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Metagenomic Approaches for Optimizing Pollution Management in the Bay of Bengal, Bangladesh: A Comprehensive Review

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Abstract: The Bay of Bengal, a vital marine ecosystem of the northeastern Indian Ocean, is struggling with growing environmental changes that hamper its ability to compromise its ecological stability and the livelihoods of many communities depending on its resources. Among the other environmental issues affecting the Bay of Bengal, urban trash, industrial discharges, and agricultural runoff severely compromise the health of its marine life. Dealing with these issues calls for a significant awareness of the existing microbial populations, since they are essential for the ecosystems functioning and the resistance against pollution. Understanding the microbial diversity of the Bay of Bengal will enable us to design focused pollution control plans that support sustainable use of its resources and preserve its unique ecosystems. Metagenomics offers unparalleled resolution in dissecting the intricate microbial assemblages inhabiting the Bay of Bengal, thereby identifying key species involved in pollution degradation and enabling targeted bioremediation programs. This approach can allow us to restore the health of the Bay of Bengal ecosystem and raise our capacity to reduce the pollution effects. Moreover, metagenomics-based research on microbial populations can facilitate the development of new biotechnological techniques for ecosystem restoration, enabling the development of targeted monitoring programs. Recent metagenomics studies highlight the importance of Proteobacteria in ecological assessments and pollution control, as they, along with various eukaryotic taxa, form a major part of the microbial consortia in the Bay of Bengal. These results support an increasing amount of research stressing the need to include metagenomics data into policy frameworks for regional sustainable environmental management. This review emphasizes the escalating environmental challenges confronting the Bay of Bengal, with a specific focus on the transformative potential of metagenomics and how it can revolutionize pollution management.

Keywords: Metagenomics, Bay of Bengal, Pollution Management, Bioremediation, Marine Microbiology, Environmental Monitoring.

Review Paper

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1. INTRODUCTION

The Bay of Bengal is the largest marine embayment in the world, characterized by its unique geographic setting in the northeastern part of the Indian Ocean, bordered by India, Bangladesh, and Myanmar. Its distinctiveness arises from the substantial freshwater influx from major river systems, most notably the Ganges and the Brahmaputra, which discharge massive loads of freshwater and sediments (Amsalia *et al*., 2022).

Geographically situated in an area prone to notable monsoonal activity, the Bay of Bengal shows clear seasonal fluctuations in weather patterns, which in turn greatly affects oceanographic conditions, including currents, upwelling, and mixing processes, including nutrient cycling and plankton development (Mili *et al*., 2021). It also protects a range of marine habitats including coral reefs, mangrove forests, and estuaries supporting a great biodiversity, providing the livelihoods of the coastal communities and playing a major part in regional fisheries (Aprilia *et al*., 2022). Comprising commercially valuable fish stocks, marine mammals, and sea turtles, these areas offer a broad range of marine species that substantially help to balance the ecosystem of the region.

Therefore, it is of utmost necessity to protect the Bay of Bengal ecosystem, maintain its water quality, and reduce environmental pollution affecting it.

Metagenomics is a powerful method for decoding microbial populations and their functional capacity within complicated environmental matrices, presenting unprecedented insight into the roles of microorganisms in biogeochemical cycling, pollutant degradation, and ecosystem functioning (Kuang *et al*., 2023). Metagenomics directly analyzes the collective genetic material acquired from an environmental sample providing a whole perspective of the genetic potential of the microbial community without the need to isolate or culture individual bacterial species. The relevance of metagenomics application is further enhanced in marine pollution assessment, offering unparalleled chances for discriminating the complex interactions between pollutants and indigenous microbial communities. This approach facilitates the identification of key microbial indicators of pollution, as well as the elucidation of biodegradation pathways. Additionally, metagenomics allows for the evaluation of the capacity of marine ecosystems to maintain functionality and resist irreversible damage when subjected to pollution, providing valuable insights into the general health and resilience of the systems (Diner *et al*., 2024; Oros, 2025). Combining multi-omics data with cutting-edge artificial intelligence techniques opens unparalleled opportunities for complete environmental management and conservation projects, as well as opening a new chapter in our understanding of the intricacy of this ecosystem.

2. Pollution Challenges in the Bay of Bengal, Bangladesh

The Bay of Bengal faces a variety of pollution along the coast of Bangladesh, posing notable environmental and health challenges. The region is being affected by several sources of pollution, such as industrial discharges, shipbreaking activities, and land-based pollutants, which are one of the few reasons behind the degradation of marine ecosystems and health risks to humans. These pollution challenges are aggravating the complex situation due to the lack of sufficient monitoring and administration mechanisms.

2.1 Sources of Pollution

- **Industrial Discharges:** Many industrial zones, including those for textile manufacturers, leather processing factories, companies, pharmaceuticals, and chemicals, abound on Bangladesh's shore. Country's freshwater resources are being polluted by about 20% due to the discharge of textile and dyeing industries in Bangladesh, contributing approximately 12.7–13.5 million m³ of wastewater annually. Heavy metals and other toxic substances are often found in high concentrations that in due course end up in the Bay of Bengal (Biswas *et al*., 2021) (Rashid *et al*., 2014).
- **Shipbreaking Yards:** The shipbreaking industry is another significant source of pollution in the marine environment. Every year around 22.5 tons of polychlorinated biphenyls (PCBs) are released into the water. This industry also contributes to heavy metal contamination in the marine environment and disrupts the ecosystems (Biswas *et al*., 2021) (Mostafa *et al*., 2024). The impact of ship breaking activities creates pollution from heavy metals (lead, chromium, arsenic, cadmium) and other physico-chemical parameters that degrade the water quality in the coastal city of Chattogram, Bangladesh. It also contributes to ecological risks and moderate heavy metal pollution, eventually disrupting marine life in the Bay of Bengal (Nath *et al*., 2023).
- **Land-Based Marine Pollution (LMP):** The Bay of Bengal faces approximately 80% of the pollution that comes from land-based activities such as agricultural runoff, sewage, and urban waste. Through river flow and direct coastal runoff, the intensive farming in the Ganges-Brahmaputra delta supplies a lot of nutrients for the Bay of Bengal. These pollutants are passed by major rivers such as the Ganges and Brahmaputra into the Bay of Bengal (Alam *et al*., 2023). This type of pollution significantly affects the Bay of Bengal by damaging water quality, damaging the marine ecosystem, reducing fisheries productivity, and causing serious health risks for coastal communities.
- **Plastic Waste:** About 3000 tons of plastic waste are being generated on a daily basis in Bangladesh. It poses a major threat to the marine environment by causing significant amounts of plastic pollution. This issue is aggravating without proper waste management infrastructure (Biswas *et al*., 2021; Islam *et al*., 2022). Microplastics (MPs) were detected in the form of different polymer types, including PE, from the estuaries of the northern Bay of Bengal coast. Their contribution to the marine pollution comes from different origins, including industrial activities aggravating the ecological risk in these estuarine ecosystems (Banik *et al*., 2023).

3. Metagenomic Technologies and Methodologies

The first step in metagenomics research is choosing an appropriate ecological or biological environment of interest that supports a broad range of microbial populations. Metagenomics is mostly applied where environments are harsh or have unique factors such as extreme acidic environments or alkaline pH, high metal concentrations, pressures, or radiation, high salinity, or extreme temperatures (Michan *et al*., 2021). Evaluating marine pollution in the Bay of Bengal via metagenomics involves the most important and critical processes, such as sample collection and processing (Figure 1). Hence, great efforts should be given to sampling tactics, preservation procedures, and DNA extraction methods.

Water column sampling, often conducted at varying depths, serves to capture the vertical stratification of microbial communities, while sediment samples provide insight into protracted pollution impacts and anaerobic degradation processes, thereby enabling a comprehensive understanding of the ecological consequences of anthropogenic activities (Akter *et al*., n.d.) (Kopprio *et al*., 2020). In addition, biofilm samples, meticulously gathered from both artificial and natural sources, decipher community-level responses to persistent pollutant exposure (Coclet *et al*., 2021; Yu *et al*., 2025). This process shed light on microorganisms' adaptation mechanisms to withstand chronic environmental stressors.

Existing metagenomics studies primarily focused on Illumina short-read sequencing platforms, with their capacity to generate an expansive volume of sequence reads at a low cost per base (Zhang *et al*., 2021). Second-generation short-read sequencing (SRS) technologies have high error rates, and incorrect reconstruction of complex microbial communities makes issues with the recovery of metagenome-assembled genomes (MAGs) essential for microbial ecology and function assessment (Grossart *et al*., 2020). To overcome the limitations, particularly in resolving complex genomics architecture and repetitive regions, long read sequencing techniques such as Pacific Biosciences and Oxford Nanopore technologies are increasingly being used (Lui *et al*., 2024). Target amplicon sequencing, 16s rRNA genes are also used to assess bacterial diversity with the help of high-throughput sequencing technologies (Michan *et al*., 2021). Metagenomic data analysis needs sophisticated bioinformatics to handle the complexity and volume of environmental sequence data. Raw sequence reads undergo rigorous quality control procedures, entailing trimming of low-quality bases and removal of adapter sequences that ensure the integrity of downstream analyses.

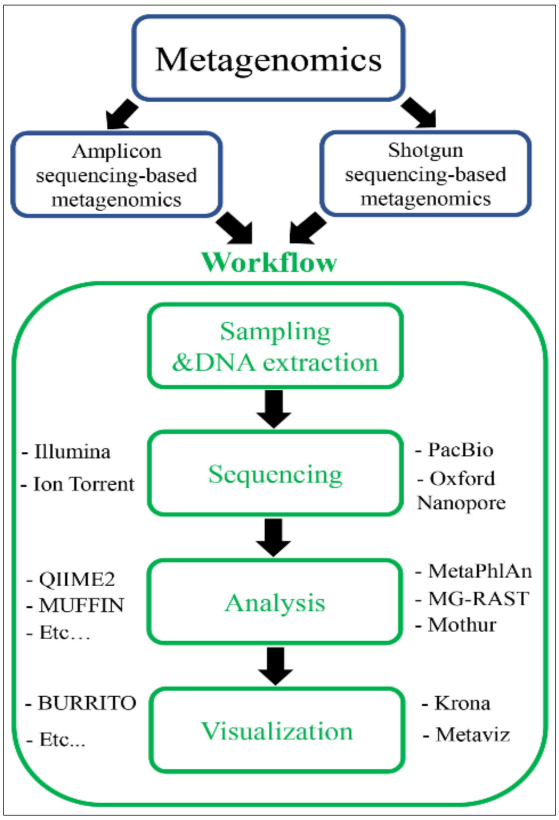

Figure 1: Classification (blue rectangles) and workflow (green rectangles) of metagenomics using different sequencing platforms and bioinformatics tools (Nam *et al*., 2023)

4. Applications for Pollution Assessment and Monitoring Identification of Microbial Communities

Metagenomics has emerged as a powerful tool for assessing and monitoring pollution in various ecosystems, including marine and freshwater environments. It plays a crucial role in pollution assessment and monitoring their functions directly collected from marine ecosystems. Metagenomics also detects any kind of novel bacteria and gene clusters that can degrade pollutants giving information about the health of marine environments. Moreover, pathogen monitoring contributes to a better understanding of pollution on marine biodiversity and ecosystem dynamics and its impacts (Datta *et al*., 2020).

4.1 eDNA Metabarcoding

Extracting and analyzing environmental DNA (eDNA) is becoming an increasingly common approach for assessing and monitoring ecosystems (Singer *et al*., 2020). To assess marine pollution a technique called eDNA metabarcoding is beneficial by distinguishing a wide range of pollutants such as oil spills, harmful algal blooms, heavy metals, ballast water, and microplastics. It allows the extraction of genetic information from environmental samples and gives information about community compositions and the indirect effects of pollution on biodiversity. eDNA is not the direct indicator of pollution but it is used as a tool to monitor ecological health changes and assess the limit of marine pollution (Rishan *et al*., 2024).

4.2 Genome-centric Metatranscriptomics

Genome-centric metatranscriptomics helped to find out chronic hydrocarbon pollution in marine ecosystems by checking the responses of microbial communities. For this process, microbial mat samples are analyzed which in turn reveal aerobic and anaerobic hydrocarbon degradation pathways. This gives important information about the dynamics of microbial communities and practical role in pollution degradation. This approach identifies active microbial populations and their metabolic pathways to assess pollution, notify bioremediation strategies, and evaluate the health of ecosystems (Vigneron *et al*., 2024).

5. Bioremediation Applications

5.1 Xenobiotic Bioremediation

The contamination caused by complex xenobiotic compounds that are highly toxic and persistent in nature, is a global environmental issue. Metagenomics is particularly useful for bioremediation to degrade or neutralize environmental pollutants including xenobiotics. Metagenomics provide detailed information of genetic and metabolic profiles to help detect distinct microbial communities for effective participation in the bioremediation process (Ottoni *et al*., 2023).

5.2 Hydrocarbon Bioremediation

Microorganisms that can degrade hydrocarbon in marine environments belonging to Proteobacteria and Actinobacteriota phyla have been identified through metagenomic approaches. Microbes that degrade hydrocarbon possess multiple copies of hydrocarbon biodegrading genes amplifying the ability to degrade various hydrocarbons. The Deepwater Horizon oil spill in the Gulf of Mexico in 2010 featured the unity of microbial communities in hydrocarbon bioremediation exhibiting highly adaptive and intricate dynamics (Weiman *et al*., 2021). This event gave new ideas to the progress of new techniques for monitoring ecosystem health and assessing bioremediation efficacy. Metagenomics also identified a particular strains *Oceanicaulis alexandrii* NP7 which have significant potential for hydrocarbon and heavy metal bioremediation (Liu *et al*., 2024) (Dell'Anno *et al*., 2021).

One notable example of a pollutant-degrading gene cluster identified through metagenomics is the alkB gene, which encodes alkane monooxygenase—an enzyme crucial for the initial oxidation of medium- to long-chain alkanes found in petroleum-based pollutants. This gene is often part of a broader operon that includes accessory proteins like rubredoxin and rubredoxin reductase, which facilitate electron transfer during hydrocarbon degradation. Metagenomic studies in oil-contaminated marine environments, such as those conducted following the Deepwater Horizon oil spill, revealed a high abundance of *Alcanivorax*, *Pseudomonas*, and *Marinobacter* species carrying alkB and related hydrocarbon-degrading genes, confirming their essential role in natural bioremediation processes (Hu *et al*., 2016).

5.3 Microplastics Bioremediation

Metagenomics, when incorporated with metatranscriptomics and metabolomics, can efficiently identify microbial communities capable of degrading microplastics. While metagenomics reveals what microbial species are present and what genes they possess (e.g., genes encoding plastic-degrading enzymes), Metatranscriptomics informs us which microbial genes are expressed in real time indicating which pathways are active under specific environmental conditions (e.g. plastic pollution) and Metabolomics examines the metabolites produced during microbial metabolism at the time of plastic degradation. This procedure enables the discovery of new enzymes and microbial consortia that can be employed in microplastic remediation efforts. Rapid screening and prediction of genes involved in polymer degradation are possible through the fusion of bioinformatics and sequencing tools, which will benefit the development of effective microplastic bioremediation strategies (Wani *et al.,* 2023).

5.4 Heavy Metal Bioremediation

Some microbes including bacteria, fungi, and archaea show innate resistance to metal toxicity and can alter metals into less harmful forms. Metagenomic approaches unveils microbial diversity and functional genes associated with heavy metal bioremediation. The application of metagenomics in heavy metal bioremediation starting from environmental sampling and sequencing can detect the diversity and function of microbial communities in polluted environments and thereby help in the selection of effective bioremediation agents (Khan *et al*., 2022), (Wimalasekara *et al*., 2023).

6. Recent Findings in the Bay of Bengal

Recent studies on deep-sea sediment metagenomes from the Bay of Bengal have shown dominance of Proteobacteria and uncovered genes involved in carbon fixation, sulfur and nitrogen metabolism, pollutant degradation (including plastics, dyes, hydrocarbons), antibiotic resistance, and metal tolerance (Marimuthu, J *et al*., 2022).

Coastal surveys in Cox's Bazar and Saint Martin Island identified dominant bacterial genera such as Alteromonas, Methylophaga, and Vibrio, alongside abundant eukaryotic groups like Ochrophyta and Dinoflagellata, with microbial communities carrying genes associated with biofilm formation, quorum sensing, antimicrobial resistance, and xenobiotic degradation (Akter, S. *et al*., 2023).

Metagenomic analysis of the Bay's virome further unveiled nearly 2,000 putative phage genomes—including large phages and giant viruses—harboring auxiliary metabolic genes, signifying a potentially significant influence on microbial food webs and biogeochemical cycling (Minch, B *et al*., 2023).

Research priorities in the Bay of Bengal should include exploration of under-examined habitats such as deep-sea and benthic zones, which may host unique microbial communities vital for ecosystem services. Longitudinal studies are needed to elucidate temporal shifts in microbial diversity and function in response to seasonal cycles and anthropogenic stressors. Investment in integrated multi-omics approaches and strengthened data infrastructure will be essential to advance collaborative research and support effective marine conservation strategies.

7. Case Studies

7.1 Microbial Diversity of USA region

Time-series analysis of sediment microbial communities in the Stellwagen Bank National Marine Sanctuary revealed that species richness inversely correlated with fishing activity levels, therefore demonstrating the effect of human activities on microbial biodiversity. Furthermore, the identification of certain biosynthetic gene clusters suggests potential medical relevance for natural product discovery. A metagenomics profiling of coastal waters near Sapelo Island recovered 45 metagenome-assembled genomes (MAGs), including members of marine group II Euryarchaeota and archaea like *Thaumarchaeota*. This work underlined the important role that microorganisms play in the biogeochemistry of coastal waters, which get organic matter from several sources. A complete dataset from Monterey Bay during a dinoflagellate bloom shed light on the bacterial and archaeal genes and their functional roles, enhancing our knowledge of microbial community dynamics during episodic phytoplankton blooms (Bruce *et al.,* 2022; Damashek *et al*., 2019).

7.2 Galicia Coastal Ecosystem

Metagenomic methods have been applied in Galicia, Spain, to track eukaryotic populations and detect possible diseases in maritime environments with important implications for the aquaculture industry and ecosystem health. The study identified several protists and toxic algae, emphasizing the use of metagenomics in evaluating the condition of marine ecosystems and spotting any hazards from invasive species and diseases (Nowinski *et al*., 2019) (Figure 2).

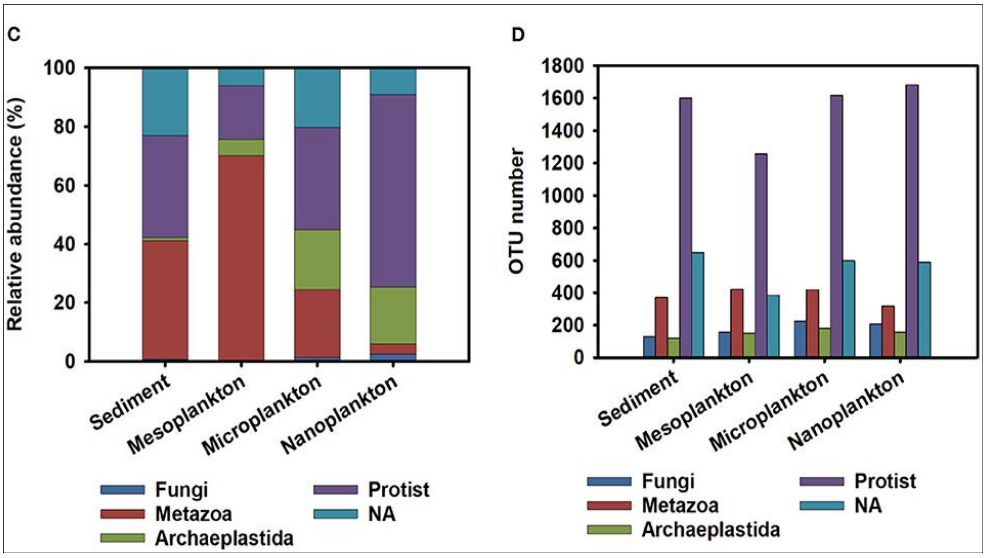

Figure 2: An overview of the variety of eukaryotic organisms found in the environment. In environmental samples (C), the relative abundance (%) of the various taxonomic groups is displayed. Analysis was done on the diversity of taxonomic groups (D) (Nowinski *et al*., 2019)

The list of invasive metazoan species found in sediment and water samples, along with their prospective invasiveness scores, is shown in Table 1 whereas Table 2 lists the multitude of possible diseases found in the environmental metazoan and fungal taxonomic groups (Ríos-Castro *et al*., 2021).

Table 1: List of invasive species of the metazoan group detected in sediment and water samples, with their potential invasiveness scores. Data adapted from Ríos-Castro *et al*., (2021), with invasiveness scores based on Tsiamis *et al*., (2020)

Invasive species	Taxonomy	Sediment	Water	Score
Xenostrobus securis	Mollusca, Bivalva	29	1763	48
Pseudodiaptomus marinus	Arthropoda, Hexanauplia	0	2501	46
Microcosmus squamiger	Chordata, Ascidiacea	2	20	42

Table 2: Variety of potential pathogens identified within the metazoan and fungal taxonomic groups present in the environment (Ríos-Castro *et al*., 2021)

Pathogenic species	Organism	Sediment	Water	Hosts
Cnidaria	*Kudoa unicapsula*	0	25	Several fish species
	Myxobolus exiguus	1	17	Myxobolids
	Parvicapsula anisocaudata	2	7	*Paralichthys olivaceus*
Platyhelminthes	*Acanthobothrium* sp.1	0	506	*Raja asterias*
	Diplectanum aequans	0	191	*Dicentrarchus labrax*
	Parvatrema sp. CG-2014	0	802	*Tagelus plebeius*
	Gymnophalloides seoi	0	610	Human intestinal parasite Oyster, second intermediate
	Bucephalus minimus	0	577	*Cerastoderma edule*
	Prosorhynchoides borealis	0	171	*Abra alba*
	Paragonimus kellicotti	1	153	Humans (consumption of undercooked crayfish meat)
	Dictyocotaster contracta	0	107	*Chelon labrosus*
Arthropoda	*Demodex folliculorum*	5	42	Human skin and eyes
Basidiomycota	*Malassezia* sp.	156	1,091	Human skin

7.3 Dinoflagellate Communities and Microbial Diversity

Using 18S rRNA amplicon sequencing, four Korean coastal areas investigated dinoflagellate communities to expose seasonal fluctuations and great species diversity that is notobservable with conventional microscopy. The investigation found dominating species causing detrimental algal blooms including *Cochlodinium sp*. and *Alexandrium sp* (Hwang *et al*., 2022) (Figure 3). A case study conducted on the northern shore of the Bay of Bengal, India, used metagenomics to investigate bacterial diversity in a contaminated environment. The study underlined the limitations of culture-dependent techniques and demonstrated metagenomics as a useful tool for revealing the large uncultured bacterial communities, therefore supporting its application in environmental monitoring (Chakraborty *et al*., 2022).

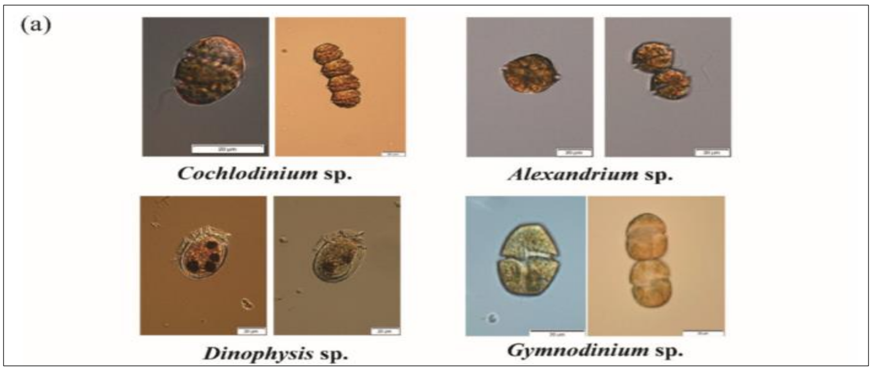

Figure 3: Seasonal distribution of red-tide-causing species through metagenome analysis in Korean coastal region (Hwang *et al*., 2022)

8. Policy Implications and Recommendations

8.1 Conservation and Marine Protected Areas (MPAs)

Metagenomics can significantly aid in our understanding of microbial diversity and ecological activities, thereby improving the design and monitoring of Marine Protected Areas (MPAs). Maintenance of biodiversity and ecosystem services is the basis of the blue economy approach as well. By means of omics technologies including eDNA metabarcoding, a reasonably affordable approach for monitoring biodiversity in vast and far-off conservation regions helps to maintain MPAs and guarantees their efficacy during conservation activities. Strong policy support and international cooperation are necessary to maximize the application of genetic technologies like CRISPR and eDNA monitoring for the preservation of threatened marine life (Jeffery *et al.,* 2022) (Van Oppen & Coleman, M. A. 2022).

8.2 Bioremediation and Pollution Management

Metagenomic helps to categorize microbial populations based on their ability to break down ubiquitous contaminants like polycyclic aromatic hydrocarbons (PAHs) present in chronically polluted marine habitats. This changing capability can improve bioremediation plans and enhancethe resilience of marine ecosystems to pollution. Evaluating microbial contributions to ecosystem processes and guiding economic valuation approaches for marine conservation, helps community genome-scale metabolic models (cGEMs) in guiding successful bioremediation strategies (Sieradzki *et al*., 2021) (Robaina-Estévez & Gutierrez, 2024).

8.3 Climate Change and Biogeochemical Cycles

Metagenomics enables the identification of metabolic pathways in marine microorganisms, which are integral to biogeochemical cycles and climate regulation. Understanding these pathways can facilitate the development of policies aimed at mitigating the impacts of climate change on marine ecosystems. The combination of metagenomics into ecological experiments and biogeochemical models can improve the foresightful understanding of microbial dynamics and their role in ecosystem-scale transformations, which is serious in the context of rapid climate change.

8.4 Biotechnology and Sustainable Resource Management

To get sustainable extraction of marine resources, metagenomic data can provide valuable insights by clarifying the functional roles of microbial communities in supporting ecosystem services. This information is vital for balancing ocean use with conservation efforts supporting a sustainable blue economy. The implementation of omics tools in marine resource management can develop the resilience of marine species against climate change and other anthropogenic disturbances, providing opportunities for the sustainable use of marine resources.

9. Challenges and Limitations

Metagenomics application in marine ecosystems provides considerable scope to understand microbial diversity and function; still it is struggling with extreme difficulties. These challenges are caused by technical, methodological, and ecological complexities in marine environments (Wani *et al*., 2023). Metagenomics has reshaped the study of previously unculturable marine microorganisms enabling the discovery of novel biosynthetic gene clusters and diverse microbial communities (Grossart *et al*., 2020). Nevertheless, the approach has its own limitations including related to sequencing technologies, data analysis, and ecological interpretation. The key challenges and limitations are briefed below-

1. Although third-generation sequencing technologies from PacBio and Oxford Nanopore, assistus to construct whole genomes data but their high error rates can complicate the assembly process and limit accuracy.
2. The tremendous diversity and complexity of marine microbial populations needs large sequencing depth and wide sample coverage to get the complete reflection of the diversity of these populations.
3. Powerful bioinformatics tools are consequently essential to manage the great volumes of data generated by metagenomic sequencing by sorting complex data and reconstructing genomes from mixed samples.
4. Identification of species within diverse microbial communities can be difficult if dealing with cryptic species that are morphologically similar but genetically distinct.
5. Although metagenomics is able to identify a vast quantity of genes, the majority of them lack functional annotation and the complex, largely uncharacterized interactions among microbes in marine ecosystems make it difficult to link metagenomically discovered genes to their specific ecological roles and their functions in biogeochemical cycling.

10. Future Directions

Metagenomics is opening exciting new doors to transform our understanding and utilization of marine biodiversity. Since most marine microbes cannot be cultured and remain largely unknown, metagenomic approaches offer a powerful means to explore the vast, hidden world of microbial life in our oceans. By combining metagenomics with the advanced analytical tools and next-generation sequencing technologies, metagenomics opens new opportunities for for biotechnological applications, ecosystem monitoring, and biodiscovery of valuable natural products.

10.1 Expanding Metagenomic Coverage and Depth

The Bay of Bengal remains largely under-researched and untapped till date. Future research should concentrate on under researched regions, most likely the deep sea and benthic zones to obtain a whole picture of how marine ecosystems function. Exploring under-researched areas to understand the impacts of human-induced changes, such as pollution and climate change, highlights the need for more advanced metagenomic techniques. (Singh, 2024) (Weiland-Bräuer *et al*., 2022).

Long-read sequencing platforms such as PacBio and Oxford Nanopore are expected to play an important role in metagenomics by enabling the retrieval of complete genes and operons. These technologies help overcome the limitations of short-read assemblies, allowing improved reconstruction of microbial genomes (Han *et al*., 2024).

10.2 Functional Metagenomics and Biotechnology

Functional metagenomics enables the identification of new enzymes and compounds for industries including pharmaceuticals, agriculture, and biofuels through screening bioactive molecules. When combined with metatranscriptomics and metabolomics, it becomes an even more powerful tool—allowing scientists to identify microbial communities capable of breaking down environmental toxins, including microplastics (Weiland-Bräuer *et al*., 2022).

10.3 Linking Metagenomics to Ecosystem Services and Biogeochemical Cycles

Ecosystem services and biogeochemical models applying metagenomics help us to understand how the motions of bacteria influence the dynamics of ecosystems. Community genome-scale metabolic models (cGEMs) can quantify the advantages of marine ecosystems and support bioremediation schemes when combined with meta-omics data. This enables the creation of natural-based economic systems (Robaina-Estévez & Gutierrez, 2024) (Grossart *et al*., 2020).

11. CONCLUSIONS

Metagenomic approach in marine environments is becoming a transforming instrument for comprehending the complex biodiversity and functional dynamics of marine life. By allowing the direct analysis of genetic material from environmental samples, metagenomics overcomes the limitations of conventional methods that often fail to capture the full taxonomic and functional diversity of usually unculturable marine microbial communities. Metagenomics has shown very successful approach by spotting undetectable species with new bioactive molecules, and improving biomonitoring initiatives helping to reveal the hidden resources of microbial communities. It has also identified the functional genomic potential of marine organisms that exposes a great range of bioactive molecules with possible uses in biotechnology such as the identification of functional genes and metabolic pathways that might be exploited for commercial use including medications and the generation of biofuel.

According to Laiolo *et al*., 2024, global initiatives like the Ocean Genome Project have further emphasized the importance of characterizing marine microbial diversity, mapping its functional potential, understanding its role in biogeochemical cycles and assessing the impact of climate change on ocean. The use of metagenomics in marine biomonitoring has shown promising aspect in rapid assessments of ecosystem health compared to traditional methods. When integrated with metatranscriptomics, metabolomics, and life science ontologies, it enables the discovery of functional and taxonomic patterns that were previously inaccessible, thus enhancing our understanding of microbial ecology and supporting informed environmental management. It enhances the ability to ask novel biological questions and improve data stewardship.

Despite its promise, metagenomics also presents challenges, particularly in terms of data analysis, storage, and interpretation. The vast amount of sequence data generated requires advanced computational infrastructure and robust data management frameworks.

Future research should focus on less-studied regions such as deep-sea and benthic habitats in the Bay of Bengal for the better understanding of the function of the microbes and the impacts of human induced pollution in marine ecosystem. While metagenomics has altered the study of marine ecosystems, it is important and relevant to recognize the complementary role of other molecular tools and traditional methods. The new challenges of metagenomic research in marine environments will be crucial to manage data and computational demands for the continued advancement.

In summary, metagenomics offers an unprecedented window into the microbial heart of marine ecosystems—unlocking biodiversity, revealing metabolic potential, and supporting targeted solutions for pollution mitigation. In ecologically vulnerable regions like the Bay of Bengal, it promises to bridge scientific discovery with informed policy-making and sustainable environmental stewardship.

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