

Isolation of a novel lipase from a metagenomic library derived from mangrove sediment from the south Brazilian coast

G.H. Couto, A. Glogauer, H. Faoro, L.S. Chubatsu, E.M. Souza and F.O. Pedrosa

Departamento de Bioquímica e Biologia Molecular, Universidade Federal do Paraná, Curitiba, PR, Brasil

Corresponding author: F.O. Pedrosa E-mail: fpedrosa@ufpr.br

Genet. Mol. Res. 9 (1): 514-523 (2010) Received November 20, 2009 Accepted January 4, 2010 Published March 23, 2010

ABSTRACT. A novel gene coding for a LipA-like lipase with 283 amino acids and a molecular mass of 32 kDa was isolated and characterized from a metagenomic library prepared from mangrove sediment from the south Brazilian coast. LipA was 52% identical to a lipolytic enzyme from an uncultured bacterium and shared only low identities $(\leq 31\%)$ with lipases/esterases from cultivable microorganisms. Phylogenetic analysis showed that LipA, together with an orthologous protein from an uncultured bacterium, forms a unique branch within family I of true lipases, thereby constituting a new lipase subfamily. Activity determination using crude extracts of Escherichia coli bearing the *lipA* gene revealed that this new enzyme has a preference for esters with short-chain fatty acids (C \leq 10) and has maximum activity against *p*-nitrophenyl-caprate (chain length C10, 0.87 U/mg protein). The optimum pH of LipA was 8.0, and the enzyme was active over a temperature range of 20 to 35°C, with optimum activity against pnitrophenyl-butyrate at 35°C and pH 8.0.

Key words: Metagenome; Lipase; Mangrove sediment

©FUNPEC-RP www.funpecrp.com.br

Genetics and Molecular Research 9 (1): 514-523 (2010)