

Diversity, Novel Taxa Identification and Enzymatic Potential of Haloalkaliphilic Bacteria from the Saline Desert of Kutch, Gujarat, India

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ABSTRACT

The microbial diversity of the Little Rann of Kutch (LRK), a unique coastal saline desert ecosystem in Gujarat, India, remains underexplored compared to other deserts worldwide. This study represents the first report on the extensive isolation, spatial distribution, 16S rRNA gene-based phylogeny, and identification of novel taxa from LRK. A total of 87 isolates were obtained from three different study sites in LRK. Based on the full 16S rRNA gene sequences, the isolates were grouped into 44 different phylotypes of four phyla: Firmicutes, Proteobacteria, Actinobacteria, and Euryarchaeota. A majority of the isolates displayed broad salt and pH tolerance. Further, six putative novel taxa were identified. Available nitrogen, pH, Organic carbon, TDS, and EC were the main environmental variables affecting the microbial diversity. Screening for extracellular enzymes revealed that 72% of the isolates produced at least one enzyme. Many strains have shown multiple enzyme activity. The enzyme activity was predominantly observed in Firmicutes as compared with other phyla. Further, Alkaline protease genes of selected protease producers were amplified and sequenced. Based on structural analysis, alkaline protease gene from haloalkaliphilic *Bacillus lehensis* was expressed in *E.coli* BL21 (DE3) and recombinant protease showed optimal activity at pH 10 and 50°C, with significant stability in various solvents and metal ions. The structural elucidation of APrBL suggests dominance of coils (45.70%), followed by α -helices (31.75%), and β -strands (22.55 %). Successful application of recombinant protease for blood stain removal and whey hydrolysis makes it good candidate for detergent and food industry. This study underscores the untapped microbial diversity of LRK and its significant potential for the discovery of novel enzymes with diverse biotechnological applications.

Keywords: Microbial diversity, Novel taxa, Haloalkaliphiles, Gene expression, Recombinant alkaline protease, Detergent additive, Whey protein hydrolysis

How to Cite

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