BIOCELL
2010, Vol. 34 (Suppl.): 1-154

ISSN 0327 - 9545
PRINTED IN ARGENTINA

- SAIB -

46th Annual Meeting
Argentine Society for Biochemistry and Molecular Biology

XLVI Reunión Anual
Sociedad Argentina de Investigación en Bioquímica y Biología Molecular

November 30 - December 3, 2010

Puerto Madryn, Chubut
República Argentina

BT-P09

CULTURE MEDIUM FACTORIAL DESIGN OPTIMIZATION FOR FIBRINOLYTIC ENZYMES PRODUCTION BY *Bionectria sp.*

Arnau VG, Rovati JI, Figueroa LIC, Fariña JI
PROIMI-CONICET. Tucumán, Argentina. E-mail: tronador17@hotmail.com

Thrombotic diseases can be clinically treated with fibrinolytic enzymes and many attempts have been made at laboratory level to increase fibrinolytic enzymes production from microbial sources and to reduce the process cost, including culture medium design, optimization of environmental conditions, and over expression with genetically modified strains. In this contribution we present the optimization of culture medium composition and incubation temperature for fibrinolytic enzyme production by *Bionectria* sp., a selected fungal strain from Las Yungas (Tucumán). Optimization was carried out at Erlenmeyer scale (100-mL working volume) via factorial design methodology. All trials included a common mineral base (%, w/v: NaCl 0.2, KH2PO4 0.05, MgSO4•7H2O 0.05). According to four factorial designs it could be demonstrated the convenience of using soy peptone as N-source, glucose as C-source, and the possibility to eliminate starch, meat peptone and meat extract from original medium composition, whilst 25°C was selected as the optimal incubation temperature. Results showed that culture medium could be successfully optimized by factorial design, achieving a reduction in the production process costs by means of a decrease in culture medium components, the improvement in culture broth rheology, mycelial morphology and mass/energy transfer, and the subsequent two-fold enhancement in productivity.

BT-P10

CORN INDUSTRY SUBPRODUCTS FOR BIOMASS PRODUCTION OF AN ATRAZINE DEGRADING BACTERIAL CONSORTIUM

Calabró López RA, Busto VD, Cuadrado V, Giulietti AM
Microbiología Industrial y Biotecnología, Fac. de Farmacia y Bioquímica, Universidad de Buenos Aires. E-mail: acalabro@ffyb.uba.ar

Bioremediation is a well known tool used to degrade or transform contaminants. Bioremediation processes can be carried out both by biostimulation and/or bioaugmentation. The last process consists in the introduction of specific competent degrading strains or consortia of microorganisms. In a previous work, in order to produce high biomass concentration of an atrazine degrading bacterial consortium, traditional carbon sources as glucose or citrate were used. Furthermore, water of maceration (MA) and syrups mixture (SM) are low cost corn industry subproducts that represent an economical alternative for cultivation of these microorganisms. The aim of this work was to study the biomass production of an atrazine degrading bacterial consortium isolated from soils of the Argentinean Humid Pampa using these subproducts as carbon and energy source. Shake flasks experiments using factorial design were carried out in 250 ml Erlenmeyer flasks using atrazine as nitrogen source and MA or SM as carbon and energy source. Biomass production and atrazine consumption were monitored over time. SM was able to replace traditional carbon sources in culture media for support consortium growth and maintain atrazine degrading capacity, being a potential substrate for biomass production useful for bioaugmentation processes.

BT-P11

PROTEOMIC STUDY OF *Rhodotorula mucilaginosa* RCL-11 REVEALED DIFFERENTIAL PROTEINS EXPRESSION UNDER COPPER STRESS

Irazusta V, Estevez C, Amoroso MJ, C. de Figueroa LI
PROIMI-CONICET, Tucumán, Argentina. E-mail: virazusta@proimi.org.ar

Organisms subjected to metal exposures in their natural environments generally have had develop resistance mechanisms. *Rhodotorula mucilaginosa* RCL-11, yeast isolated from a copper filter plant at the province of Tucumán, Argentina, has the ability of supporting high amounts of copper metal by a slow down in its growth rate. In order to understand the mechanism involved in RCL-11 resistance to copper it was conducted a proteomic approach. Results of atomic absorption spectroscopy showed that copper concentration in the medium decreased from 0.5 to 0.2mM 48 h later inoculation occurred. Analyzing by mono-dimensional gel electrophoresis the crude cells extracts, it was observed differential bands expressions between cells with or without copper. Further, with the aim of studying these differences, two-dimensional electrophoresis analyses was carried out. Gels were silver-stained, scanned and analyzed with Image Master Program. 2-D analysis of RCL-11 revealed that 48 h copper exposure produced an over-expression of 20 proteins; some of them increased their expression according to the time of copper exposure (16, 24 and 48 h). The results obtained in the present work show that when exposing *R. mucilaginosa* RCL-11 to 0.5mM copper concentration, it is produced a differential protein expression probably involved in cell resistance mechanisms.

BT-P12

DYNAMICS OF A MARINE-MICROBIAL COMMUNITY DURING BIODEGRADATION OF BILGE WASTE HYDROCARBONS

Nievas ML[1], Ferrero M[2], Olivera NL[1], Dionisi HM[1], Commendatore MG[1], Esteves JL[1], Bucala V[3]
[1]CENPAT (Puerto Madryn), [2]PROIMI (Tucumán), [3]PLAPIQUI (Bahía Blanca), CONICET, Argentina. E-mail: nievas@cenpat.edu.ar

The aim of this study was to identify the dominant taxons of a hydrocarbon-degrading microbial community enriched from bilge waste oily phase, and to assess its population dynamics during bilge waste biodegradation. Samples were retrieved from an aerated batch bioreactor with 2.1 g/L total hydrocarbons in seawater medium during a 14-day biodegradation experiment. Total DNA was analyzed by PCR-DGGE, and the relative intensity of each dominant band calculated. Members of the genus *Marinobacter* were dominant in the enrichment, and *Pseudomonas*, *Shewanella* and *Halomonas* were also detected. During the biodegradation experiment, the exponential-growth phase agreed with n-alkane depletion and an increase in the prevalence of *Pseudomonas* and *Shewanella*. Only after emulsification, biodegradation of other more recalcitrant hydrocarbons found in an unresolved complex mixture (UCM) occurred, associated with a predominance of *Marinobacter* and *Shewanella*. Cluster analysis from DGGE fingerprints showed shifts in the microbial community structure which matches with the pattern of sequential hydrocarbon biodegradation found (n-alkanes-UCM). *Shewanella*, a genus which can use diverse electron acceptors such as metals and colonizes emulsified oil from spills, showed high prevalence during both n-alkane and UCM biodegradation of bilge wastes, suggesting a promising potential for bioremediation.