Abstracts

XVIth National Congress of Biochemistry

Ponta Delgada, São Miguel, Açores
October 22—25, 2008

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S11.P9 *Petrotoga mobilis* possesses two pathways for the synthesis of the rare compatible solute mannosyl-α-1,2-glucosylglycerate
Chantal Fernandes, Nuno Empadinhas, Vitor Mendes, Joana Costa, Helena Santos, Milton S. da Costa

S11.P10 Identification of genes putatively involved in the synthesis of cyanobacterial exopolysaccharides
Sara Pereira, Ângela Brito, Andrea Zille, Pedro Moradas-Ferreira, Paula Tamagnini

S11.P11 A unique combination of genetic systems for the synthesis of trehalose in *Rubrobacter xylanophilus*: Characterization of the first bacterial TreT
Ana Nobre, Susana Alarico, Nuno Empadinhas, Milton S. da Costa

S11.P12 Genetic diversity among azorean isolates of *Steinernema carpocapsae*
L. Esteves, R. Montiel, N. Simões

S11.P13 Metalloproteases produced by the entomopathogenic bacteria *Photorhabdus* sp.Az29: expression studies and characterization of the prtA and prtS genes
C. M. Cabral, R. Montiel, G. Nascimento, N. Simões

S11.P14 The sugar phosphotransferase system (PTS) is involved in the uptake of the quorum sensing molecule AI-2 in *Escherichia coli*
Antota Santos, Catarina S. Pereira, João C. Marques, Karina B. Xavier

Symposium 12: **BIOTECHNOLOGY**

Invited Speaker

S12.IS Biotechnological approaches to fruit related allergens
Margit Laimer

Selected Comunications

S12.C1 A new analgesic peptide: From biophysical screening to in vivo tests
Marta M. B. Ribeiro, M. Heras, E. Bardaj−,M. Pinto, I. Tavares, Miguel A.R.B. Castanho

S12.C2 Molecular phytopatology: From plant pathogen diagnosis to the research on resistance mechanisms
D. Mendonça, I. Foroni, M. S. Lopes, S. Leitão, A. da Câmara Machado

S12.C3 Improvement of naringinase activity and stability via immobilization techniques
M. I. Amaro, M. H. Ribeiro

S12.C4 HE-TAIL PCR, a powerful tool for identification of *Trichoderma harzianum lip1* gene
L. Jorge, F. González, E. Monte, A. Choupina

Poster Presentations

S12.P1 Maintenance of catalytic activity in complex steroid bioconversion
Marco P.C. Marques, Filipe Carvalho, Gabriel A. Monteiro, Joaquim M.S. Cabral, Pedro Fernandes

S12.P2 Aminopeptidase N from *A. thaliana:* expression and characterization
Rui Cruz, Rosário Faro, Euclides Pires, Carlos Faro, Paula Ver−ssimo

S12.P3 Identification of cytotoxic proteins of*Bacillus thuringiensis*
Ana Duarte, Vera Gouveia, Rafael Montiel, Carla Cabral, Luisa Oliveira, Nelson Simões

S12.P4 scFv antibodies selected by phage display technology that target gp41 and gp120 are strong candidates to inhibit HIV-1 fusion process
Andreia Couto, Pedro Lucas, João Gonçalves

S12 C4 HE-TAIL PCR, a powerful tool for identification of *Trichoderma harzianum lip1* gene

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Trichoderma harzianum is a widespread soil fungus, known as a biocontrol agent against soilborne plant pathogens. Species of *Trichoderma* are commercially applied as biological control agents against plant fungal pathogens based on different mechanisms, such as antibiosis, competition for nutrients and mycoparasitism.

One of the mechanisms involved is the production of several lytic enzymes. In *T. harzianum* has been identified several glucanases, celulases, chitinases and proteases, but nothing are already known about its lipolytic system.

In this work we described the identification of *lip1* from *T. harzianum*, a gene encoding the first extracellular triacylglicerol lipase known in this species. A cDNA library of *T. harzianum* CECT 2413 cloned in pBluescript SK+ was screened, and the expressed sequence tags (ESTs) with more similarity against lipase gene sequences in international databases selected and sequenced. Elucidation of complete gene nucleotide sequence of *lip1*, including 52 bp of the open reading frame at the N-terminal region and 693 bp of the promoter region were achieved by high-efficiency thermal asymmetric interlaced (HE-TAIL) PCR (Michiels *et al.*, 2003), which confirmed to be a powerful tool to identify flanking regions from short known sequences.

Lip1 codifies a 558 amino acids protein, with 59322.6Da and a calculated global iso-electric point value of 4.56.

The GenBank/EMBL/DDBJ accession number for the sequence reported in this paper is AM18087.
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