ABSTRACT

Biodiversity of India is a unique asset, which can be harnessed through use of modern biotechnological tools of research. Since, we are not able to culture majority of these organisms, there is a demand for novel techniques and effective strategies to tap the unexplored diversity. Modern molecular techniques have enabled us to assess microbial diversity without culturing them. 16S rDNA-based molecular techniques have been used for community-level analysis of differences in microbial composition associated with different environments. The detailed analysis of microbial diversity within an environment can be divided into two broad categories: culture dependent and culture independent studies.

Microbial diversity from six different environments has been studied using culture dependent and culture independent methods. Microbial communities in coastal subsurface sediments are scarcely investigated and have escaped attention so far. Soil is a very complex habitat dominated by the soil solid phase. Natural products derived from soil samples can continue to play a major role in the development of new biocatalysts and drugs. ETPs represent a biological wastewater treatment facility that receives wastewater from different processes or industries. The exploitation of biological waste material as a renewable resource for bioenergy and byproducts development continues to be a major challenge for biotechnology. Use of different isolation parameters i.e. pH, salt, temperature and metal concentration have enhanced the identification of distinct microbial types. Segregation of microbes by antibiotic susceptibility assay has provided a preliminary identification. Using culture-based techniques 18 different genera (represented by 110 isolates with 73 phylotypes), belonging to the phyla Actinobacteria, CFB group, Firmicutes, α-, β- and γ- Proteobacteria, were identified. These isolates have a wide range of amylase, protease and lipase producing abilities. Twenty different genera (represented by 81 clones with 44 phylotypes) from the phyla Actinobacteria, CFB group, Firmicutes, α-, β-, δ- and γ- Proteobacteria were identified. A majority of sequences retrieved here were ≤95% related to closest database matches. Shannon-Weiner diversity index (H) varied a lot in all the samples, i.e from 2.35 for nitrogen rich soil to 3.21 for oil refinery ETP sludge sample. It was found to be highest for oil refinery ETP sludge.
sample, followed by 2.70 for vegetable waste sample, indicating that highly diverse species were present in these samples.

In this study, 16S rDNA sequence analysis was carried out for identification of bacteria. We can anticipate their vital role in consistent performance of ETPs, particularly in case of digester failure. A consortia of these microbes can be maintained on the diluted effluent and used to replenish the loss of microbial mass in case of accidental loading with toxic or novel feed/wastewaters.