



Category: Metagenomics

An Insight into the Microbial Community Structure of White Rann of Kachchh: A Study towards Functional Aspects and Taxonomic Profiling

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Abstract

The desert environment owns a distinctive set of microbial communities as compared to other environment across the globe. Saline desert has unique ecosystem containing well adapted microflora exclusive to the niche. In spite of the importance of ecological processes in saline desert ecosystem, diminutive amount of knowledge is known and understood about indigenous microbial community, functional diversity, biotechnologically potential genes, biogeochemical processes and carbon sequestration abilities. The present study describes the microbial community composition and their functional inheritance from the White Rann of Kachchh. The microbial population was pre-dominantly fashioned by bacteria species followed by archaea and eukaryota. The abundance of bacterial species *Salinibacter* (7.4%), *Burkholderia* (4.3%) of phylum Proteobacteria and Firmicutes, respectively was evidently observed, while archaeal population abundantly contains *Haloarcula* (14%) and *Natromonas* (8%) of phylum *Euryarchaeota* and *Crenarchaeota*, respectively. The functional capabilities were shaped by primarily by genes involved in amino acid transport and metabolism, carbohydrate transport and metabolism, energy production and conversion. This study revealed that the microbial community has developed mechanisms for carbon fixation, stress response, synthesis of osmoregulant to cope up with fluctuations of high and low osmotic pressure in this saline environment. The diversity indices suggested that this profound study may perhaps be more appropriate for better understanding of ecology, White Rann of Kachchh.

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