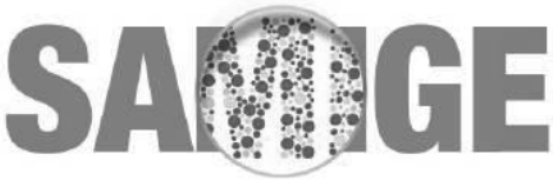
LVI SAIB Meeting



XV SAMIGE Meeting

SAIB-SAMIGE Joint Meeting 2020 *on line*

MI-C30-197
PROTEOMIC AND PHYSIOLOGICAL CHARACTERIZATION OF COPPER EFFECT ON QUORUM SENSING REGULATION IN *PSEUDOMONAS CAPEFERRUM*
Leguina AC, Lacosegliaz M, Fernández PM, Castellanos de Figueroa LI, Nieto Peñalver CG.

16:30-18:30 CELL BIOLOGY III

Chairpersons: Graciela Boccacio – Javier Valdez Taubas

16:30-16:43
CB-C016-084
GUANINE QUADRUPLEXES AS POTENTIAL REGULATORY ELEMENTS OF THE SARS-COV-2 VIRUS
Bezzi G, Piga E, Armas P

16:45-16:58
CB-C017-086
EFFECTS OF GENETIC POLYMORPHISMS ON RNA GUANINE QUADRUPLEX AFFECTING THE TRANSLATION HUMAN ONCOGENS
Bezzi G, Piga E, Armas P
Instituto de Biología Molecular y Celular de Rosario (IBR) – CONICET-UNR.

17:00-17:13
CB-C018-185
INFLUENCE OF CIRCULAR TARGET RNA TOPOLOGY ON miRNA STABILITY AND FUNCTION
Fuchs Wightman F, Lukin J, Giusti S, Refojo D, De la Mata M

17:15-17:28
CB-C019-255
MOLECULAR AND PHENOTYPIC ANALYSES OF SULFITE TOLERANT *S. CEREVISIAE* STRAINS CARRYING WILD TYPE OR ABERRANT PROMOTERS OF THE *SSU1* GENE
Raymond Eder ML, Bragato M, Rosa AL

17:30-17:43
CB-C020-284
AUGMENTED FERREDOXIN LEVELS IN TRANSPLASTOMIC TOBACCO PLANTS COUPLE ALTERNATIVE ELECTRON FLOW WITH ENDOGENOUS PHOTOPROTECTIVE MECHANISMS
Lobais C, Bilger W, Blanco NE

17:45-17:58
CB-C021-018
KNOCKDOWN OF THE CYTOCHROME P450 CYP4PR1 IN PYRETHROID-RESISTANT TRIATOMA INFESTANS INCREASES SUSCEPTIBILITY TO DELTAMETHRIN.
Dulbecco AB, Moriconi DE, Pedrini N.

18:00-18:13
NS-C02-096
DIFFERENTIAL GENE EXPRESSION TRIGGERED BY NEUROTOXIC INTOXICATION IN *TRIATOMA INFESTANS*, VECTOR OF CHAGAS DISEASE
Traverso L, Latorre-Estivalis J, Fronza G, Lobbia P, Mougabure-Cueto G, Ons S

microorganisms are an important source of proteolytic enzymes. They could act on soybean proteins and release biofunctional peptides that may possess antioxidant properties. Therefore, the aim of this work was the study of the antioxidant activity of the biopeptides released from soybean protein isolate (SPI, which contains only glycinin and β-conglycinin) by three lactic acid bacteria (*Enterococcus italicus* LET 302, *E. faecium* LET 303 and *Lactobacillus brevis* LET 216) previously isolated from soybean flour. To this end, each strain was incubated for 16 h in broth with SPI as the sole protein source. Then, the supernatants were recovered by centrifugation and sterilized by filtration with 0.22 µm pore membranes. In order to obtain different peptidic fractions, the supernatants were centrifuged with 10 kDa filters, and the filtrates were centrifuged again with 3 kDa filters. This way, three fractions were obtained for each strain: M1 (peptides > 10 kDa), M2 (3 kDa < peptides < 10 kDa), and M3 (peptides < 3 kDa). Protein concentration was assessed by Bradford, and the amount of protein on each fraction was adjusted to 0.3 µg before the antioxidant activity was determined by DPPH assay. Antioxidant activity was observed on the three fractions from all strains, and M3 presented the highest activity in all cases. Comparing the respective fractions from different strains, higher antioxidant activity was always showed by *E. faecium* LET 303, followed by *E. italicus* LET 302 and *L. brevis* LET 216. In conclusion, the proteolytic enzymes expressed by the strains of lactic acid bacteria studied could act on soybean proteins, releasing peptides with antioxidant activity. The hydrolysis of these proteins, in a treatment before their consumption by poultry or *in situ* by these bacteria administered as feed additive, could improve their digestion as well as collaborate with the oxidative metabolism of cells in the digestive system.

MI-C30-197

PROTEOMIC AND PHYSIOLOGICAL CHARACTERIZATION OF COPPER EFFECT ON QUORUM SENSING REGULATION IN *PSEUDOMONAS CAPEFERRUM*

Leguina AC[1], Lacosegliaz M[1], Fernández PM[12], Castellanos de Figueroa LI[13], Nieto Peñalver CG[13].
[1]PROIMI-CONICET (Tucumán), [2]Fac. de Ciencias Exactas y Naturales (UNCA), [3]Fac. de Bioquímica, Química y Farmacia (UNT).
E-mail: carolinaleguina12@gmail.com

Copper has largely been used for the control of phytopathogen fungi in agriculture, even though to its non-degradability, it tends to accumulate in soils reaching prejudicial levels for soil microorganisms, including rhizomicroorganisms. The rhizosphere is characterized by intense and complex interactions that take place in it. Many of these intra- and interspecies interactions occur through quorum sensing (QS) systems. QS is a cell-to-cell signaling mechanism that control the microbial physiology in a population density manner. Several soil bacteria use QS circuits to regulate important phenotypes. In this work we studied the influence of copper on QS regulation in the plant growth-promoting rhizobacterium (PGPR) *Pseudomonas capeferrum* WCS358. Firstly, the QS system of the bacterium was inactivated using a quorum quenching strategy. Secondly, intracellular proteins of *Ps. capeferrum* WCS358 QS^+ and QS^-, cultured in the presence or absence of copper, were analyzed using liquid chromatography coupled to mass spectrometry. Furthermore, the effects of copper and QS on other activities such us motility, biofilm production and oxidative stress response were also evaluated in *Ps. capeferrum* WCS358. The QS activity and the presence of metal modified the relative abundance of proteins involved in amino acid and carbohydrate metabolism, oxidative stress defense and nutrient absorption. Besides, results indicated that QS system is implicated in the regulation of motility, biofilm production and oxidative stress response in *Ps. capeferrum* WCS358 and that copper had a negative effect on these activities. The results presented in this work indicate that QS regulates important traits in *Ps. capeferrum* WCS358 and that contamination with copper could be detrimental for the QS-dependent phenotypes in this rhizobacterium. Since the modifications observed are related to activities that are significant for the survival and fitness of bacteria, they suggest that QS may confer a competitive advantage to *Ps. capeferrum* WCS358 and that copper could alter the competence of this PGPR in its natural niche.

MI-C31-204

MECHANISMS ASSOCIATED WITH PROLINE METABOLISM AND REDOX BALANCE IN PEANUT MICROSYMBIONTS EXPOSED TO WATER STRESS

Villa JF[1], Castro SM[1], Bianucci EC[1], Becker D[2], Furlan A[1,2]
[1] Instituto de Investigaciones Agrobiotecnológicas (INIAB-CONICET), FCE,F-QyN, UNRC. Río Cuarto, Córdoba, Argentina. [2] Dep. Biochemistry, Redox Biology Center, University of Nebraska-Lincoln, Lincoln, NE 68588, USA.
E-mail: afurlan@exa.unrc.edu.ar

The exposure of microorganisms to adverse environmental conditions can affect the possibility of establishing interaction with plants. Proline, an osmoprotective amino acid and determinant of cellular redox balance, could increase tolerance to drought stress. Thus, proline addition to peanut inoculants would mitigate drought stress in crops. The objective was to elucidate the fundamental mechanisms of protection against water stress mediated by proline in peanut microsymbionts, exploring the participation of its metabolism in the cellular redox balance. To evaluate whether the addition of proline activates the catabolism of the enzyme and the antioxidant system, we used the microsymbionts recommended as peanut inoculants, *Bradyrhizobium* sp. SEMIA6144 and *Bradyrhizobium* sp. C-145. Cultures in exponential phase were treated with different proline doses (0 - 50 mM) for 0 - 60 min to determine viability (CFU ml^{-1}), the transcription of genes from proline catabolism (*putA*) and antioxidants, catalase (*cat*) and thioredoxins (*trx*). Next, we analyzed the effect of proline on growth and redox metabolism of microsymbionts exposed to water stress. Proline concentration was selected by studying microorganisms' viability and priming effect on peanut seeds. The drought stress condition was imposed by Polyethylene glycol (PEG) addition,