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

MI-P57

ABUNDANCE OF POLYCYCLIC AROMATIC HYDROCARBON-DEGRADING POPULATIONS IN PATAGONIAN COASTAL SEDIMENTS

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The aim of this project was to quantify polycyclic aromatic hydrocarbon (PAH)-degrading bacterial populations in coastal sediments of Northern Patagonia. We analyzed the relative abundance of various genes encoding PAH dioxygenases by qPCR, in DNA extracted from intertidal sediment samples collected at Fracasso Beach, a protected area, and Córdova Cove, a chronically polluted site. We quantified the following catabolic genes: *phnA1* (*Cycloclasticus* spp.), *nahAc* (*Pseudomonas* spp.), *phnAc* (β-*Proteobacteria*) and C, a novel dioxygenase gene previously detected in Subantarctic sediments. Additionally, we quantified 16S rRNA genes using a universal primer set. Physico-chemical parameters, including ORP, granulometry, organic matter, ammonium and hydrocarbon concentrations, were also measured in these samples. *phnA1* genes were abundant in polluted sediments, and their abundance was found to be two orders of magnitude higher in sediments with twice the concentration of 3-ring PAHs. The other analyzed genes were found to be present, although below quantification limit for this technique. These results suggest that *Cycloclasticus*, a marine obligate hydrocarbonoclastic bacterium, plays an important role in the biodegradation of low molecular weight PAHs in coastal sediments of Patagonia. Laboratory scale studies are being performed to analyze population dynamics after crude oil or PAH exposure7

MI-P58

STATISTICAL EVALUATION OF MEDIUM COMPONENTS OF ENTOMOPATHOGENIC PROTEIN PRODUCTION

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Bacillus thuringiensis produces proteins with entomopathogenic action. Advances in the production of bio-insecticides involve the application of suitable fermentation technologies, especially with the use of appropriate media, overcoming the metabolic limitations of the microorganisms. The use of agro-industrial residues as substrate in the production by fermentation can significantly reduce the final price and add value to low-cost materials. The objective of the present work was to screening substrates that have a positive impact on the production of entomopathogenic proteins from *Bacillus thuringiensis* RT. Evaluation was performed by Plackett-Burman experimental design. Eleven medium components were evaluated. Mortality bioassays were carried out using 3rd instar larvae of *Spodoptera frugiperda*. The most significant variables affecting positively the production were starch, milk powder and whey. Medium with highest protein production (0,8 mg/ml) was 4 times better than Luria Bertani medium (0,2mg/ml). There were significant differences in mortality with the media tested. In conclusion, many substrates were identified to improve production, which could be considered for optimization medium and studies in bioreactors.

This work was supported by grants PIP-CONICET 297 and CIUNT 26/D409.

MI-P59

PROTECTION OF OILSEED RAPE (*B. napus*) TOWARD FUNGAL PATHOGENS BY STRAINS OF BIOCONTROL PGPR

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The aim of this work is to evaluate the effects of treatment of oilseed rape (*Brassica napus*) with indigenous bacterial strains isolated from soybean rhizosphere. Antifungal activities of two of these isolates, previously identified and designated as *Pseudomonas fluorescens* BNM296 and *Bacillus amyloliquefaciens* BNM340, were assayed by dual culture with two serious fungal pathogens to *Brassica* species, *Botrytis cinerea* and *Sclerotinia sclerotiorum*. Oilseed rape seeds were inoculated with each of the bacterial suspensions and colonization of seedling roots was evaluated. In addition, the treated plants were assessed for their resistance to the fungal pathogens using detached leaves assays. The dual bacterial culture of BNM340 inhibited the myceliar growth of *B. cinerea* (66.4±1%) and *S. sclerotiorum* (71.1±5.2%) with respect to each of the fungi growing alone. In the case of BNM296, the relative growth of *B. cinerea* and *S. sclerotiorum*, in the presence of the bacteria, were also inhibited 46.1±4.6% and 37.6±6%, respectively. The quantification of bacteria adhering to the surface of inoculated *B. napus* seeds and roots showed that both of tested bacteria effectively colonized them. Leaves of treated plants with BNM296 and BNM340 exhibited an enhanced state of resistance against *S. sclerotiorum* and *B. cinerea*, demonstrating that these bacterial suspensions are capable of inducing ISR.

MI-P60

MOLECULAR IDENTIFICATION OF *Enterococci* ISOLATED FROM ARTISANAL CHEESES

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Enterococci are relevant for improving and developing the flavor and quality of cheese. *E. faecalis* is the commonest specie isolated from artisanal cheeses. Strains of *E. faecium* (EVR) are also recovered from artisanal cheeses, being the reason of human infections. EVR develops multi-resistance to different antimicrobials such as aminoglycosides, ß lactams and glycopeptides.

Aims: To correlate the phenotypic and genotypic identification of the enterococci isolates from artisanal cheese manufactured in farms settle in Tandil, BA province.

Methods: 21 artisanal cheeses were processed. The phenotypic characterization was performed by the API System, whilst the molecular identification of the strains was undertaken by PCR amplification of *tuf* and *sodA* genes.

Results: 13 strains of enterococci were isolated from cheeses, by which 9 strains were phenotypically identified as *E. faecalis,* whilst 4 isolates were not typified. PCR revealed that all the strains tested were identified as *E. faecium*.

Conclusions: The phenotypic characterization is not a reproducible and reliable method to identify enterococci. In contrast, the genotyping techniques, allows a fast and accurate identification of those strains. In artisanal dairy products is pivotal to identify other species than *E. faecalis* that may become as emergent pathogens in human (EVR).