

Journal of Chemical, Biological and Physical Sciences



An International Peer Review E-3 Journal of Sciences

Available online at www.jcbps.org

Section B: Environmental Biotechnology

CODEN (USA): JCBPAT

Abstract

Cloning Of Microbial Lipase Of A Metagenomic Library Of Aquifer From Yucatán

Castro Avilés Jaime¹, Chi Manzanero B¹, Ramos Jiménez S¹, Canseco Pérez M¹, De los Santos Briones C¹, Apolinar Hernández M¹, Rivera Muñoz G⁴, Prieto Davó A², Rojas Herrera R³, O' Connor Sánchez A¹, Canto Canche B¹.

¹Centro de Investigación Científica de Yucatán A.C Unidad de Biotecnología, Mérida Yucatán 43No. 130 col. Chuburná de Hidalgo C.P 97200, Canto Canche Blondy.

²Facultad de Química, Unidad Sisal. Universidad Nacional Autónoma de México, Puerto de Abrigo S/N, municipio de Hunucmá, C.P. 97156, Sisal, Yucatán, México.

³UNAM.Facultad de Ingeniería Química. Periférico Norte Kilómetro 33.5.Tablaje Catastral 13615. Colonia Chuburná de Hidalgo Inn. C.P.97203.Merida, Yucatán.

⁴Instituto Tecnológico de Mérida Av. Tecnológico km 4.5 S/N, calle 60, colonia Plan de Ayala, C.P.97118, Mérida, Yucatán, México.

Abstract: The microbial lipases represent an important group of enzymes for biotechnological applications, given that they are specific for certain substrates, stable in organic solvents and they have a high regio-enantioselectivity. The strategy implemented was a screening of a metagenomic library of the Yucatan's aquifer, with the objective of finding lipase genes. We analyzed 6600 clones on selective medium containing rhodamine B and olive oil, obtaining 15 positives clones that showed lipolytic activity, among these, we selected the clones with biggest fluorescent halos on plate screening. Afterwards it was purified for the sequencing and supercontig of 32 kb was assembled. By using bioinformatics tools we found the predicted ORFs for some hypothetic proteins and sequences with no hits. Further Blast analysis retrieved a sequence of phospholipase from *Fusarium Oxysporum*, however the E-value denoted that data possibly is not reliable, reason why we will search the lipase sequence by lose of function though the use of transposition *in vivo*. Likewise, we will know if the data obtained by bioinformatics analysis is true.

Keywords: Metagenomic, lipase, plate screening, *in silico*, fosmid, ORF.

Corresponding author: Blondy Canto Canché

James_av@live.com.mx