

Taxonomy and diversity of marine microbes

01

K. S. Sobhana

ICAR-Central Marine Fisheries Research Institute, Kochi

Marine microbes form a diverse and complex group that plays a crucial role in the functioning of marine environments. They encompass a wide range of organisms, including bacteria, archaea, viruses, and microeukaryotes, each contributing uniquely to marine ecosystems' dynamics and functions. For the initial 2-3 billion years of planetary and biological evolution, microbes stood as the sole life forms. It is widely believed that life emerged in the oceans, making marine microorganisms the closest extant descendants of these primordial life forms. These early marine microbes played a crucial role in setting the stage for subsequent life forms. Around two billion years ago, photosynthetic marine microorganisms began generating oxygen, profoundly altering the chemical landscape in which plants, animals, and all other life evolved. This transition was monumental, as the generation of oxygen facilitated the development of aerobic life forms and shaped Earth's habitability. Beyond oxygen production, marine microbes continue to be indispensable. They act as microscopic factories, catalyzing essential chemical reactions within biogeochemical cycles. Their metabolisms, both aerobic and anaerobic, enable them to perform crucial steps within these cycles that other organisms cannot accomplish. The smooth operation of these biogeochemical cycles is vital for sustaining life on our planet. From nutrient cycling to carbon sequestration, marine microbes play a pivotal role in maintaining Earth's ecological balance. Without their contributions, the intricate web of life would cease to function effectively. Thus, acknowledging and understanding the significance of marine microbes is imperative for preserving the health and continuity of life on Earth.

The diversity of microbial life in the sea is vast, encompassing organisms from all three domains of life—archaea, bacteria, and eukarya—as well as viruses, although viruses are often not classified as living organisms by most authorities. These groups or taxa exhibit distinct differences in morphology, physiology, and phylogeny, spanning both prokaryotic and eukaryotic domains. The remarkable adaptability of microorganisms to

thrive under diverse physicochemical conditions underscores their critical role in maintaining ecosystem balance. Given their significance, it is essential to catalog their diversity comprehensively. However, their microscopic size renders them invisible to the naked eye, posing challenges for effective classification.

The diversity of microbial communities varies significantly within and between marine habitats. These habitats can be categorized based on several factors:

Presence of other organisms: This includes symbiotic relationships, free-living microbes, and biofilms

Proximity to ocean features: Marine habitats can be distinguished based on their depth and location, such as euphotic zones (0-150 m), mesopelagic zones (150 – 1000 m), bathopelagic zones (>1000 m), and benthic habitats within sediments

Nutrient concentrations: Habitats can also be classified as oligotrophic (low nutrient concentrations), mesotrophic (moderate nutrient levels), or eutrophic (high nutrient levels)

Interfaces between different habitats are often biodiversity hotspots, such as air-water, water-sediment, water-ice, and host macroorganism-water interfaces. However, studying these interface habitats in detail is challenging due to their sub-millimeter scale of physical and chemical variability.

The recent focus on biogeography in microbial diversity studies is due to the small size of microorganisms and the complexity of their environments (Fierer, 2008). Environmental complexity plays a crucial role in shaping microbial diversity, with spatial heterogeneity leading to the formation of numerous niches within a habitat. Tools like metagenomics provide valuable nucleic acid sequence data, allowing for direct identification of microorganisms and comparison of microbial diversity profiles across habitats. Alpha diversity refers to diversity within a specific location or community, while beta diversity measures differences in community composition between multiple locations. Gamma diversity applies to larger regions,

encompassing continents and biomes, and is larger in scale compared to alpha diversity. These concepts help researchers understand the distribution and composition of microbial communities across various marine habitats.

Understanding microbial diversity is a challenging yet crucial aspect of marine biodiversity research, as it sheds light on biogeography, community assembly, and ecological processes (Pedros-Alio, 2006). While species richness has traditionally been a key metric in ecological and conservation studies, the concept of biodiversity encompasses much more than just the number of species present. Estimating microbial diversity often involves statistical approaches that extrapolate species numbers from relatively small sample sizes. Hughes *et al.* (2001) highlighted the effectiveness of rarefaction and richness estimators in predicting bacterial species numbers, emphasizing the utility of nonparametric estimators in microbial diversity studies. However, these estimators rely on operational taxonomic units (OTUs), which may treat divergent and redundant taxa equally. To address this limitation, recent advancements have introduced statistical techniques from population genetics and systematics to estimate species richness and phylogenetic diversity without solely relying on sequence frequencies (Martin, 2002). Measures such as the reciprocal of Simpson's index ($1/D$), F-statistics (FST), and phylogenetic grouping of taxa (P tests) have been applied to microbial datasets as indicators of diversity. These metrics, widely used in ecological studies, offer a more nuanced understanding of microbial diversity by considering both species richness and phylogenetic relationships among taxa (Stach *et al.*, 2003). By combining species richness estimates with measures of diversity like phylogenetic relationships, researchers can gain deeper insights into marine microbial diversity, enabling more informed ecological analyses and conservation strategies.

Within ocean-surface bacterioplankton communities, the dominant clade is the heterotrophic SAR11, while non-photosynthetic protists of diverse origins regulate picoplankton populations and nutrient supply into marine food webs. Collectively, bacterial, archaeal, and protist communities constitute over 90% of oceanic biomass and are responsible for 98% of primary production. Archaea stand out for their ability to thrive in extreme environments, differing from bacteria notably due to the

absence of peptidoglycan in their cell walls. Both domains, archaea, and bacteria, play crucial roles in shaping marine environments, contributing significantly to ecological processes and nutrient cycling essential for marine life. Over the past two decades, molecular studies utilizing gene sequences encoding the small subunit rRNA (SSU rDNA) have unveiled a plethora of new marine microorganisms. Marine microbiologists are experiencing a sense of living in an era of continual discovery, with no foreseeable end in sight. However, much of this newfound diversity remains undescribed due to the necessity of pure cultures to define a species.

Recent investigations into microbial diversity have yielded remarkable revelations about previously unknown microorganisms, many of which exert significant impacts on oceanic processes (Zinger *et al.*, 2012). Among these discoveries are vast populations of picoplankton encompassing diatoms, dinoflagellates, picoflagellates, and cyanobacteria. These picoplankton serve as primary drivers of carbon fixation, orchestrating nitrogen cycling and forming the foundation of the traditional marine food web. Modern technologies, including molecular techniques and automated fluorescence cell sorting, have revolutionized our understanding of microbial life in the oceans. These advancements have unveiled the immense abundance and diversity of microbial forms, particularly through DNA sequencing of environmental genomes, also known as metagenomics. Metagenomics has become crucial in studying microbial communities, especially since an estimated 99% of the microbial population is considered uncultivable using traditional methods. One of the significant findings of molecular techniques is the identification of SAR11 as a dominant clade within ocean-surface bacterioplankton communities. Bacteria belonging to the SAR11 clade, specifically within the Pelagibacteraceae family, constitute approximately one-third of cells at the ocean's surface. In fact, SAR11 bacteria are estimated to represent between a quarter and a half of all prokaryotic cells in the ocean, showcasing their remarkable prevalence. These SAR11 bacteria are classified as alphaproteobacteria and include the highly abundant marine species known as *Candidatus Pelagibacter ubique*, which has gathered attention for its ubiquity and ecological significance in marine environments. This species has not yet been validly published, though the strain

HTCC1062 has been successfully isolated in pure culture (Rappe *et al.*, 2002), and therefore the species name does not have official taxonomic standing.

Taxonomic classification on marine microbes

In modern microbial taxonomy, a polyphasic approach is utilized to define a microbial species, combining both phenotypic and genotypic characteristics. When proposing a new taxon, it is crucial to isolate the organism in pure culture and assess its characteristic features under standardized conditions. Consistency in phenotypes among all strains within a species is essential. A designated type strain of a species serves as the reference specimen for that species. The 16S rDNA sequences play a vital role in species delineation. Organisms with 16S rDNA sequences $\leq 98.5\%$ identical are considered members of different species. However, uncultured microbes cannot be assigned to a specific species since their phenotype remains unknown. Instead, they may be designated as 'Candidatus' provided their 16S rRNA sequence aligns with known species' identity principles. A concept pertinent to taxa lower than the strain level is the ecotype. Ecotypes refer to microorganisms that occupy specific ecological niches and are adapted to the conditions prevalent in those niches (Koeppel *et al.*, 2008). This adaptation often leads to genetic and phenotypic divergence, reflecting the diverse ecological roles microorganisms play in their environments.

Numerical taxonomy

Numerical taxonomy is a method that utilizes a range of biochemical, morphological, cultural, and susceptibility characteristics, including responses to antibiotics and inorganic compounds, to assess the similarity between organisms. Typically, between 50 to 200 traits are considered for each organism. The degree of similarity, expressed as a coefficient or percentage, is then calculated between strains, where each strain represents a single isolate from a specimen. Using these similarities, a dendrogram or similarity matrix is constructed, organizing individual strains into groups based on their degree of similarity. This dendrogram places groups that share higher similarity closer together, providing a visual representation of the relationships between different strains and groups.

While 16S rDNA sequences have caught attention as a powerful tool for delineating species uniqueness, numerical taxonomy,

which relies on phenotypic traits from a broad range of species, holds its ground as a robust approach. In fact, it compares favourably with genotypic data and aligns well with modern taxonomy practices. This methodology, by considering a diverse array of characteristics, offers valuable insights into the relationships and classifications of organisms based on their observable traits and behaviours.

Polyphasic taxonomy

In the polyphasic approach to microbial taxonomy, researchers aim to provide a comprehensive description of organisms by integrating phenotypic, genotypic, and phylogenetic information. Phenotypic characteristics encompass colony traits, cell morphology, cell wall composition, pigmentation patterns, protein profiles, and other chemotaxonomic markers. Genotypic features are derived from nucleic acids (DNA/RNA), providing insights into the genetic makeup of the organism. Phylogenetic information plays a crucial role and is often obtained by studying sequence similarities in specific genes such as 16S rRNA or 23S rRNA for bacteria and 18S rRNA for fungi. Various molecules are employed to delineate and describe taxa, with certain components like 16S rRNA genes, phenotypic traits, and chemotaxonomy being mandatory. Optional components may include amino-acid sequencing of specific proteins or DNA-DNA hybridization, which are included as needed for accurate taxonomic descriptions.

The DNA barcoding approach is gaining popularity in assessing microbial diversity, although the availability of comprehensive datasets, especially for eukaryotic microbes, remains somewhat limited. However, advancements in sequencing technologies have led to faster and more cost-effective methods, improving the availability and accuracy of genetic information for microbial taxonomy.

Marine microbes under the three domains of life

Bacteria

Bacteria, forming the Domain Bacteria, represent one of the earliest branches on the tree of life and are genetically distinct from both archaea (Domain Archaea) and eukaryotes (Domain Eukarya). They are ubiquitous in all marine environments, playing a crucial role in sustaining life on Earth by facilitating the recycling of essential nutrients within oceanic food webs. Despite their fundamental importance, our understanding

of bacterial biology in marine environments remains limited. This is primarily due to the fact that only a small fraction, averaging around 1%, of marine bacteria can be successfully cultured under laboratory conditions. This limitation hinders our ability to study the vast majority of bacterial diversity and their ecological roles in marine ecosystems. Majority of bacterial isolates obtained from marine environments, belong to the five major bacterial phyla: Proteobacteria, Cyanobacteria, Firmicutes, Actinobacteria, and Bacteroidetes:

Phylum Proteobacteria

Includes diverse groups of Gram-negative bacteria, such as Alpha-, Beta-, Gamma-, Delta-, and Epsilon-Proteobacteria, each with distinct metabolic capabilities and ecological roles. They contribute significantly to nutrient cycling, bioremediation, and symbiotic relationships with plants and animals. Some Proteobacteria are of medical importance due to their pathogenicity, highlighting the diverse ecological roles and impacts of this phylum in ecosystems and human health.

Phylum Cyanobacteria

Autotrophic Gram-negative bacteria that can obtain biological energy by photosynthesis, which contribute significantly to primary production in marine ecosystems. Certain Cyanobacterial species are capable of nitrogen fixation, converting atmospheric nitrogen into a usable form for plants and other organisms. This process is essential for maintaining nitrogen levels in marine ecosystems. Under certain conditions, Cyanobacteria can undergo rapid population growth, leading to harmful algal blooms (HABs). Some Cyanobacteria produce toxins harmful to marine life and humans, causing water quality issues and impacting aquatic ecosystems.

Phylum Firmicutes

A significant marine phylum comprising Gram-positive bacteria, possessing the unique ability to form spores. These spores serve as resting stages characterized by inactivity, strong dehydration, and high resistance to environmental stresses. Despite being dormant, spores contain sufficient energy for germination and are specifically adapted to swiftly respond to substrate availability. Upon encountering favourable conditions, spores undergo germination, giving rise to vegetative cells capable of replication and growth. This adaptability allows Firmicutes to effectively navigate varying environmental challenges

and exploit opportunities for growth and proliferation in marine habitats

Phylum Bacteroidetes

Known for their ability to degrade complex organic compounds and plays a key role in nutrient cycling. Their metabolic versatility and ability to degrade complex organic compounds make them significant contributors to ecosystem stability and functioning.

Phylum Actinobacteria

Actinobacteria are prevalent inhabitants of marine sediments, thriving in the nutrient-rich and diverse environments found in oceanic sediments. Their presence is crucial for the decomposition of organic materials and nutrient cycling within these ecosystems. Actinobacteria are renowned for their ability to produce a vast array of bioactive secondary metabolites, including antibiotics, antifungals, and anticancer compounds.

Bacteria play a significant role in marine ecosystems, constituting a major portion of the organic matter that sustains countless bottom-dwelling animals. As organic particles sink through the water column, they are predominantly composed of bacteria. These bacteria primarily feed on dead organic material, contributing to nutrient recycling and energy transfer within marine food webs. Notably, some bacteria, such as cyanobacteria, are photosynthetic, making them the most abundant photosynthetic organisms in the ocean due to their small size and prolific distribution. Beyond their roles as free-living organisms, some bacteria have evolved to form symbiotic relationships with other marine organisms. These symbiotic associations have led to the evolution of organelles found in eukaryotic organisms, originating from symbiotic bacteria. Ultimately, bacteria are crucial in the decomposition of organic matter in oceans, contributing significantly to nutrient cycling and ecosystem functioning in marine environments.

Archaea

Archaea, part of the Domain Archaea, represent some of the earliest and most basic life forms known. The discovery of 3.8-billion-year-old fossils resembling archaeal structures underscores their ancient lineage and potential significance in the early evolution of life on Earth. These prokaryotic organisms are unicellular and lack a nucleus and membrane-bound organelles, distinguishing them from eukaryotic cells. The existence of Archaea in

extreme environments initially earned them the title of "Extremophiles". They were first identified in extreme terrestrial settings like hot sulphur springs, saline lakes, and environments with highly acidic or alkaline conditions. The exploration of extreme marine habitats revealed that archaea are also prevalent in deep-sea environments, where they endure pressures ranging from 300 to 800 atmospheres. Notably, certain archaea thrive in the extreme temperatures of hydrothermal vents, with some unable to grow below 70-80°C. Impressively, a particular hydrothermal vent archaeon has been found to survive at an astonishing 121°C, marking it as the most heat-tolerant organism known to date. The diverse habitats where archaea are found highlight their resilience and adaptation to extreme conditions, providing valuable insights into the boundaries of life and the potential for life to exist in extreme environments. The majority of archaea from marine environments, comprising over 80% of their population, belong to several major phyla that are distinctive in their characteristics and ecological roles:

Phylum Euryarchaeota

One of the largest and most diverse archaeal phyla found in marine environments. Members of this phylum are known for their ability to thrive in extreme conditions such as high salinity, high temperatures, and anaerobic environments. They encompass diverse metabolic capabilities, including methanogenesis (methane production), sulphate reduction, and acetogenesis. Euryarchaeota includes methanogens, halophiles, and thermophiles, exhibiting diverse adaptations to extreme marine environments.

Phylum Thaumarchaeota

A significant phylum in marine ecosystems, particularly in oceanic waters. They are known for their involvement in the nitrogen cycle, specifically in the oxidation of ammonia to nitrite (ammonia oxidation). Thaumarchaeota are important contributors to nitrification processes in marine environments, influencing nutrient cycling and ecosystem dynamics.

Phylum Crenarchaeota

A diverse phylum of archaea found in various marine habitats, including deep-sea environments, hydrothermal vents, and sediments. They are often adapted to extreme conditions, such as high temperatures and acidic pH levels. Some members of

Crenarchaeota are involved in sulphur metabolism, ammonia oxidation, and other metabolic pathways crucial for marine ecosystems.

Phylum Nanoarchaeota

A less studied but intriguing phylum of archaea that includes extremely small and symbiotic organisms. They are often associated with other microorganisms, such as thermophilic archaea, forming symbiotic relationships. The ecological roles and metabolic functions of Nanoarchaeota in marine environments are areas of ongoing research and discovery.

Phylum Korarchaeota

A lesser-known group of archaea that has been primarily identified in high-temperature environments, such as hydrothermal systems and geothermal areas. However, their presence and significance in marine environments are still areas of active research and exploration.

These major archaeal phyla demonstrate the diversity, adaptability, and ecological significance of archaea in marine ecosystems. Archaea possess a diverse range of metabolic capabilities, including photosynthesis, chemosynthesis, and heterotrophy. Among archaea, a significant proportion are methanogens, which are anaerobic organisms capable of metabolizing organic matter to produce energy, with methane as a byproduct. Within the Archaea domain, the Halobacteria are notable photosynthetic organisms that thrive in environments with high salinity levels. These organisms utilize bacteriorhodopsins, purple proteins that enable them to trap light energy, facilitating photosynthesis even in extreme saline conditions. The adaptation of Halobacteria to high salinities and their unique light-capturing abilities highlight the diversity and resilience of archaeal organisms in varied environmental niches. Their metabolic capabilities, ranging from methane production to nitrogen cycling, contribute to nutrient dynamics, energy flow, and ecosystem stability in marine habitats. Understanding the roles and interactions of these archaeal groups is essential for comprehending marine microbial communities and their impact on global biogeochemical cycles.

Microeukaryotes

Marine microbial eukaryotes are an integral part of marine ecosystems, belonging to various kingdoms such as Protista, Fungi,

Plantae, and Animalia. Unlike prokaryotes, which are predominantly unicellular, eukaryotes encompass both unicellular and multicellular organisms. The majority of marine microbial eukaryotes are classified under the Kingdom Protista, which contribute significantly to primary production and trophic interactions in marine food webs. This diverse group includes organisms that can be autotrophic (capable of producing their own food) or heterotrophic (relying on external sources for nutrition). Among these microbial eukaryotes are algae, diatoms, dinoflagellates, zooxanthellae, coccolithophores, foraminiferans, radiolarians, ciliates, and marine fungi. Algae are a significant component of marine microbial eukaryotes, playing a crucial role in primary production and nutrient cycling. Diatoms, with their intricate silica shells, are abundant in marine environments and are essential primary producers. Zooxanthellae are symbiotic algae found in coral reefs, providing essential nutrients to corals through photosynthesis. Coccolithophores, characterized by their calcium carbonate plates, are vital contributors to marine carbon cycling and play an important role in climate regulation. Foraminiferans and radiolarians are amoeboid protists with intricate shell structures, contributing to marine biodiversity. Ciliates are diverse protozoans with cilia for movement and feeding, occupying various niches in marine ecosystems. Marine fungi, although less studied compared to their terrestrial counterparts, play roles in nutrient recycling and decomposition processes. Overall, the diversity of marine microbial eukaryotes underscores their importance in marine food webs, nutrient cycling, and ecosystem dynamics.

Viruses

Viruses, although not classified as living organisms, play a crucial role in marine ecosystems, particularly in the marine food web. Viruses are essentially particles composed of nucleic acid, either RNA or DNA, enclosed in a protein coat. They are obligate parasites, relying on living cells for their replication and development. Unlike organisms which possess the ability for independent cell division and the machinery for DNA duplication and cell division, viruses lack these capabilities. Instead, they depend on infecting living cells to replicate their genetic material and produce new virus particles. Due to this dependency, viruses do not fall under any of the three domains of life. Despite their non-living status, viruses are immensely significant for generating and maintaining

genetic diversity across all three domains of life through horizontal gene transfer. They play a crucial role in the microbial food web and biogeochemical cycles by promoting nutrient production and maintaining high diversity, thereby preventing the dominance of specific microorganisms. Viruses primarily parasitize bacteria and plankton, releasing organic matter into the ocean. Studies suggest that viruses may be responsible for up to half of bacterial mortality in aquatic ecosystems and substantial mortality in phytoplankton populations. The abundance of viruses in an environment correlates directly with the abundance of microbial life they infect, highlighting their regulatory role in microbial populations. Viruses, although not alive in the true sense, are integral to marine ecosystems, contributing to nutrient cycling, genetic diversity, and the balance of microbial communities in marine environments.

Marine microbial diversity and ecological roles

Marine microbial diversity and ecological roles are fundamental to the functioning of marine ecosystems.

Functional diversity

Photosynthetic microbes like cyanobacteria and phytoplankton play a crucial role in marine primary production, contributing substantially to the ecosystem's energy input. On the other hand, heterotrophic bacteria and archaea act as decomposers, nutrient cyclers, and symbionts, engaging in organic matter degradation and nutrient recycling processes vital for ecosystem functioning. The diversity of viruses also plays a significant role, impacting microbial community structure, genetic exchange, and nutrient dynamics through both lytic and lysogenic cycles, thus influencing the overall balance and stability of marine ecosystems.

Spatial and temporal dynamics

Vertical stratification in microbial communities within water columns is influenced by factors like light availability, nutrient gradients, and predation pressure. This stratification creates distinct niches for different microbial species, contributing to overall ecosystem diversity and functioning. Seasonal variability further adds to microbial dynamics, with fluctuations in diversity and abundance driven by changes in temperature, nutrient availability, and daylight hours,

showcasing the dynamic nature of marine microbial communities over time.

Ecological interactions

Ecological interactions within marine ecosystems are incredibly diverse and dynamic, encompassing a multitude of relationships and processes that collectively shape the functioning and stability of these environments. Symbiotic interactions are of paramount importance in marine ecosystems, where they often involve mutually beneficial or parasitic relationships between microbes and host organisms such as corals, sponges, and other marine fauna. These symbiotic associations play a pivotal role in various ecosystem functions, including nutrient cycling, habitat provision, and even defence mechanisms against environmental stressors. For example, symbiotic algae living within coral polyps contribute significantly to coral reef productivity through photosynthesis, while certain bacteria can provide essential nutrients to their host organisms. Predation and grazing activities by protists (such as zooplankton) and metazoans (like fish and invertebrates) have a profound impact on microbial communities within marine ecosystems. Predators and grazers regulate the abundance and diversity of microbial populations by consuming them directly or indirectly through grazing on primary producers. This predation pressure can influence the structure and composition of microbial communities, affecting their resilience to environmental changes and their role in nutrient cycling.

The interactions between predators, grazers, and microbes help regulate population sizes within marine ecosystems. Predation acts as a natural control mechanism, preventing the unchecked proliferation of certain microbial species that could otherwise disrupt ecosystem balance. Grazing by marine organisms also influences the distribution and abundance of microbes, shaping community dynamics and contributing to overall biodiversity. Predation and grazing not only regulate population sizes but also have a significant impact on the composition and diversity of microbial communities. Selective feeding by predators and grazers can favour certain microbial taxa over others, leading to shifts in community structure and function. These changes can ripple through the entire ecosystem, influencing nutrient cycling, productivity, and resilience to environmental perturbations.

Collectively, these ecological interactions contribute to the overall balance and stability

of marine ecosystems. By regulating population sizes, influencing community composition, and participating in nutrient cycling processes, symbiotic relationships, predation, and grazing help maintain the health and resilience of marine ecosystems in the face of environmental challenges and disturbances

Factors shaping marine microbial diversity

Numerous factors influence marine microbial diversity, reflecting the intricate web of interactions within marine ecosystems. These factors encompass physical, chemical, and biological variables, each exerting varying degrees of influence on microbial communities. Key variables shaping marine microbial diversity include turbulence, light availability, temperature gradients, nutrient levels (such as nitrogen and phosphorus), salinity variations, pH levels, UV radiation, solar influx, surfaces/interfaces, redox potential, metal concentrations, and the presence of macroorganisms like invertebrates and macroalgae. These factors collectively contribute to the richness and composition of microbial communities, yet the precise extent of their influence and their significance across different environmental contexts remain subjects of ongoing research. Climate change is poised to emerge as a pivotal top-down force shaping marine microbial communities, primarily through alterations in ocean temperatures. These changes are anticipated to bring about unforeseen shifts in community diversity and structure. Additionally, pollution, notably anthropogenic nitrogen inputs arising from human activities, profoundly impacts marine microbial diversity. Anthropogenic nitrogen influxes now constitute nearly half of the total nitrogen inputs to oceans, contributing to the emergence of extensive dead zones in coastal regions and an escalation in harmful algal blooms. These anthropogenic impacts underscore the urgency of understanding and mitigating human-induced pressures on marine microbial ecosystems. Understanding the complex interplay of these factors is crucial for predicting and managing changes in marine microbial diversity, especially in the context of ongoing environmental challenges such as climate change and pollution

Conclusion

The taxonomy and diversity of marine microbes are fundamental to understanding the structure, function, and resilience of marine ecosystems. Advances in molecular techniques have revolutionized our ability to

study and characterize these diverse microbial communities, shedding light on their ecological roles, interactions, and responses to environmental changes. The wealth of sequence information, such as 16S rRNA sequences, genome sequences, and metagenomes, along with rRNA-targeted probes like Fluorescent *In Situ* Hybridization (FISH), has facilitated the discovery of numerous new bacterial groups. In the realm of marine microbial genomics, ranging from model organisms' genome studies to various meta-omics approaches (*e.g.*, metagenomics, metatranscriptomics, and metaproteomics), researchers have made significant strides in understanding roles played by microbes in the marine environment. Recent advancements in technology have the potential to revolutionize how we characterize, identify, and study microbial communities. Innovative tools like microbial ecological DNA microarrays, such as PhyloChip and GeoChip, have been developed to comprehensively investigate microbial community composition and function. These microarrays offer a high-throughput platform for analyzing microbial diversity and metabolic potential. Another groundbreaking approach is Single Cell Genomics, which allows for the amplification and sequencing of DNA from individual cells directly obtained from environmental samples. This approach is particularly valuable for obtaining genomes from uncultured phyla, providing insights into the genetic make-up and potential functions of previously elusive microbial groups. The advent of Single Cell Genomics promises to reshape the field of microbiology by enabling the study of individual cells within complex microbial communities. Future research efforts aimed at unravelling the complexities of marine microbial diversity will contribute significantly to marine conservation, biotechnology, and ecosystem management

References

- Fierer, N. 2008. Microbial biogeography: Patterns in microbial diversity across space and time. In: Zengler K. (Ed.).
- Accessing uncultivated microorganisms: From the environment to organisms and genomes and back.* ASM Press, Washington DC, USA, pp. 95-115.
- Hughes, J. B., Hellmann, J. J., Ricketts, T. H. and Bohannan, J. M. 2001. Counting the uncountable: statistical approaches to estimating microbial diversity. *Appl. Environ. Microbiol.*, 67: 4399–4406.
- Koepfel, A., Perry, E.B., Sikorski, J., Krizanc, D., Warner, A., Ward, D.M. 2008. Identifying the fundamental units of bacterial diversity: A paradigm shift to incorporate ecology into bacterial systematics. *Proc. Natl. Acad. Sci. USA*, 105(7): 2504–2509.
- Martin, A. P. 2002. Phylogenetic approaches for describing and comparing the diversity of microbial communities. *Appl. Environ. Microbiol.*, 68 :3673–3682.
- Pedros-Alio, C. 2006 Marine microbial diversity: Can it be determined? *Trends Microbiol.*, 14(6): 257–263.
- Rappe, M. S., Connon, S. A., Vergin, K. L. and Giovannoni, S. J. 2002. Cultivation of the ubiquitous SAR11 marine bacterioplankton clade. *Nature*, 418 (8): 630-632
- Stach, J. E. M., Maldonado, L. A., Masson, D. G., Ward, A. C., Goodfellow, M. and Bull, A. T. 2003. Statistical approaches for estimating actinobacterial diversity in marine sediments. *Appl. Environ. Microbiol.*, 69: 6189–6200.
- Zinger, L., Gobet, A. and Pommier, T. 2012. Two decades of describing the unseen majority of aquatic microbial diversity. *Mol. Ecol.*, 21(8): 1878–1896