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Mini Review

Variability of Chromophytic Phytoplankton in the Pacific Ocean and Indian Ocean: A Review

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Abstract

Generally, phytoplankton exhibits high species diversity and wide range of variation which makes them most successful primary producer in contemporary global oceanographic regimes. When compared to its counterpart of terrestrial ecosystem, phytoplankton species diversity is twelve-fold lower, however, taxonomic divisions are eight times higher than terrestrial plants. Therefore, it is important to investigate the detailed composition of phytoplankton and study their spatiotemporal distribution in the marine environment. In the present review, we have assessed the detailed community composition of cormophytic phytoplankton with their variability in the world oceans.

Introduction

In aquatic ecosystem, primary production mostly depends on the photosynthetic process carried out by autotrophic organisms which include phytoplankton, phytobenthos and macroalgae. Although phytoplankton are responsible for only 1-2% of the total global biomass, they produce 30-60% of the global annual fixation of carbon on Earth. This ultimately leads to providing the necessary energy for consumers and ultimately, to human beings. In marine ecosystem primary productivity is mainly focused in euphotic zone and marine phytoplankton are the key players which carry out carbon fixation via photosynthesis. Generally, phytoplankton community structure is characterized by suits of approaches including light microscopy, flow cytometry and pigment analysis. Recently, new technologies such as molecular methods (Next generation sequencing and 18s rRNA) have revolutionized the characterization of phytoplankton. However, due their evolutionary conserved nature and multiple copies, 18s rRNA may not provide high resolution and sometimes fail to identify phytoplankton at species or at genus level. Whereas, functional genes are based on selected functional aspect of organisms and achieve greater resolution of community structure. Moreover, these functional genes provide insights of element metabolism (e.g. carbon and nitrogen), which are potentially linked to biogeochemical cycling in oceans.

Recently, functional gene markers including rbcL (encoding RuBisCO enzyme), increasingly being used in deciphering community composition of chromophytic phytoplankton. Generally, RuBisCO enzyme involved in Calvin-Benson cycle which assimilate carbon dioxide to organic carbon. RuBisCO contains four different forms (Form I, II, III and IV). Form I contain 8 large and 8 small (L8S8) subunits. It is mainly found in all plants and few bacteria. Whereas form II (L2) is found in Dinoflagellates and few bacteria. Form III has been recovered from some archaea, while form IV which is also known as RuBisCO-Like Protein (RLP) is identified from variety of microbial group. Among all these forms, large subunit is widely distributed in all the four forms. It contains more conserved sequences making it a suitable gene marker for phylogenetic analysis. Specifically, Form I RuBisCO gene is divded into green and red lineages whereas, non-green phytoplankton contain form ID RuBisCo and termed as chromophytic phytoplankton. Numerous previous studies based on large subunit have recognized its importance in decrypting community structure of chromophytic phytoplankton and their vast distribution in different ecological settings of world oceans.

Pacific Ocean

Pacific Ocean is the largest ocean and numerous studies have been carried on chromophytic phytoplankton. Generally, studies were carried out at east Pacific Ocean, north Pacific Ocean and west Pacific Ocean. In the region of west Florida continental shelf, the study carried out by Pichard et al. [3] on Form I rbcL gene showed dominance of Prochlorococcus and Synechococcus in euphotic zone. However, in the in deep euphotic zone, they observed manganese-oxidizing bacterium, ultimately suggesting that chemoautotrophs might have contributed to the diversity of carbon fixing organisms in the marine euphotic zone. Another study carried out at costal part of west Pacific Ocean i.e., Monterey Bay costal upwelling zone by Bhadury et al. [2], showed dominance of bloom forming Diatoms including Pseudo-nitzschia sp., and Thalassiosira sp. Moreover, they have also observed the dominance of Haptophycea groups such as Emiliania huxleyi.

However, this study concluded that obvious environmental parameters such as temperature and nitrate did not strongly correlate with species abundance. Contrast to these results of upwelling zone, the study carried out by our group Pujari et al. [3] Accepted and in printing) showed strong correlation to the most of environmental parameters present in the mindano upwelling zone located at West Pacific Ocean. West Pacific Ocean is composed of western boundary currents which play the key role in maintaining world climate. These currents are the most dynamic and intensive mass water transportation system in the world. Our study showed that warmer, low saline and nutrient limited conditions regulated the Cyanophyceae (mainly Prochlorococcus) group in surface and subsurface depths. Further, we also observed dominance of Haptophyceae group species such as Chrysochromulina dominated the deeper depths which were correlated with high salinity and fairly high concentration of dissolved nutrients. Moreover, one of the key species of upwelling zone was dominated by Pelagomonas of Pelagophyceae group. It was influenced by availability of upwelled nutrients, and adapted to light limited conditions. Similarly, one of the studies based on monthly observation for two years carried out in Station ALOHA and North Subtropical Gyre (NPSG) of Pacific Ocean by Li et al. [5] showed that despite of prevailing oligotrophic conditions, diatoms, prymnesiophytes and dinoflagellates were dominant with varying concentration. qPCR analysis showed that these groups gene abundance often varied more than order of magnitude between successive months. Specifically, Diatoms rbcL gene abundance was more apparent at upper and lower regions of the euphotic zone. Whereas Prymnesiophytes and Pelagophytes were significantly high in number at lower euphotic zone than in the upper euphotic zone. One of the iron enrichment experimental studies based on quantification of rbcL transcripts using qRT-PCR by Endo et. al. [6] in Bering Sea of Northern Pacific Ocean showed that, regardless of Fe availability, the transcript abundance of rbcL gene decreased in the high CO_2 treatments (600 and 1000 ppm). This ultimately showed that projected future increase in seawater pCO_2 could reduce the RuBisCO transcription in Diatoms, resulting in decreased primary productivity and there could be possible shift in the food web structure of the Bering Sea.

Indian Ocean

Indian ocean is the third largest ocean in the world. And covers almost 20% of the water on Earth's surface. Within Indian ocean, there are few marginal seas, including Bay of Bengal, Arabian Sea, Laccadive Sea, Somalia Sea and Andaman Sea. Although Indian Ocean is one of the largest seas, it is significantly ignored for the distribution and ecology of chromophytic phytoplankton. Only few studies are carried out in the Indian Ocean region. One of such study was carried out by our group, Pujari et al. [4] in the Bay of Bengal. This study serves as the first report of chromophytic phytoplankton from that region. Study was carried out with the combination of techniques (molecular and traditional taxonomy using stereo microscope) to decipher the community structure of chromophytic phytoplankton. Our study observed variation in spatial distribution of chromophytic phytoplankton using rbcL genes and morphologically identification which was likely impacted by coastal freshwater input, winter monsoons, and upwelling. Moreover, as this study report first molecular related characterization of chromophytic phytoplankton, numerous new lineages were reported. One of such genus was Bolidomonas which ubiquitously distributed but only constitute minor component of phytoplankton community. Bolidomonas is a unicellular alga and with the isolated strains by comparing nuclear, plastidal and mitochondrial gene markers, Ichinomiya et al. [7] combined Bolidomonas and Triparma and included them into Parmales. Further, phylogenetic analysis showed that Parmales (Bolidophyceae) are closely related to Diatoms Unlikely open oceans or coastal regions, one of the studies was carried out by Samanta and Bhadury, (2014) in the Sundarbans mangrove ecosystem of the Bay of Bengal for decrypting spatiotemporal community composition of chromophytic phytoplankton.

The Sundarbans which is the part of the largest deltaic mangrove ecosystem located at the apex of the Bay of Bengal. It encompasses over 102 islands with a network of countless rivers, rivulets and creeks. Bay of Bengal is vast deltaic region which covers almost area of 10000 km^2, and generally it is influenced by the coastal waters from the Bay of Bengal. As observed in other mangrove ecosystem of South Asia and South East Asia, diatoms outnumber other chromophytic phytoplankton assemblages. Similarly, Samanta et al. [8] observed by far high clone libraries of Diatoms (Bacillariophyceae). Moreover, for the first time from Sundarbans mangrove ecosystem, this study detected other chromophytic phytoplankton community, including Cryptophyceae, Haptophyceae,

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Pelagophyceae, Eustigmatophyceae and Raphidophyceae. To summarize, numerous studies were undertaken for deciphering community composition of chromophytic phytoplankton. Moreover, as we are progressing towards new technologies to assess the diversity of these phytoplankton, new species are being discovered. Many recent studies are being able to identify the new species which were not reported in the particular niche.

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