



Category: Metagenomics

Microbial diversity assessment within continuous subsurface sediment core of estuarine region of Mahi river basin, Western India

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Abstract

The Mahi estuary is located at the western fringe of the Gujarat alluvial plain in Mainland Gujarat and presents an interesting geomorphic set up. Subsurface microbial diversity plays a vital role in maintenance of good soil health, because microorganisms are involved in many essential functions such as soil formation, elemental cycles, contaminant degradation, and the maintenance of groundwater quality. In the Indian subcontinent, subsurface microbial processes and the diversity are not well studied. Understanding of subsurface microbial diversity of Mahi river basin will help to understand microbial ecology of the Indian subcontinent. Here we examined depth related bacterial diversity pattern within different strata of a vertical sediment section of estuarine region of Mahi river basin. Sediment core samples were collected by core drilling method from Chokari (~17 m deep) (CRD). Upper ~8 m part of sediment core comprises of an estuarine sequence (Holocene age) which is underlain by fluvial sequence (pleistocene age) that continues further down the core. We selected two samples from depth 61.25 cm and 187.5 cm (CRD 2 and CRD 6, respectively) which lie within estuarine sequence and one sample (CRD 27) from 1000 cm depth which lies within fluvial sequence for microbial diversity analysis by using Illumina based sequencing of V3-V4 region of 16S rRNA gene. Total 642462 reads (~ length 250 bp) were obtained which comprised of 32763 OTUs (Operational Taxonomic Units). Abundant OTUs were affiliated with *Actinobacteria*, *Bacteroidetes*, *Proteobacteria*, *Plancomycetes*, *Firmicutes*, *Chloroflexi*, *Cyanobacteria*, *Acidobacteria*, and *candidate division TM7* phyla. *Actinobacteria*, *Proteobacteria*, *Firmicutes*, *Cyanobacteria* and *candidate division TM7* decreased significantly as the depth decreases. Within paleosols of late pleistocene age (CRD 27) *Bacteroidetes* were comprise of 75.32% OTUs while within Holocene samples it comprises of only 19.78% and 1.63% OTUs (CRD 2 and CRD 6, respectively). Taxonomic patterns of OTUs were similar within Holocene samples while pleistocene sediment sample shows different pattern based on pairwise beta-diversity patterns. Conclusively microbial diversity within subsurface sediment core of estuarine region of Mahi river basin are highly diverse indicating availability of different energy source and electron acceptors in microhabitats within the estuarine region of Mahi river basin.

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