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92 **Resúmenes de las Comunicaciones presentadas en formato E-Póster**

BPE123-dependent manner, indicating that interaction with translocated BPE123 might also be occurring during the intracellular phase of *B. abortus*. Moreover, down-regulation of the expression of ENO1 in HeLa cells infected with *B. abortus* affected intracellular replication, demostrating a role of ENO1 in *Brucella* intracellular lifestyle. To investigated if the interaction between BPE123 and ENO1 affects the catalityc activity of ENO1, activity assays were performed and demostrated that ENO1 activity is enhanced not only in HeLa cells ectopically expresing BPE123 but also in *B. abortus*-infected THP-1 macrophages. These results suggests that interaction between BPE123 and ENO1 induces structural and/or functional changes accounting for the activation of host cell alpha-enolase during the infection process. Further experiments are underway to study the changes of the kinetic parameters of ENO1 in the presence of BPE123.

Keywords: Brucella abortus; Type IV secretion; intracellular replication; alpha-enolase; BPE123

(1283) **CR(VI) AND LINDANE REMOVAL BY *Streptomyces sp.*M7 IS IMPROVED BY MAIZE ROOT EXUDATE**

María Zoleica Simón Solá (1), Daiana Emilce Perez Visñuk (2), José Sebastián Dávila Costa (1), Marta Alejandra Polti (1), Analía Álvarez (1)

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Environmental mixed pollution by both organic and inorganic compounds are detected worldwide. Phytoremediation techniques have been proposed as ecofriendly methods for cleaning up polluted sites. Several studies have demonstrated enhanced dissipation of contaminants at the root-soil interface through an increase in microbial activity caused by the release of plant root exudates (REs). The aim of this study was to evaluate the effectiveness for Cr(VI) and lindane removal by *Streptomyces* M7 cultured in a co-contaminated system in presence of maize REs. In order to evaluate the performance of *Streptomyces* M7 on lindane and chromium removal, flasks with minimal medium (MM) with 1 g L^{-1} glucose were artificially contaminated with 2 mg L^{-1} lindane and/or 25 mg L^{-1} of Cr(VI), and inoculated with *Streptomyces* M7. Then, in order to evaluate the effect of maize REs on lindane and chromium removal by *Streptomyces* M7, flasks with MM (without glucose) were supplemented with maize REs (0.4 gC L^{-1}). Then, MM was contaminated with 2 mg L^{-1} lindane and/or 25 mg L^{-1} of Cr(VI) and inoculated with *Streptomyces* M7 .Flasks were incubated at 30 ºC, 150 rpm, five days. Microbial growth and contaminants concentrations were determined. Our results showed when REs were added to the contaminated MM as the only carbon source, microbial removal of Cr(VI) and lindane increased significantly in comparison to contaminant removal obtained in MM with glucose 1 g L^{-1}. The maximum removal of 91% of lindane and 49% of Cr(VI) were obtained in the co-contaminated system. *Streptomyces* M7 showed plant growth promoting traits which could improve plant performance in contaminated soils. The results presented in this study provide evidence that maize REs improved growth of *Streptomyces* M7 when REs were used as a carbon source in comparison to glucose. Lindane and Cr(VI) removal was considerably enhanced making evident the phytoremediation potential of the actinobacteria-plant partnership.

Keywords: *Streptomyces*, Root exudates, Bio/phytoremediation, Co-contamination

(1681) **SEQUENCE ANALYSIS OF FLAVONOL SYNTHASE, KEY IN THE POLYPHENOL METABOLISM OF *LIGARIA CUNEIFOLIA***

Maria Valeria Ricco (1), Melina Laguía Becher (1), Martín León Bari (1,2), Rafael Alejandro Ricco (3), Marcelo Luis Wagner (3), María Alejandra Alvarez (1)

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Ligaria cuneifolia (R. et P.) Tiegh (Santalales, Loranthaceae) is an hemiparasitic plant with several pharmacological activities (antioxidant, antiproliferative, antitumor, hypolipidemic and antimicrobial) attributed to its flavonoids. However, there is no information about the sequences of the enzymes involved in the synthesis of these metabolites in *L. cuneifolia*. Hence, our goal is to elucidate the sequence of the Flavonol synthase protein (FLS), a key enzyme for the production of flavonols.

For this purpose, we have made an exhaustive search for the FLS sequences of the Div. Magnoliophyta in the databases. We have selected a total of 15 sequences from orders close to Santalales (according to phylogenetic tree APG3) as there is not a sequence from Santalales in the databases. Then, degenerate primers were designed using the CODEHOP software (COnsensus-DEgenerate Hybrid Oligonucleotide Primer). Those primers come from conserved regions from a multiple alignment of proteins that will be amplified by PCR in order to identify homologous genes. Once the primers were designed, total RNA was extracted from foliar tissue and used as a template to synthesize the first strand of copy DNA (cDNA) using the Superscript II retrotranscriptase. Different combinations of the degenerate primers were used to amplify the cDNA by PCR. The PCR product (338 bp) was cloned into the pGEM-T vector and sequenced. With the obtained fragment a search was made in the database Nucleotide collection (nr / nt) of GenBank using the program Blastn. Only FLS alignments of vascular plants were obtained. In following experiments, the RACE technique will be used to obtain the complete enzyme sequence. The knowledge generated in this work would be of relevance for future applications in metabolic engineering of *L. cuneifolia* flavonoids.

Key words: *Ligaria cuneifolia*, flavonol synthase, flavonoid, CODEHOP.

(1738) **BIO-INFORMATIC ANALYSIS OF BACTERIOPHAGES ACTIVE ON *Staphylococcus aureus* ISOLATED FROM HUMAN NOSTRILS.**

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Lab. Microbiol. Molecular. Fac. Cs. Médicas UNR

The rise of Multi-Drug resistant bacteria has triggered worldwide concern. Novel antibiotic molecules are urgently needed to fight those patogens. An alternative strategy lays in the utilization of bacteriophages which are natural bacterial predators, this strategy was put forward but left aside due to the availability of natural and synthetic antibiotics.

Staphylococcus aureus causes several mild to life threatening pathologies in humans and animals; circulating in health centers as well as in the community. Our group has studied *S. aureus* nasal carriage by health staff at a major public hospital; as part of that project we screened by nasal swabs for bacteriophages active against this pathogen. During this process we isolated 23 temperate bacteriophages whose description in terms of genomic sequence, bioinformatic analysis and host range is reported.

The genomes annotation, function prediction and domain search was carried out using BLASTP, pfam and Interproscan. Our results yielded a bacteriophage (named Mat_T), displaying a broad host range comparable to that of the most active lytic bacteriophage reported, bacteriophage K (87% and 85% of activity against 43 *S.aureus* local isolates respectivelly). In spite of a detailed analysis of integrase and anti-repressor genes encoded in the isolated bacteriophages, we were not able to find an explanation for the high killing activity of bacteriophage Mat_T.

Keywords: *Staphylococcus aureus*; temperate bacteriophages; bacteriophage integrases and excissionases.

(1887) **CHARACTERIZATION OF THE INTERACTION OF KELCH DOMAIN FORM KEAP-1 WITH PEPTIDES DERIVED FROM NRF2 TRANSCRIPTION FACTOR.**

Federico Issoglio (1), Nadine Alaimo (2), Mariana Gallo (3), Daniel Cicero (2), Dario Estrin (1)

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