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Functional metagenomics: A modern tool for enzyme-based bioremediation**Chandni Sidhu, Vipul Solanki, Krishan Gopal and Anil Kumar Pinnaka**
Institute of Microbial Technology, India

Increase in population and progress in science, technology and industry has led to the introduction of a lot of contaminants in the environment which poses a serious health risk to living systems due to their carcinogenic properties. A large number of microbial enzymes have been reported to carry out efficient biodegradation of these toxic pollutants. Among these enzymes, oxygenases are the fundamental enzymes and play a crucial role in xenobiotic degradation. Due to the limitation of cultivability of microbes in standard laboratory conditions, we have used functional metagenomics technique to directly clone the environmental DNA from contaminated sites and explore the oxygenase diversity and their ability to degrade recalcitrant compounds. Here, we constructed a functional metagenomic library in fosmid carrying ~40 kb DNA from activated sludge and screened it by activity-based approach using catechol as a substrate. Positive fosmid clones were further sequenced and oxygenase genes were identified using bioinformatic tools. One of the positive fosmid clone SD3 suggested the presence of catechol 2,3-dioxygenase (SD3-C23O), 2,3-dihydroxybiphenyl 1,2-dioxygenase (SD3-bphC), gentisate 1,2-dioxygenase (SD3-G12O) and taurine dioxygenase (SD3-TDO) in ~38 kb fragment. Recombinant versions of these enzymes were constructed and enzymes were purified to examine their degradation ability in the presence of various contaminants. We have completely characterized SD3-bphC which encodes a gene of 891 bp corresponds to 297 amino acid residue protein. BLAST results using the protein sequence of bphC_SD3 showed the similarity of 74% and 72% with glyoxalase of *Sphingomonas* spp. MCT13 and *Caulobacteraceae* bacterium OTSz A272 respectively. BphC protein from both the species has not been characterized yet. Biochemical characterization showed that it is a halotolerant enzyme that can tolerate up to 4 M NaCl. Taxonomy binning suggested that the cluster of SD3 is from uncultured bacteria. SD3-bphC is able to degrade 2, 3-dihydroxybiphenyl > catechol > 3-methylcatechol > 4-chlorocatechol in an efficient manner. The properties of SD3-bphC make it as a potential candidate for decontamination of saline and hypersaline environments like salt marshes, oil fields and saline industrial effluents.

Biography

Chandni Sidhu is pursuing her PhD under the supervision of Dr. P Anil Kumar (Senior Scientist, MTCC, CSIR-IMTECH Chandigarh, India). She has published more than 60 papers in reputed journals. She has research experience and expertise in the field of microbiology, molecular biology, metagenomics, proteomics and bioinformatics. Her research work includes oxygenase-based bioremediation of contaminated environments by functional metagenomics.

chandnisidhu20@gmail.com

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