
List of Figures

Figure 1.1: Schematic presentation of metagenomic analyses of environmental samples	6
Figure 1.2: Phylum level distribution of culturable (cultivable isolates) and unculturable bacterial communities obtained from various subsurface ecosystems.....	16
Figure 1.3: Auger, cable-tool, and rotary drilling process of core sample collection.....	17
Figure 1.4: Diagram showing types of rock core barrels	18
Figure 1.5: Microbial activities that occur in the terrestrial ecosystem and some of the important roles of microbes in biogeochemical processes.....	20
Figure 1.6: Overview of the predominant terminal electron-accepting processes (TEAPs) take place in sedimentary environments.	25
Figure 1.7: Microbial mediated bioremediation of heavy metals/metalloids.	27
Figure 1.8: Model demonstrating the influence of lithology on organic matter metabolism in deep aquifers..	29
Figure 1.9: Microbial mediated process involved in the decomposition of organic matter and weathering of rocks for pedogenesis.	30
Figure 1.10: Indicators of soil health.	31
Figure 1.11: Map of the alluvial plain of the Mahi River.....	33
Figure 1.12: Geomorphic map of the lower Mahi River basin..	34
Figure 2.1: Location map of core drilling sites and cross-sections showing core locations.....	38
Figure 2.2: (a) Rotary drilling rig at Chokari, Rayka, and Rampura (b) Labeled and sealed plastic core liners.	39
Figure 2.3: Schematic diagram of the packed bed columns used in a microcosm study.....	52
Figure 3.1: Cross-section of CRD core drilling site.	57
Figure 3.2: Litholog of Chokari (CRD) sediment core showing stratigraphic sequences (lithofacies) together with depositional phases.	58
Figure 3.3: Microbial enzyme activities within Chokari (CRD) core.	60
Figure 3.4: Enzymatic stoichiometry within Chokari (CRD) core.	61
Figure 3.5: Counts of culturable bacteria and gene abundance in CRD core samples.	63
Figure 3.6: Principal component analysis (PCA) between sediment depth, physicochemical characteristics and microbial parameters within CRD core.....	64

Figure 3.7: Pearson correlation analysis between sediment depth, physicochemical parameters and microbial parameters	64
Figure 3.8: Genus level identity (based on 16S rRNA gene partial sequence) of bacterial strains obtained from CRD core samples.....	65
Figure 3.9: 16S rDNA PCR-DGGE clustering of microbial communities of the CRD core samples.....	68
Figure 3.10: Taxonomic affiliation of DGGE band sequences (based on NCBI-BLASTn) obtained from CRD core samples	69
Figure 3.11: Distribution of OTUs, cumulative percentage reads encompassed by shared OTUs and taxonomic affiliation of top 10 shared OTUs.....	72
Figure 3.12: Cumulative percentage reads encompassed by shared OTUs and percentage reads covered by the top 10 unique OTUs and their taxonomic affiliation	74
Figure 3.13: Distribution of bacterial taxa within Chokari (CRD) core samples.. ..	75
Figure 3.14: Circos plot of CRD core samples displaying percentage distribution of different functional groups of bacteria based on METAGENassist prediction tool.	77
Figure 4.1: Cross-section of RYD and RMD core drilling sites.....	85
Figure 4.2: Comparative litholog of RYD and RMD cores.....	86
Figure 4.3: Box plots of physicochemical attributes and elemental content that showed a significant difference ($p < 0.01$) between the RYD and RMD cores.....	87
Figure 4.4: Microbial enzyme activities within RYD and RMD sediment core sections.....	89
Figure 4.5: Enzymatic stoichiometry within RYD and RMD core.	90
Figure 4.6: Counts of culturable bacteria in RYD and RMD cores.....	92
Figure 4.7: Gene abundances within RYD and RMD core samples by qPCR.....	93
Figure 4.8: Principal component analysis (PCA) of physicochemical attributes, grain size distribution data and major oxides with microbial characteristics within RYD and RMD core profiles.....	94
Figure 4.9: Principal component analysis (PCA) of trace elements and rare earth elements (REEs) with microbial characteristics within RYD and RMD core profiles.....	95
Figure 4.10: Pearson's correlations of microbial parameters with geological variables within RYD and RMD vertical core sections.	97

Figure 5.1: Genus level and phyla/class level distribution of bacterial strains obtained from Rayka (RYD) and Rampura (RMD).110

Figure 5.2: Heavy metal [Hg(II), Cd(II), Cr(VI), Cu(II), and Ni(II)] tolerance of bacterial strains obtained from RYD and RMD cores111

Figure 5.3: Percent survival and removal of chromate by selected bacterial strains obtained from RYD and RMD cores in R2A and SE + peptone broth amended with 2, 5, 10, 15, and 20 ppm Cr(VI).114

Figure 5.4: Morphology of *Bacillus* sp. RYD 15.1A and *Streptomyces* sp. RMD 42.2B.115

Figure 5.5: Effect of *Bacillus* sp. RYD 15.1A and *Streptomyces* sp. RMD 42.2B on chromate removal in the leachate of packed bed columns filled with the soil of different consistency.116
