

BIOCATALYSTS GENE SEQUENCE RECOVERY FROM METAGENOMIC DNA OF ATLANTIC FOREST SOIL

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Metagenomics has made possible to access the vast genetic resources hidden in unculturable microorganisms genomes. New enzymes and metabolic pathways leading to the production of biomolecules with industrial and pharmacological applications can be discovered by analyzing metagenome libraries. Here we describe the sequencing and analyses of a 40kb insert of a clone isolated from library constructed with metagenomic DNA from the Atlantic Forest soil of Paraná State. Three metagenomic libraries containing 100,032 clones were screened for lipase activity on tributirin (316 positive clones), tricaprilin (10 positive clones) and triolein (1 positive clone). The metagenomic DNA insert of the triolein degrading clone was fully sequenced. The final sequence was assembled using the Phrep-Phrap-Consed package and compared to the non-redundant SwissProt database using BlastX and BlastP program. A lipase gene with low identity to lipase gene sequences of database (45%) was identified. Bioinformatics analysis indicated the presence of a LipA multidomain of the Esterase/Lipase superfamily (EC: 3.1.1). The result suggest the isolation of a new lipase gene with no counterpart in the protein database. Moreover, the insert contains genes for 22 additional proteins, including a PKS type 3, Zn-dependent metallopeptidase, dipeptidil aminopeptidase, serine phosphatase, metyltransferase, mandelate racemase, N-acetyl-gamma-glutamyl-phosphate reductase, serine O-acetyltransferase, diguanylate cyclase and a two component system composed by a sensor histidine kinase and a heavy metal response transcriptional regulator. These results reinforce the potential of Metagenomics for prospection of new biotechnological products. Supported by: CNPq/MCT, Instituto do Milênio, Fundação Araucária/CNPq, Pronex

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