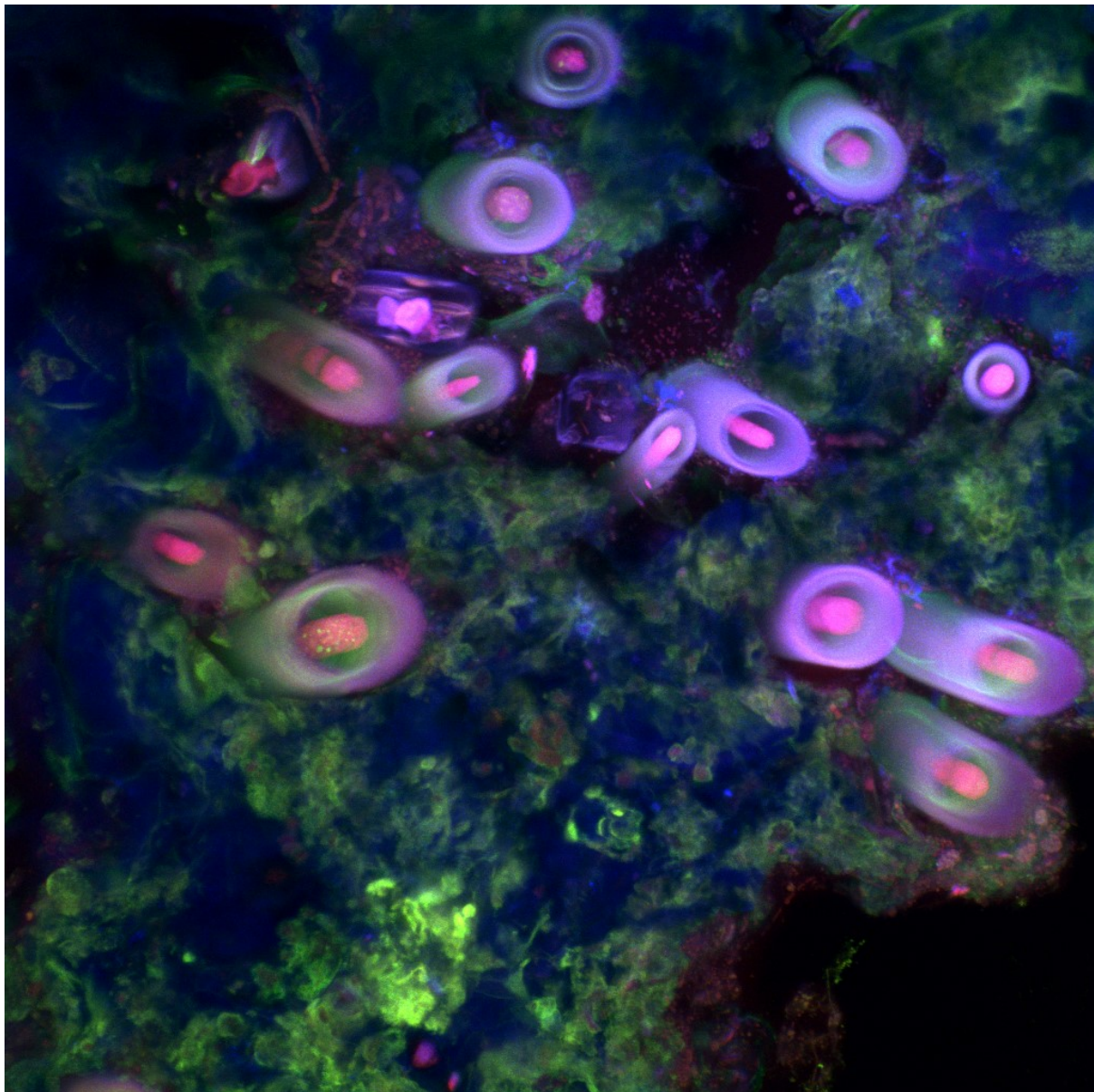




LVI SAIB Meeting - XV SAMIGE Meeting



SAIB-SAMIGE Joint Meeting 2020 – *Online*

Cover image:

Mineral–microorganisms interactions

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A Confocal Laser Scanning Microscopy image of a resin-embedded microbialite from Laguna Negra (Puna-Catamarca), stained with calcein (a fluorescent dye that produces a stable complex in the presence of calcium and fluoresces in the green region of visible light). Mineral aggregates are observed in blue. Their surfaces are partially stained with calcein, indicate the presence of free Ca²⁺ ions. Diatoms and *Rivularia halophila* filaments are visible in red thanks to their photosynthetic pigments.

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Argentine Society for Biochemistry and
Molecular Biology
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MI-C29-186

ANTIOXIDANT PEPTIDES RELEASED FROM SOYBEAN BY LACTIC ACID BACTERIA WITH PROTEOLYTIC ACTIVITY

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Biopeptides are fragments encrypted in a precursor protein. They possess a particular amino acid sequence and specific biofunctional attributes that can influence the main systems of an organism when released by proteolysis. Glycinin and β -conglycinin are the main proteins in soybean (which in turn is the main protein source in poultry feeds), and many amino acid sequences with different features, such as antioxidant properties, are included in them. On the other hand, 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 μ m 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 < 10kDa), and M3 (peptides < 3 kDa). Protein concentration was assessed by Bradford, and the amount of protein on each fraction was adjusted to 0.3 μ g 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*

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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 controls 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 *P. 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 as motility, biofilm production, and oxidative stress response were also evaluated in *P. 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 the QS system is implicated in the regulation of motility, biofilm production and oxidative stress response in *P. 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 *P. 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 *P. capeferrum* WCS358 and that copper could alter the competence of this PGPR in its natural niche.