Chapter 9

Marine Microbes: Early Warning Indicators of Climate Change

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Abstract: Microbes are responsible for the production of primary and massive secondary metabolites of the marine ecosystem. The great diversity of microorganisms in the oceans plays a significant role on the regulation of biogeochemical cycles. The role and function of microorganisms in climate change have not been thoroughly investigated, despite - anthropogenic causes and consequences of the gases have gained substantial attention. Previous studies that assessed the role of marine microorganisms under different environmental conditions revealed that marine microbes had a major effect on climate change. Therefore microorganisms should be considered as the viable candidate in indicating climate change and related assessments. Microbes have played a major role in the evolution of the earth by influencing the quantity of greenhouse gases in the atmosphere, such as carbon dioxide (CO_2), methane (CH_4), and nitrous oxide (N_2O). Microbes are excellent model to review the impact of climate alteration scenarios on detoxification process in marine environment due to their inherent characteristics, including their quick generation time, small size, and operational role in biogeochemical cycles. This chapter focus on the potential of marine microbes as “early warning indicators” for the climate change.

Keywords: Climate change, marine microbes, bioindicators, pollution, biogeochemical cycles.

1. Introduction

Biological indicators, also referred to as indicator species, are organisms that are able to be used to monitor changes in the environment and habitat conditions for particular niches (McGeoch and Chown, 1998, De Cáceres

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et al., 2010). Kolkwitz (1908) developed one of the first signal systems to gauge the level of contamination in waterways by looking for the existence of saprophytic (ciliates and flagellates) and macroorganisms (e.g. insect larvae, molluscs, bivalves, annelids, and crustaceans). Marine systems' responses to climate change will depend on how they interact with other human-caused disturbances to the oceanic environment. For example, worldwide fishing has reduced the population of huge fish at more complex trophic levels (Jackson et al., 2001, Myers and Worm, 2003) even if more commercial, domestic, and agricultural activity has led to the nutrient rich of many coastlines (Schindler, 2006).

Microorganisms are essential to the worldwide food chain, agriculture, plant and animal health, continuous supply of nutrients and carbon, and the well-being of humans. They are the only living forms can be found in certain places, such as the depths below and "extreme" habitats, yet they exist in every ecological niche on earth. Microorganisms have been on Earth for at least 3.8 billion years before life began, and it is likely that they will persist long after any potential extinction events. Since then, a number of biomonitoring initiatives have been created and successfully implemented in estuarine and freshwater ecosystems by evaluating indicator species within the macrobenthic invertebrate community, such as AUSRIVAS (Australian River Assessment Scheme), RIVPACS (River Invertebrate Prediction and Classification System), SIGNAL (Stream Invertebrate Grade Number Average Level), (European Union Water Framework Directive). Biomonitoring techniques used to monitor the coral reef which is considered as an important species in ocean to maintain the marine ecosystem significantly (Cooper et al., 2009).

The influence of marine biota on climate variations was only briefly discussed in Intergovernmental Panel on

Climate Change, then, the possibility of several marine biota reactions to climate/environmental change and feedback to the climate system has come into greater focus. Compared to terrestrial plants, marine phytoplankton has far higher turnover rates and is distributed across a larger surface area, making it less susceptible to seasonal fluctuations (Behrenfeld, 2014). Due to the significant contribution of microbes to the generation and consumption of CO_2, CH_4, and other greenhouse gases, they known as the main drivers of climate changeand also thought to be more reactive than plants and animals (Panikov, 1999). On a global scale, phytoplankton reacts to climatic changes quickly according to the scientific reports (Litchman et al., 2012).

The phytoplankton bloom cycles, which are influenced by both top-down (such as grazing and viruses) and bottom-up (such as the availability of vital nutrients and vertical mixing) controls, make it difficult to predict how climate change would affect primary productivity (Hutchins and Boyd, 2016, Behrenfeld, 2017). According to a story in Down to Earth (February 28, 2001), the Chloralkali factory in Tamil Nadu (Southern India) is dumping wastewater into the Gulf of Mannar and Palk Bay. As a result, heavy metals such as lead, cadmium, and mercury have been found in the local water bodies.

The contaminations eventually result in environmental problems, such as the elimination of the renowned pearl-bearing oysters which are indigenous in the area (Selvin et al., 2009). Therefore, appropriate biological markers are needed to track pollution and its effects on the establishment and survival of local flora and fauna. The current level of research about the broad effects of marine microbes on climate change as well as various environmental stresses is summarized in our paper.

1.1. Why marine microbes called bioindicators?

Naturally occurring bioindicators are a crucial tool for identifying environmental changes, both positive and negativeeffects on human society. They are used to evaluate the health of the environment as well as to monitor environmental changes. The transmission of light, the presence of water, temperature, and suspended particles are some of the variables that control the presence of bioindicators in the environment. By using bioindicators, forecast prediction is possible in a region's ecological state or the extent of contamination (Khatri and Tyagi, 2015).

The biological indicator must respond to pollution quickly and correctly, be suitable for the intended use, and recognize changes in an ecosystem caused by poor management, inappropriate land use, pollution, and/or climatic changes. Microorganisms are frequently utilized in assessing ecosystem contamination in marine and coastal settings because of their rapid development, faster reaction to pollution, even at low levels, and show clear indicators of ecosystem alterations. Furthermore, because of their abundance in maritime habitats, they are easy to recognize and readily available (Gerhardt, 2002, Khatri and Tyagi, 2015). Microbiota is much easier to monitor than any other species, although their regulation might merely be a result of poisons making their communities better. The microbial consortium can regulate pollutants in the ecosystem by modifying its activity levels, biomass, and group composition, which is a mixture of bacteria. These factors are crucial in determining how well-developed a certain ecosystem (Butterworth et al., 2001). The comparative diversity study of marine microbial populations as a whole represents, today, as molecular technologies and their accompanying computer methodologies evolve, a significant indicator of the consequences of human interference on marine ecosystems. Utilizing DNA-based molecular techniques that span the entire population, diversity loss may be easily tracked for a very long time (Dupont et al., 2007). In conjunction with computer-based analysis of such data, marine ecological (meta) genomics may develop rarefaction curves that are in fact indicative of consequences at an ecosystemic scale. Additionally, the identification of mechanisms utilized by bacteria to respond to environmental changes and adapt to human demands, as well as -omic based analyses of the metabolic behaviors of microbial communities, may be used for environmental monitoring purposes: The evolution of response-specific functional indices using microbial biodiversity as a starting point integrates intricate interactions across microbial communities (Desrosiers et al., 2013).

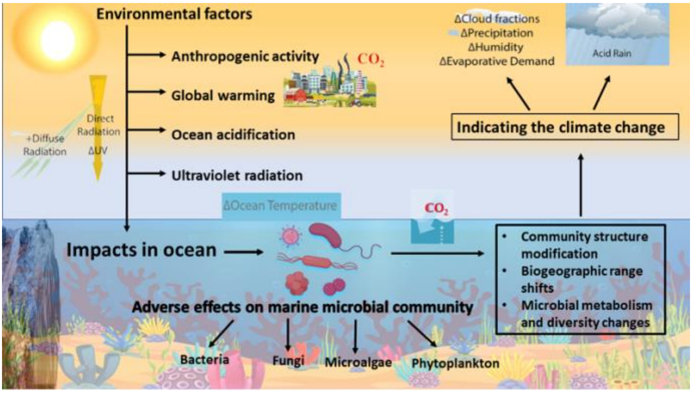

Figure 1. Marine microbial functions towards climate change

1.2. Marine microbes: Environmental pollution indicators

Certain pollution-indicating water quality measures, including aerobic heterotrophic bacteria, total coliform (TC), faecal coliform (FC), dissolved oxygen (DO), and nutrients, are used to analyse marine environmental pollution (NO_2-N, NO_3-N, NH_4-N and PO_4-P). When compared to their corresponding values in the open sea, DO and nutrient concentrations in the water at various sample points vary significantly (Turki and Mudarris, 2008). In many regions of the world, aquaculture activities are expanding quickly, raising awareness of and concern for their possible effects on the coastal marine environment and leading to significant management applications (Barg and Phillips, 1998). Recreational waters typically have a variety of microorganisms, whether they are naturally occurring or come from outside sources including sewage, industry, farming, and other industrial activities. When a sufficient amount of a pathogen colonises an ideal growth location in the body and causes an illness, this microbial mixture could be dangerous for swimmers (WHO, 1998, Elmanama et al., 2005).

The existence of many species, including plants, insects, fish, bacteria, and viruses, is evaluated using biological methods as an environmental indicator. Some bacterial species, such as Coliform, *Escherichia coli, Streptococcus* sp., *Pseudomonas* sp., *Vibrio* sp., *Clostridia* sp., *Bifidobacterium pseudolongum*, *Arcobacter* sp., *Thiobacillus* sp., and others, have been utilised as indicators in the monitoring of environmental quality. The bacteria are markers of several types of pollution, such as heavy metal, petroleum, and other types of pollution, as well as domestic trash (human and animal waste) and waste from households (Sumampouw and Risjani, 2014). As a possible indicator organism, the bacteria linked to the sea sponge *Fasciospongia cavernosa* were assessed to monitor the environmental quality. Bacteria demonstrated resistance to the heavy metals, including *Streptomyces* sp. (MSI01), *Salinobacter* sp. (MSI06), *Roseobacter* sp. (MSI09), *Pseudomonas* sp. (MSI016), *Vibrio* sp. (MSI23), *Micromonospora* sp. (MSI28), *Saccharomonospora* sp. (MSI36) (Selvin et al., 2009).

One of 24 congeners, the worldwide species *Corollospora maritime* is the only one that is frequently seen on sandy beaches in temperate and tropical waters. This species possesses qualities that make it a good indicator that might be used to monitor changes and assess ecological damage on sandy coastal beaches (Kohlmeyer and Kohlmeyer, 1979). Because it is acknowledged as a natural prey for many species and since the International Organization for Standardization (ISO) has normalized its use, the calanoid copepod *Acartiatonsa* can be used as a bioindicator (Støttrup and McEvoy, 2003). Naturally occurring microbial communities may be useful indicators of ecological balance and facilitate delicate environmental pressure predictions.

Table 1. Marine microbes as pollution indicators

Microbial indicators	**Location**	**Contaminant**	**References**
Streptomyces sp. and *Saccharomonospora* sp.	Gulf of Mannar	Cd and Hg	Selvin et al., 2009
Vibrio fischeri	In vitro Mediterraneanlaguna	Wide range of chemicals Pathogens	Parvez et al., 2006
Fecal coliforms, *Escherichia coli*, enterococci, somatic coliphages, and F+-specific coliphages	South Florida beach	Fecal	Bonilla et al., 2007
Escherichia coli, Enterococcus spp.,	Goa, central west coast of India	Sewage-pollution	Nagvenkar and Ramaiah, 2009
Oleiphilus messinensis	Harbor sediments (Messina Italy)	Hydrocarbon-degrading	Yakimov et al., 2007
Thiobacillus sp.	Gulf ofManado	Mercury (Hg) pollution	Ijong and Suwetja, 2003
Chromatium sp.	Niger mangrove ecosystem	Crude oil pollution	Essien and Antai, 2009.
Kocuria palustris, *Bacillus pumilus* and *Bacillus subtilis*	Pelagic waters	Degrade low-density polyethylene	Harshvardhan and Jha, 2013
Vibrio spp., *Aeromonasspp., Campylobacter* spp. and *Arcobacter* spp.	Mandovi and Zuarithe central west coast of India	Sewage-pollution	Nagvenkar and Ramaiah, 2009

2. Climate change: various factors affecting marine microbes

The stringent physiological thresholds that marine bacteria have also make them susceptible to even minor changes in temperature, nutrition, salinity, oxygen, and a variety of anthropogenic pollutants. These factors make microbes excellent markers for warning about manmade stressors such as climate change in the marine ecosystem.

2.1. Impact of temperature

A significant component causing the range shifts of marine creatures due to climate change is changing ocean temperatures (Thomas et al., 2012). There has been a lot of research done on how sensitive pathogenic bacteria react and respond to high temperatures. Increased pathogen prevalence and virulence, the facilitation of novel pathogen invasions, or decreased host adaptability and resilience are all effects of elevated seawater temperatures that can have an impact on the frequency and severity of disease outbreaks (Sutherland et al., 2004). As temperatures rise, oxygen levels drop, and metabolic rates rise, potentially putting some creatures under increased respiratory stress. The intriguing possibility that a decline in the well-being of the host organisms may be the cause of a rise in the prevalence of illnesses linked with elevated seawater temperatures is raised by the fact that outbreaks of disease appear to be caused by a wide species of pathogens, including viruses, bacteria, fungi, and parasites (Webster and Hill, 2007, Dutta and Dutta, 2016). Alternatively, as is the case with the coral parasite *Vibrio shiloi*, rising temperatures may change a pathogen's virulence pathways. The pathogenicity of this coral pathogen has been the subject of extensive research (Toren et al., 1998). Temperature fluctuations may have an effect on important biological functions. For example, the spread, plenty, biology, and yield of phytoplankton communities worldwide are changed in response to warming, acidifying, and stratifying oceans (Ducklow et al., 2009, Polovina et al., 2008). Although *Trichodesmium* and *Crocosphaera* may perish from portions of their existing tropical habitats where future warming may surpass their maximum thermal tolerance limits, thermally induced changes towards higher latitudes are also predicted for N_2-fixing cyanobacteria (Breitbarth et al., 2007, Thomas et al., 2012). Both marine and freshwater microalgae are affected by temperature in terms of growth rates. These creatures react spontaneously to climatic changes (Butterwick et al., 2005). On shorter durations, these changes first appear as changes in the aquatic algae species, but longer timescales can result in changes to algal assemblages (McCormick and Cairns, 1994).

2.2. Impact of Ocean acidification (OA)

Numerous microbial functions can be impacted directly or indirectly by a cascade of consequences brought on by non-microbial groups' reactions and/or modifications to the chemistry of saltwater. While the phrase "ocean acidification" describes the decrease in pH, it is not an indication that the ocean's surface waters are going to become acidic (that is, below 7) (Caldeira and Wickett, 2003). If current trends in CO_2 emissions continue to climb, the pH of the world's surface waters could decrease by about 0.4 units by the end of the millennium compared to before industrialization periods (Orr et al., 2005). The microbial communities that are linked with the coral, for instance, may be impacted by this physiological pH change, which could then have an impact on the physiology and health of the coral. pH levels of 7.3 and 8.2 (ambient seawater) were used in the study to compare the bacterial communities in the coral *Acroporaeurystoma's* mucus, tissue, and skeleton changed as a result (Meron et al., 2011). Joint et al. (2011) stated recently that marine biogeochemical processes driven by phytoplankton, bacteria, and archaea will not undergo catastrophic alterations because microbial assemblages have always experienced fluctuating pH environments. In a meta-analysis of published data, Liu et al. (2010) hypothesised that modifications to microbial structure and function are possible. Ocean acidification may also affect other parts of the nitrogen cycle in addition to nitrogen fixation. Ammonia fluctuations caused by pH can have an impact on nitrification (NH_3), which plays major role in ocean acidification. According to Beman et al. (2010), nitrification rates may drop by 3-44% within a few decades. These experiments have shown that the changes in bacterial activity and abundance under conditions of elevated PCO_2 can be caused by phytoplankton shifts (Grossart et al., 2003, Allgaier et al., 2008). On the other hand, increased CO_2 levels may alter the algal community's composition and intensity of competition. The resulting effect would be the culmination of intricate interactions between environmental elements such as climate change and other factors (Beardall and Raven, 2004). The distribution of algae species is a significant effect. Hence, it is important to address the effect of ocean acidification on microbial function with closer attention to local or regional conditions.

2.3. Impact of Ultraviolet radiation (UVR)

The ability of various bacterial groups to repair UVR-induced damage and their susceptibility to UVR has also been demonstrated to vary (Fernández Zenoff et al., 2006, Santos et al., 2012). Since bacteria in aquatic environment have basic haploid genomes that offer little to no functional redundancy, UVR is a significant stressor for these organisms (Garcia-Pichel, 1994). In a number of aquatic habitats, gammaproteobacteria have been found to be the group that is mostly resistant to UV (Alonso-Sáez et al., 2006, Santos et al., 2012). The Bacteroidetes group has been found to be UV resistant in field experiments (Alonso-Sáez et al., 2006) whereas, the

Alphaproteobacteria group noted to be UV-sensitive (Alonso-Sáez et al., 2006). The SAR11 cluster of Alphaproteobacteriamay be the highly widespread group of heterotrophic marine bacteria was discovered to be especially vulnerable to solar UVR (Ruiz-González et al., 2012). Recent observations of the elimination of *Pelagibacter*-affiliated sequences in wild Patagonian bacterioplankton groups after 8-day exposure to PAR, PAR+UVA, and PAR+UVA+UVB provide more evidence for the SAR11 group's UV sensitivity (Manrique et al., 2012).

The biogeochemical effects of increased UVR depend critically on the varying UVR sensitivity displayed by the most prevalent bacterial species in the bacterioplankton. Comparative studies on several phytoplankton species' swimming habits (avoidance tactics) also revealed significant interspecies variation. After two to three hours of exposure to solar radiation, some species, which were less vulnerable to UV radiation and tended to gather close to the surface, start to slow down and produce less motile cells. Additionally, when irradiances are strong (local noon), cells travel deep in the water column (Richter et al., 2007). Issues related to climate change, such as the shallowing of the upper mixed layer, may alter swimming behavior by preventing cells from migrating deep into the water column, favoring UV-resistant species. Therefore, the main markers of climate change are modifications in the structure of the bacterial community brought on by increased UVR.

3. Marine microbial responses to climate change

The bacteria have also been impacted by the numerous changes that microorganisms have caused about in the global environment (Zimmer, 2010). In reality, a number of microbes may be impacted by climate change, which might have an adverse effect on the environment, the economy, and society as well (French et al., 2009). Micro-, nano-, and picoplankton, which include bacteria and archaea, dominate the mechanics of the oceanic carbon cycle (Stewart, 2003). Massive populations of photosynthetic microbes can be found in oceans, particularly in polar region (like Arctic Sea ice), and these organisms extract enormous amounts of atmospheric carbon. Ideally, the ocean's bacteria have captured around one-fourth of the anthropogenic CO_2 produced since 1960 (Weiman, 2015). Additionally, the ocean's water supports a huge number of viruses (around 41030), which have the potential to lyse up to 50% of oceanic bacteria per day. They significantly alter the way biological matter accumulates and respirates, a key driver of climate change, in this way, which has an impact on global geochemistry (Suttle, 2007).

Methanotrophic bacteria reduce the impact of extremely high CH_4 emission levels in some conditions (Singh et al., 2010). For instance, they consume massive amounts of CH_4 produced by abrupt good blowouts like the Deepwater Horizon leak as well as by marine sediments (Zimmerman and Labonte, 2015). Natural CH_4 emissions are mostly caused by anaerobic archaea that live in wetlands, oceans, rumens, and termite guts. Approximately these emissions would be around 250 million tonnes, or 2.5 1011 kg/year (Singh et al., 2010). Compared to regions where there is an active water flow, saltier wetlands are home to microbial communities that release less methane (Dutta and Dutta, 2016).

Additionally, the climate is influenced by and responded to marine biogeochemical processes. Population growth is causing the atmospheric CO_2, the most prominent greenhouse gas, to rise significantly. The amount of atmospheric carbon that has increased since pre-industrial times (150 Gt C) is equal to how quickly the marine planktonic ecology cycles through carbon (Denman et al., 1996). A density-driven mechanism will also cause the surface combined layer to become thinner over a large portion of the ocean, keeping microbial communities nearer the surface where solar radiation is strongest. The future ocean is predicted to lose a significant amount of oxygen due to a combination of reduced oxygen solubility (in warmer surface waters) and stratification-driven isolation from atmospheric ventilation (in deeper waters).

The global spread of hypoxic waters will have significant effects on microbial diversity and metabolism (Hutchins and Fu, 2017). Changes to the planet in the future, especially climate change and decreased nutrition availability, may cause a shift in the phytoplankton population away from giant cells like diatoms and toward smaller species like picocyanobacteria, according to modeling studies (Dutkiewicz et al., 2015). There is compelling evidence that the biogeographic boundaries of marine bacteria and phytoplankton have begun rapidly shifting in response to climate change, much like those of plants and animals (Poloczanska et al., 2013).

Physical ocean circulation patterns in currents or eddies limit microbial expansions into new habitats (Doblin and Van Sebille, 2016). Invasive microorganisms including poisonous algae can be introduced into new ecosystems by anthropogenic transport vectors like ship ballast water transfers (Doblin et al., 2004). Scientists can now evaluate the structure and function of microorganisms in a variety of habitats, including soil, sediment, water, and inside of animal and plant hosts, thanks to recent advances in molecular technologies. The responses of marine microbial communities to climate change offer an essential experimental framework for comprehending how future changes in human-induced pollution, microbiological relationships, and climate change may affect marine ecosystems.

4. Conclusion

In addition to being the cause of climate change, microbes also react differently to it. They are sensitive to changes in the world, but it is unclear how they will react. This is due to the fact that microbes exist in a variety of communities and engage in intricate interactions with one another and their surroundings. Considering the stated uncertainties, it is clear that understanding the direct and indirect effects of climate change on these bacteria and their related long- and short-term responses will help to comprehend the possible roles of the microbes. If applied appropriately, microbes have the potential to be a vital natural resource for identifying climate change. We must conduct in-depth research on this subject, fully understand the underlying mechanics, and then apply what we determine to finding solutions. In order to increase awareness and involvement among the scientific community on the relationship between microbial interaction and climate change, special issues or research themes in particular journals might be created based on analysis of emerging trends and revolutionary shifts in the same sector.

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