LIST OF TABLES

Table 2.1: Overview of genetic fingerprinting techniques.

Table 3.1: Standard zone of inhibition by various antibiotics at standard concentrations.

Table 3.2: Antibiotic sensitivity test of different isolates.

Table 3.2a: Segregation of the isolates into their respective subzones for each antibiotic, depending upon its zone of inhibition (diameter in mm).

Table 3.2b: Segregation of the isolates with respect to their subzones for each antibiotic.

Table 3.2c: Frequency of occurrence of different isolates within each group.

Table 3.2d: Frequency of different isolates within each group in ascending order.

Table 4.1: Source and isolation conditions for different microbes used in this study.

Table 4.2a: Antibiotic sensitivity assay of microbial strains isolated from diverse environmental samples used in this study.

Table 4.2b: Frequency of occurrence of different isolates within each group on the basis of resistance and sensitivity towards various antibiotics.

Table 4.2c: Response pattern of isolates for different antibiotics.

Table 4.3: Identification of microbial isolates from marine coastal water sample 16S rDNA sequencing.

Table 4.4: Identification of microbial isolates from nitrogen rich soil sample 16S rDNA sequencing.

Table 4.5: Identification of microbial isolates from Oil Refinery ETP sludge sample by 16S rDNA sequencing.

Table 4.6: Identification of microbial isolates from nitro aromatic ETP sludge sample by 16S rDNA sequencing.

Table 4.7: Identification of microbial isolates from vegetable waste sample by 16S rDNA sequencing.

Table 4.8a: Frequencies of phylotypes (OTUs) within the bacterial domain derived from the 16S rDNA gene sequences of isolates from Marine coastal water sample.
Table 4.8b: Frequencies of phylotypes (OTUs) within the bacterial domain derived from the 16S rDNA gene sequences of isolates from Nitrogen rich soil sample.

Table 4.8c: Frequencies of phylotypes (OTUs) within the bacterial domain derived from the 16S rDNA gene sequences of isolates from Oil refinery sludge sample.

Table 4.8d: Frequencies of phylotypes (OTUs) within the bacterial domain derived from the 16S rDNA gene sequences of isolates from Nitro aromatic sludge sample.

Table 4.8e: Frequencies of phylotypes (OTUs) within the bacterial domain derived from the 16S rDNA gene sequences of isolates from Vegetable waste sample.

Table 4.9: Comparison of phylotype richness, diversity and evenness values for different environmental samples studied.

Table 4.10a: Hydrolytic activities of bacterial isolates from different environmental sample.

Table 4.10b: Bacterial isolates from different environmental samples showing range of hydrolytic enzymes activities.

Table 4.11a: Diversity distribution of clones from 16S rDNA library of pharmaceutical industry.

Table 4.11b: Frequencies of phylotypes (OTUs) within the bacterial domain derived from the 16S rDNA gene sequences from pharmaceutical effluent.

Table 4.11c: Comparison of Closest database matches obtained from culture dependent and culture independent methods.

Table 4.12: Comparison of phylotype richness, diversity and evenness values for the pharmaceutical ETP sludge sample cultured and uncultured bacterial communities.