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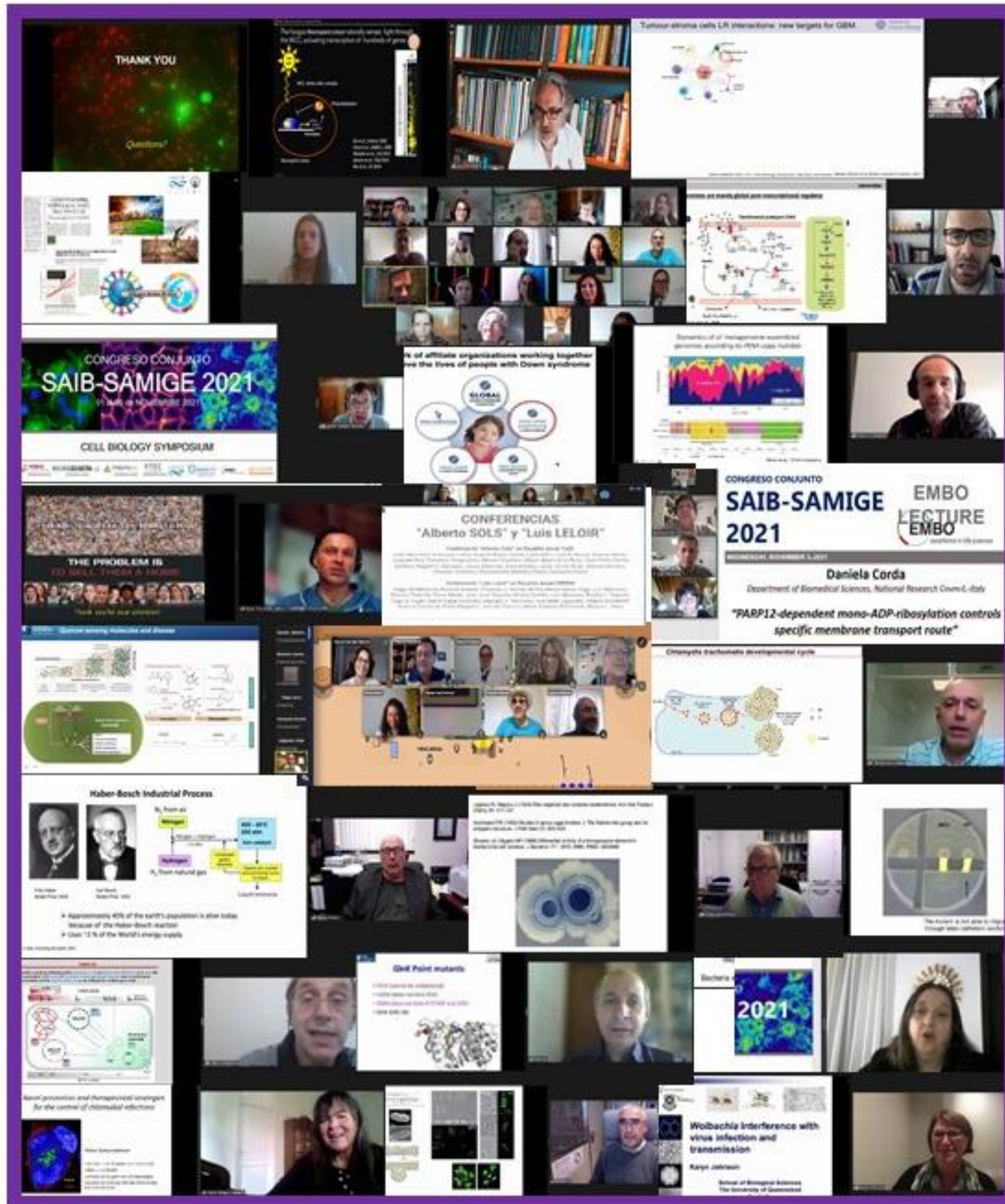
SAIB - SAMIGE Joint meeting
2021 *on line*



November 1-5, 2021

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LVII Annual Meeting of the Argentine Society for Biochemistry and Molecular Biology Research (SAIB)

XVI Annual Meeting of the Argentinean Society for General Microbiology (SAMIGE)

SAIB - SAMIGE Joint meeting 2021 *on line*

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SAIB-SAMIGE Joint meeting 2021 - Program at a glance

	Monday, Nov 1st	Tuesday, Nov 2nd	Wednesday. Nov 3rd	Thursday, Nov 4th	Friday, Nov 5th
9:00-9:15	**Opening ceremony**				
9:15-11:15	**PARALLEL SYMPOSIA** *Cell Biology* *Microbiology I: Host-pathogen Interactions*	**PARALLEL SYMPOSIA** *Plants* *Microbiology II: Biotechnology & Environmental Microbiology*	**PARALLEL SYMPOSIA** *Lipids* *Microbiology III: Molecular Microbiology* *Signal transduction*	**PARALLEL SYMPOSIA** *Glycobiology* (*Tribute to Dr. J.L. Daniotti*) *Microbiology IV: Microbial Ecology & Physiology*	**SYMPOSIUM** *Young investigators*
11:15	**Break**	**Break**	**Break**	**Break**	**Break**
11:30-12:30	**SAIB Plenary lecture "A. Sols"** *Consuelo Guerri*	**SAMIGE Plenary lecture** *Francisco García del Portillo*	**SAIB Plenary lecture EMBO** *Daniela Corda*	**SAMIGE Plenary lecture** *Dennis Dean*	**Closing ceremony**
12:30	**Break**	**Break**	**Break**	**Break**	
13:30-13:50		*Tribute to Dr. Israel Algranati*		*Tribute to Dr. Juan Dellacha*	
14:00-15:00	**SAMIGE Plenary lecture** *Luis Larrondo*	***SAIB*** **Plenary lecture "Héctor Torres"** *Joaquín Espinosa*	**SAMIGE Plenary lecture** *Josep Casadesus*	***SAIB*** **Plenary lecture "Ranwel Caputto"** *Beatriz Caputto*	
15:00-15:15	**Break**	**Break**	**Break**	**Break**	
15:15-17:15	**Poster session**	**Poster session**	**Poster session**	**Oral communications**	
17:15-17:30	**Break**	**Break**	**Break**	**Break**	
17:30-19:30	**Oral communications**	**Oral communications**	**Break** **19:00 SAIB Assembly**	**Break** **19:00 SAMIGE Assembly**	

safe release into the environment. All the strains analyzed reverted into faster growing and non-NH_4^--excreting clones in 16-20 bacterial cell generations under regular conditions for *A. vinelandii* culture under laboratory conditions. However, preliminary experiments in which the mutant strains with the inducible allele of *glnA* were inoculated into sterile soil increased the NH_4^+ content of the soil and allowed the isolation at a high frequency of clonal strains conserving the characteristic mutant phenotype after two months of inoculation, suggesting a greater genetic stability under these conditions. These results encourage further research of the genetic engineering strategy used in this study to improve *A. vinelandii* and/or any other robust plant growth-promoting bacteria to align fertilization efficiency and environmentally safe use.

MI-P038-294

EVALUATION OF PROBIOTIC PROPERTIES ASSOCIATED WITH THE CELL SURFACE IN *Bifidobacterium* FOR APPLICATION IN POULTRY

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Currently, consumers seek to include in their diet minimally processed products that are organic in origin. In this context, the poultry industry has reviewed its production practices and focused on the use of strategies, such as the introduction of probiotic microorganisms, to promote animal health and welfare. Probiotics are able to competitively exclude pathogens that cause food transmitted diseases and eliminate antinutritional factors present in feed, such as lectins, but these properties are strain dependent and should be thoroughly studied to select effective probiotics. The objective of this work was to analyse the ability of 15 *Bifidobacterium* strains isolated from poultry to self-aggregate, co-aggregate with pathogens, and capture lectins on their surface. Most of the bifidobacteria presented autoaggregation percentages between 9.4 and 25%, and co-aggregated with 3 different serotypes of *Salmonella* and *Escherichia coli.* Some bifidobacteria co-aggregated with one or more pathogenic strains, standing out *B. boum* LET 413 that co-aggregated with all the pathogens evaluated, followed by *B. boum* LET 414 that only failed to co-aggregate with *Salmonella enteritidis*, and *B. pseudolongum* subsp. *pseudolongum* LET 404, which did not co-aggregate with *E. coli*. The rest of the strains interacted with at least one pathogen. In addition, the capture of different FITC-labelled dietary lectins was studied. All the strains captured wheat lectin (WGA) on their entire surface, but showed varied binding to the lectins PNA (peanut lectin) and PHA–P (bean lectin) in specific regions of their surface. *B. thermacidophilum* LET 406, *B. boum* LET 413, *B. pseudolongum* subsp. *globosum* LET 403, and *B. pseudolongum* subsp. *pseudolongum* LET 405 and LET 412, bound PNA only in specific regions. *B. boum* LET 414 was the only strain that could capture PNA in its entire surface. Because capsular polysaccharides were not detected for these strains, their affinity to certain lectins was directly linked to glycoproteins or glycolipids bound to the cell wall. Based on the results, we can conclude that the studied strains showed good aggregation and interaction with *Salmonella* and *E. coli*, which could contribute to the elimination of pathogenic bacteria during digestion. The study of capture of antinutritional factors such as lectins, on the bacterial surface, makes it possible to estimate the ability to capture soy lectin (SBA), this cytotoxic phytoagglutinin, present in poultry feed, through binding to lectins of similar affinity, such as PNA and PHA-P.

MI-P039-295

BIOETHANOL PRODUCTION: OPTIMIZATION OF REGIONAL CIDER WASTE PRE-TREATMENT AND SELECTION OF NATIVE *Saccharomyces cerevisiae* STRAINS

Fontanini JM [1], Origone AC [2], GorordoMF[1], Lopes CA [1,2], Sangorrín MP [1], Rodríguez ME[1].
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The use of lignocellulosic biomass (LB), in addition to the potential of yeasts to ferment reducing sugars, has proved to be a robust feature for bioethanol production that could replace the use of limited, environmentally damaging petroleum-derived resources. However, it is necessary to apply suitable pre-treatments of the LB in order to ensure both availability of fermentable sugars and the absence of compounds that can inhibit fermentation. The aim of the present work was to study the behaviour of a pool of *Saccharomyces cerevisiae* yeast strains from different origins (including wine, apple chicha and Toddy beverages) under stress conditions encountered during the bioethanol production. Furthermore, the optimization of apple bagasse (AB) pre-treatment was evaluated for its possible application in the production of bioethanol as well as to reduce its availability as a waste from the cider industry. A total of 60 *S. cerevisiae* stains were assayed in microplates containing 0-15% (v/v) ethanol. OD growth data were fitted to Gompertz function and kinetic parameters (μ_{max} and λ) were obtained. Twelve yeast strains were selected for their ethanol tolerance (higher than 12% v/v ethanol). The selected strains showed the shortest λ (media of 11.83±0.89 h) and the highest μ_{max} (media of 0.15±0.01 h^{-1}). Later analysis for their tolerance to temperature (25-45°C), pH (2-5), glucose (2-300 g/L), Na_2SO_4 (0-50 g/L) and acetic acid (0-8 g/L) concentrations evidenced that glucose and Na_2SO_4 did not affect the growth. However, all the strains were able to grow at temperatures below 40°C and at pH 3, 4 and 5, as well as at 3g/L of acetic acid. The AB pre-treatment involved an initial screening, using a fractional factorial design, to establish the significant variables for optimization. For the phosphoric acid (PA) pre-treatment, a Central Compound Design (CCD) was assayed with 16 runs and 3 factors: solid:liquid ratio (1:5-1:7), temperature (121-131°C) and PA concentration (0.2-1% w/v).