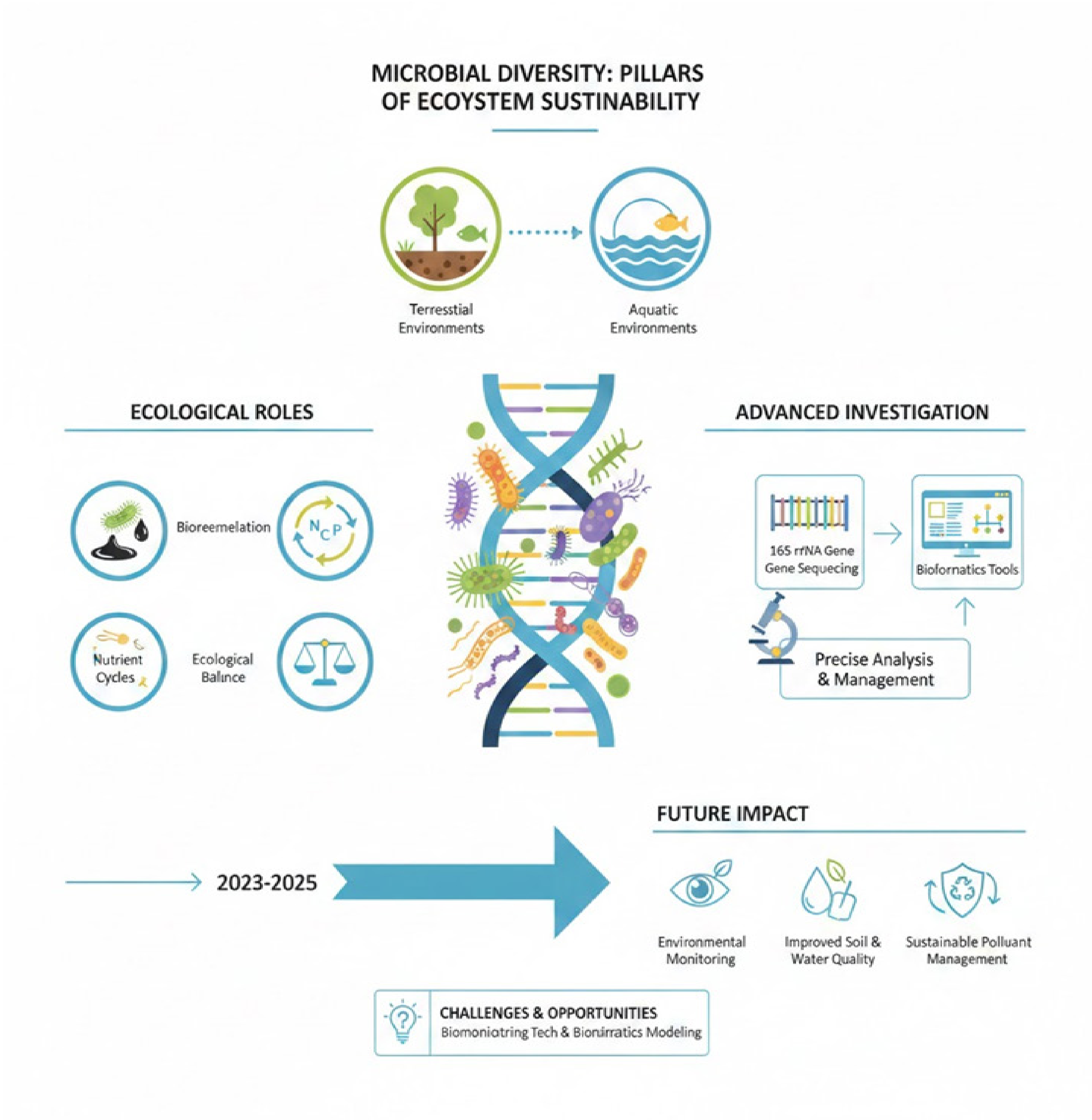
Graphical Abstract



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Introduction

Life on Earth is inextricably linked to the hidden activities of microorganisms. These microscopic entities, ubiquitous in every habitat from the deepest ocean trenches to arid deserts, are responsible for executing the vital processes that sustain the biosphere(Nandal et al., 2025). Their ecological functions encompassing the cycling of key elements like carbon, nitrogen, and phosphorus, the decomposition of organic matter, and the establishment of symbiotic relationships with plants and animals form the foundation of ecosystem health and resilience (Ogidi et al., 2024). Microbial biodiversity extends beyond species counts to encompass genetic, functional, and metabolic diversity within communities This high diversity confers stability and adaptability to ecosystems. In soil, for instance, a diverse microbiome can simultaneously support multiple functions, such as nitrogen fixation, phosphorus solubilization, and the production of plant growth hormones, directly impacting agricultural productivity(Kumar et al., 2021) In aquatic environments, microbes channel energy from dissolved organic matter to higher trophic levels through the microbial loop, playing a central role in primary production and nutrient cycling (Chinthala, 2016) Despite their importance, our understanding of microbial community dynamics was long hampered by the limitations of traditional culture-based techniques. These methods identify only a small, biased fraction of environmental microbes, leading to the great plate count anomaly and a profoundly incomplete picture of ecosystem function (Satyanarayana et al., 2019). The dawn of the NGS era in the early 21st century marked a watershed moment in environmental microbiology. These technologies allow for the sequencing of total community DNA (metagenomics) or RNA (metatranscriptomics) directly from an environmental sample, bypassing the need for cultivation(Chandran et al., 2020). The enormous volume of data generated by these approaches, often termed the data deluge, is unmanageable without sophisticated bioinformatics tools. Bioinformatics now serves as the backbone of omics analyses, performing essential tasks such as quality control, sequence assembly, gene annotation, and comparative community analysis(Ininbergs et al., 2015). This review aims to provide an integrated perspective on these recent advances. We first examine the ecological functions and microbial diversity in terrestrial and aquatic ecosystems. We then introduce the novel biotechnological and bioinformatic approaches that have enabled this new level of insight. Finally, we discuss the practical applications of this knowledge in environmental monitoring, management, and restoration.

Ecological Functions and Microbial Diversity in Ecosystems

Terrestrial Environments: The Role of Soil as a Living Ecosystem

Soil is a living, dynamic natural resource whose health is directly dependent on its resident microbial community. The soil microbiome is arguably the most complex and diverse biome on the planet , and its key functions include nutrient cycling, in which bacteria and fungi act as the primary agents of mineralization by converting organic matter into plant-available forms; nitrogen fixation, performed by symbiotic bacteria such as *Rhizobium* and free-living bacteria such as *Azotobacter*, represents one of the most critical biogeochemical processes on Earth. In addition, soil microorganisms play a vital role in plant health, as plant growth–promoting rhizobacteria (PGPR) and mycorrhizal fungi enhance plant fitness through hormone production, increased nutrient uptake, and induced resistance against pathogens and pests (Banerjee & Van Der Heijden, 2023). Microbes also contribute significantly to soil structure, particularly fungi, which produce extracellular polymeric substances that bind soil particles into stable aggregates, thereby improving water infiltration, aeration, and resistance to erosion. Furthermore, indigenous soil microbial communities possess remarkable catabolic potential for bioremediation, enabling them to degrade a wide range of pollutants, including petroleum hydrocarbons, pesticides, and heavy metals, and thus providing a sustainable, green solution for the remediation of contaminated land (Bronick & Lal, 2005; Sax et al., 2013)

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Aquatic Environments: The Engines of Oceans and Freshwater Systems

Microbes also contribute significantly to soil structure, particularly fungi, which produce extracellular polymeric substances that bind soil particles into stable aggregates, thereby improving water infiltration, aeration, and resistance to erosion; furthermore, indigenous soil microbial communities play a crucial role in maintaining soil functionality through their diverse metabolic activities(Negi et al., 2025).

New Approaches in Biotechnology and Bioinformatics

The Omics Revolution: Beyond Single Gene Sequencing

Omics technologies provide a holistic and unbiased view of microbial communities by integrating multiple high-throughput approaches. Metagenomics, through sequencing of the total DNA extracted from a sample, reveals the collective genetic potential or metagenome of the community and enables the discovery of novel metabolic pathways as well as previously unknown taxa (Mathuria et al., 2024), etabarcoding, a widely used complementary technique, focuses on sequencing specific marker genes such as the 16S rRNA gene for bacteria and archaea or the ITS region for fungi to assess taxonomic diversity and overall community composition(Falkowski et al., 2008). Metatranscriptomics extends this analysis by sequencing total RNA, or the metatranscriptome, thereby identifying which genes are actively expressed under particular environmental conditions and offering insight into the real-time functional state of the community. Finally, metaproteomics and metabolomics examine the total protein complement (metaproteome) and the complete set of small molecules (metabolome), respectively, providing the most direct representation of the biochemical activities occurring in situ(Antil et al., 2023).

The Critical Role of Bioinformatics

Analyzing the massive datasets generated by omics approaches is impossible without bioinformatics. Standard software pipelines and platforms, such as QIIME 2 for metabarcoding analysis and MG-RAST for metagenomic data, perform crucial tasks including raw data processing through demultiplexing, quality filtering, and removal of adapter and primer sequences(Dixit et al., 2024). These tools also handle clustering or denoising by grouping sequences into Operational Taxonomic Units (OTUs) or more precise Amplicon Sequence Variants (ASVs). In addition, they enable taxonomic and functional annotation by assigning taxonomic identities to sequences using reference databases such as SILVA and Greengenes, and by predicting functional potential from gene data using tools like PICRUSt. Finally, bioinformatics platforms support comprehensive statistical analyses, including the calculation of diversity metrics such as alpha diversity, which reflects within-sample richness, and beta diversity, which measures between-sample dissimilarity and the identification of patterns associated with environmental variables(Smith et al., 2020).

Applications in Environmental Monitoring and Management

The integration of microbial ecology with new technologies has led to numerous practical applications. One of the most important of these is biological monitoring (biomonitoring), in which changes in the structure or function of microbial communities can serve as an early-warning system for environmental disturbances. For example, a reduction in overall microbial diversity accompanied by a relative increase in metal-resistant taxa can indicate soil contamination with heavy metals. Similarly, in coastal waters, monitoring shifts in microbial community composition can help predict harmful algal blooms (HABs) before they become visually detectable(Esposito et al., 2025). Another key application is bioremediation. By identifying the microorganisms or genes responsible for degrading specific pollutants, the efficiency of environmental cleanup processes can be significantly improved. This enhancement can be achieved through bioaugmentation, which involves introducing highly efficient microbial strains into contaminated sites, or through biostimulation, which focuses on optimizing environmental conditions such as nutrient availability to stimulate the activity of indigenous pollutant-degrading microorganisms. In addition, microbial ecology plays a critical role in sustainable ecosystem management. In agriculture, analysis of the soil microbiome can guide the development of biofertilizers and biopesticides, thereby reducing dependence on chemical inputs. In conservation efforts, assessing the microbial health of sensitive ecosystems such as coral reefs or wetlands provides valuable information for management decisions and supports effective restoration and conservation strategies (Nandy et al., 2022).

Conclusion and Future Perspectives

The integration of modern biotechnology, especially next-generation sequencing (NGS), with advanced bioinformatics analyses has revolutionized our understanding of the diversity and ecological functions of microorganisms. These approaches have enabled the study of microbial communities on an unprecedented scale and have created a link between fundamental knowledge and practical applications. The focus of research has shifted from the mere identification of microorganisms to understanding their function and response to the environment. Despite significant progress, challenges and opportunities remain, such as the integration of multi-omics, the transition from correlation to causation, and the development of predictive models. Ultimately, effectively harnessing the potential of the microbial world will play a key role in achieving sustainable development and facing the environmental challenges of the 21st century.

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