

Exploring biogeographic patterns of marine planktonic cyanobacteria in coastal habitats- integrating uncultured and cultured approaches

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The structure of marine planktonic cyanobacterial communities in coastal habitats can strongly influence rates and fluxes of coastal carbon cycling. Biogeographic patterns of marine planktonic cyanobacterial assemblages were elucidated from four coastal habitats namely, Baltic Sea (BL), Monterey Bay (MB), South China Sea (SCS) and Sundarbans (SB) based on deep phylogeny of 16S rRNA sequences generated using next generation sequencing and Sanger sequencing approaches. Based on 16S rRNA phylogeny, four major taxonomic orders of marine planktonic cyanobacteria were recovered in varying proportions with several novel 16S rRNA sequences in each of the four targeted habitats. Members of the order Synechococcales were dominant in all the habitats (~94% sequences) while the orders Chroococcales and Oscillatoriales were only detected in SB and SCS, respectively. In the phylogenetic tree, *Synechococcus*-like sequences showed overwhelming dominance in SB and they were found in three other habitats. *Prochlorococcus*-like sequences were found in sizeable number in MB and SCS but were absent in SB and coastal BL. *Synechococcus*-like sequences were represented by three major marine clusters (5.1, 5.2, and 5.3). Three novel clades as part of *Synechococcus* cluster were detected only in SB and one novel clade in BL. These clades could have potential functional significance in coastal carbon cycling. Interestingly, cultured based approaches also revealed a new species of *Synechococcus*, *Synechococcus moorigangaii* from SB which has the ability to grow across a range of salinity and metabolize different forms of nitrogen as well as fix di-nitrogen. This reflects the potential vast unexplored functional diversity of marine planktonic cyanobacteria in coastal habitats which needs to be identified and can help towards understanding of export of carbon in coastal oceans. Overall the study has revealed that majority of the marine planktonic cyanobacterial OTUs were found to be exclusive to each habitat, whereas some were shared by two or more habitats based on beta-diversity analysis.

Keywords: Coast, marine planktonic cyanobacteria, diversity, 16S rRNA