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Exoenzyme Profiling of Economically Important hydrolytic enzymes from bacteria in Forest Soil

Western Ghats is considered, as a global biodiversity hotspot and Thattekad Bird Sanctuary is a part of Western Ghats famous for avian biodiversity. The topography of the area mostly contains long running plains, adorned with continuous tropical forests and this region consisting of an unexplored microbial community, is selected as the study area for the present investigation. The high demand for microbial enzymes in the industry directed the focus of this study to exoenzyme profiling of relevant bacterial isolates from forest soil samples mainly focusing on multienzyme producers. The soil was collected from five different sites of Thattekad and morphologically different bacterial colonies were selected after serial dilution followed by spread plate method. All the isolates were subjected to the production of the following enzymes: amylase, cellulase, ligninase, pectinase, xylanase, gelatinase, caseinase, esterase, and lipase. In order to determine enzymatic activities, isolates were streaked on specific minimal media supplemented with an appropriate substrate for extracellular hydrolytic enzyme detection. The Enzymatic Index (EI) in each enzyme assay was measured after incubation, expressed as EI= (colony diameter + halo zone diameter)/colony diameter . Qualitative enzyme assays were carried out in six independent experiments, and standard deviation was determined using descriptive statistical analysis. The strains produced 2 or more enzymes on repeated exoenzyme screening trials were selected for further studies. All the selected sites produced multienzyme producing strains and 150 different bacterial strains producing different enzymes were isolated. Site 2, the moist deciduous type of forest was the best area with 45 different enzyme producers and it was followed by Site 2 comprised of evergreen type of forest with 34 strains. In our study the site 5, with sandy soil was the least enzyme producing microbial strains and only 15 strains were isolated from that site. Identification of the isolates was performed using the microbiological techniques like cultural characteristics, biochemical methods and molecular techniques. For molecular characterization, the data of 16S rRNA gene sequences were identified using the BLAST-N search program in the National Centre for Biotechnology Information (NCBI). Based on the taxonomic classification, the identified strains come under two different categories of phylum; firmicutes and proteobacteria. 34 bacterial 16S rDNA sequences were deposited in NCBI Gene bank and are given accession numbers from National Center for Biotechnology Information (NCBI). Phylogenetic tree was constructed and the evolutionary relationship of strains based on 16S rRNA gene sequences has been determined by following the Maximum Likelihood and Bootstrap consensus method to categorize isolates into specific clades. The geographic location selected for this study turned out to be a natural source of potent strains of hydrolytic enzyme producers that had not been explored till now to the best of our knowledge. Multienzyme producing microbial strains can gain significant role in the enzyme industry for various .

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Biography

Mrs.Achamma Thomas has completed her masters in Microbiology and currently doing Ph.D. in Microbiology, in the field of Metagenomics under the guidance of Dr.S.Mohan In M.G University. She is also an entrepreneur in Biotechnology.