

Microbial Diversity in a Mapping Perspective : A Review

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Abstract

This review article briefly describes about tracing the microbial diversity by using advanced technologies viz. Remote sensing and Geographic Information System, which would help reduce the long term process of identification of potential microbes for their novel bioactive principles for the use of humankind and establishing new species from the coastal and marine environments. This article also addresses the evolution of the species for microbial mapping in the perspective of geochemical, geological and geographic features. This will greatly help the future workers to pursue research in the field of microbial biogeography, to discern microbial diversity, both spatially and temporally.

Keywords: Diversity, Geographic Information System (GIS), Microbes.

Introduction

In the recent years, research has indicated that the earth contains microbial diversity that has the potential for remarkable scientific, social and economic impact. In spite of these recent research activities, it remains largely undiscovered, and an understanding of its global distribution and temporal variability remains elusive. Recognized is the need to integrate microbiological data and geographical locations in order to enrich our knowledge of the spatial and temporal patterns of microbial diversity.

The term, Geographic Information System (GIS) was introduced in 1960 (Tomlinson *et al.*, 1976) and it became operational in the late seventies. Nowadays, GIS is an important tool in research and it is one of the advanced technologies which is used by a large number of scientists. GIS paves way for new approaches and analysis. GIS is being widely used in many fields including the marine realms and a good amount of research has been carried out. Coastal resources such as mangroves (Kamal *et al.*, 2014; Sudhir *et al.*, 2013), coral reefs (Andrefouet 2014; Velloth *et al.*, 2014) and seagrasses (Nobi *et al.*, 2013) were studied by using GIS. It has also been used in chlorophyll mapping (Nikolaidis *et al.*, 2014), monitoring of oil spills and pollutants etc., and management of coastal zones by studying shoreline changes, coastal zone hazards etc., (Parvin *et al.*, 2014, ManiMurali *et al.*, 2009). Though, there are many articles published on the mapping of the coastal zones and resources using GIS, this technology has not been applied in mapping of marine microbes.

Study of biogeography offers insights into the mechanisms that generate and maintain diversity such as speciation, extinction, dispersal and species

interactions. Previously, biologists have investigated the geographic distribution of mangroves, seagrasses, plankton, etc. More recently, geographic distributions of microorganisms has been studied well and the molecular based methods are allowing sampling and studying the microbial diversity more deeply and widely than ever before, since the culture-based study skips much of the microbial diversity; microbial biogeography stands to benefit tremendously from these advances, although there is still debate as to whether microorganisms exhibit any biogeographic patterns (Martiny *et al.*, 2006) or not.

There are internet-accessible databases that are devoted to include microbial diversity, but are limited in the geographical and geochemical information content. Traditional microbial diversity databases are not designed to display the information in map form and do not contain the compilation of geochemical information needed for ecological studies or the geographical information for discerning long term trends in global distribution (Stonner *et al.*, 2001). There is a development of a prototype database that "maps" microbial diversity of the geochemical and geological environment and geographic location (Stonner *et al.*, 2001). This prototype database is the first of its kind that links microbiological data with geochemical and geographical information. When it is fully implemented, researches will be able to conduct database searches, construct maps containing the information of interest, download files and enter data in the internet.

Influence of temporal and spatial variations on the microbial community composition was assessed in the unique coastal mangroves of the Sundarbans using parallel 16SrRNA gene pyrosequencing (Basak *et al.*, 2014). The total sediment DNA was extracted and subjected to the 16SrRNA gene pyrosequencing, which

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resulted in 117 Mbp of data from three experimental stations. The taxonomic analysis of the pyrosequencing data revealed 24 different phyla. In general, Proteobacteria were the most dominant phyla with predominance of Deltaproteobacteria, Alphaproteobacteria, and Gammaproteobacteria within the sediments. Besides Proteobacteria, there were a number of sequences affiliated to the following major phyla detected in all the three stations in both the sampling seasons: Actinobacteria, Bacteroidetes, Planctomycetes, Acidobacteria, Chloroflexi, Cyanobacteria, Nitrospira, and Firmicutes. Further, taxonomic analysis revealed the abundance of micro-aerophilic and anaerobic microbial populations in the surface layers, suggesting anaerobic nature of the sediments in the Sundarbans.

Results of this study have added valuable information about the composition of microbial communities in the Sundarban mangroves and shed light on possible transformations promoted by bacterial communities in the sediments. In addition, temporal changes in the microbial diversity of the sampling stations during the post-monsoon and monsoon seasons have been highlighted to understand the role of climate and other parameters in shaping the sediment microbial communities in the Sundarbans. This work is also important in building a database and an understanding of as to how the microbial communities vary geographically and with anthropogenic intervention.

Zettler *et al.* (2014) have laid the foundation for an integrated database (MICROBIS) for searching lipid related data with other molecular and geospatial data. Further, the MICROBIS has been updated which can cross-reference lipidomic, taxonomic DNA sequence, and geospatial data. Further, International Census of Marine Microbes (ICoMM) is designing a search-engine-supported mass spectrometry library wherein cross-referencing between the Lipid Maps and the mass spectrometry database is done by the LIPID identifications that will be linked to geospatial data. Thus at the global level, MICROBIS will provide with a user-friendly interface that will allow searching for taxonomic data using DNA sequences, and phylogenetic information, enabling biogeochemists to link lipid data to genomic and geospatial data.

Recently, Priyanka (2014) has made a novel approach in GIS based microbial mapping to explore the spatial diversity of the microbes (bacteria) of the Neil and Havelock Islands of the Andamans, where bacterial detection was done using molecular techniques (16S rDNA analysis) and the strains were assigned to different genera and to different habitats. In this study, mapping the spatial distribution of bacteria was also done using the GIS with Landsat 8 image.

In conclusion, it can be stated that mapping of the marine microbes would pave the way for the future workers to pursue research in the field of microbial biogeography, to discern microbial diversity, both spatially and temporally. This would greatly help explore the useful and potential microbes from the appropriate marine and coastal locations, for use in biotechnology, bioprospecting, biomonitoring and bioremediation.

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