Abstract

Although research on microbial biogeography has made great progress in the past decade, knowledge of the influence of various physiochemical parameters on microbial characteristics within subsurface floodplain deposits is still lacking in the Indian subcontinent. River floodplains have great economic importance as river catchments are used for various human activities including agricultural and industrial developments. Moreover, microbial activities of subsurface river floodplains play an essential role in maintaining global biogeochemical cycling, bioremediating various pollutants, and improving groundwater quality. Therefore, discovering microbial parameters and their correlation with surrounding geological parameters within subsurface floodplain ecosystems requires special attention for improving subsurface ecosystem functioning.

The Mahi River is the third largest west-flowing river of India after the Narmada and Tapi. Here, the Mahi River basin is used as a model of the river floodplain ecosystem. It encompasses older and younger terraces of which the older terrace comprises aeolian, fluvial, and marine Late Pleistocene sediment deposits, while the younger terrace comprises tidal-flat estuarine sediment deposits of the Holocene period (deposited above Pleistocene fluvial deposits). The vertical stratification of the Mahi River floodplains comprises strong heterogeneity in their geochemical characteristics and offers a highly complex ecosystem for determining key abiotic factors that link with microbial characteristics.

In the present work, core samples from three different locations of the Mahi River basin were collected by rotary drilling method and the study of these core profiles is organized into three Chapters. The first part of the study includes microbial characterization and their correlations with physicochemical parameters of ~17 m deep core of the Mahi river estuary [at Chokari (CRD)-22°13’49"N, 72°55’41"E] lies within a younger terrace of the river basin. The second Chapter includes microbial characterization and their correlations with geological parameters within two laterally deposited Rayka (RYD) (22°26'55"N, 73°05'27"E) and Rampura (RMD) (22°23'0.3"N, 73°05'15"E) cores spanning ~28 m depth and lies within the older terrace. Microbial parameters determined in these studies include analysis of selected *in situ* enzyme activities, determination of microbial abundance by culturable method, gene abundances by qPCR based approach, microbial diversity assessment via isolation and identification of culturable heterotrophs, denaturing gradient gel electrophoresis (DGGE), and metagenomics analysis (16S rRNA amplicon sequencing). The third part of the study includes the determination of heavy metals tolerance ability [Cu(II), Ni(II), Cd(II), Cr(VI), and Hg(II)] of bacterial isolates obtained from RYD and RMD cores and their Cr(VI) removal ability in liquid media as well as in soil of different consistency determined by microcosm experiment (packed bed column experiment).

Metagenomics, DGGE, and culturable microbial diversity revealed the presence of bacterial communities dominated by phyla *Actinobacteria*, *Proteobacteria*, *Bacteroidetes*, *Firmicutes*, *Chloroflexi*, and *Acidobacteria* in the CRD core. Similarly, RYD and RMD cores exhibited dominance of bacterial isolates affiliated with phyla *Actinobacteria*, *Proteobacteria*, *Firmicutes*, and *Bacteroidetes*. Further, sustainable microbial abundance was observed throughout all three cores. Detectable microbial enzyme activities throughout depth in all three cores revealed the role of the Mahi River floodplain in C, N, P, and S cycling. Principal component analysis (PCA) and Pearson correlation analysis between microbial and sediment physicochemical parameters indicated that bulk total organic C (org. C), salinity, P_2O_5, Fe_2O_3, MgO, Cu, Ni, V, and Zn are critical determinants for microbial activities in the CRD. core In RYD and RMD cores, various trace and rare earth elements, K_2O, P_2O_5, EC, TDS, and salinity link significantly with microbial parameters with different directions (i.e. positive or negative correlations) and magnitudes (i.e. strength of correlation). Additionally, total org. C content did not significantly influence microbial enzyme activities in these two cores while in the estuarine core (CRD) org. C content has a positive impact on microbial enzyme activities. Salinity and elemental contents exhibit distinct correlations with microbial parameters in all three cores suggesting that site-specific geochemistry influences microbial parameters differently in all three sedimentary profiles of the Mahi river basin under study. This might be reflected due to different dynamics of *in situ* mineral-microbes interactions and/or due to discrepancies in the bioavailability of elements. This finding could assist the future investigation to altered microbial characteristics via deviating physicochemical parameters that link with microbial parameters to improve sediment ecosystem functioning of the region. Furthermore, the multi-metal tolerance, Cr(VI) removal ability of bacterial strains from the liquid media, as well as prevention of Cr(VI) leaching through sediments of different consistency by bacterial strains obtained from RYD and RMD cores highlights the implication of subsurface microbes in removing Cr(VI) contamination from soils/sediments comprising different textural characteristics.