LVII SAIB Meeting - XVI SAMIGE Meeting

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**	

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

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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). Experiments were carried out in 100 mL Erlenmeyers, incubated during 40 min, and both total reducing sugars and glucose concentrations (g/100 g dry weight) were determined. The optimization conditions suggested by the model were: 1:5 of S:L, 121°C, PA 0.2% w/v. On the other hand, the alkali pre-treatment showed optimal conditions of NH_4OH 6%, at room temperature for 24 h. The subsequent hydrolysis of the pre-treated AB was optimized using a cocktail of enzymes (endo-β-glucanase, pectinase and cellulose) at equal concentrations, with 10 runs and 2 factors: cocktail concentration (1.88-6.12%) and time (190-530 min). The optimal conditions obtained were 6.12% cocktail for 360 min. The pre-treated and hydrolyzed AB evidenced an increase of 20 and 22% of glucose and reducing sugar content. In addition, the calculation of bias and precision factors close to 1 indicated a good fit of the models. This results and the tolerance to stress factors of selected strains suggest the possibility of producing bioethanol using regional industry wastes.

MI-P040-307

IMPROVEMENT OF NUTRIFUNCTIONAL PROPERTIES OF CHICKPEA (*Cicer arietinum L.*) FLOUR BY FERMENTATION WITH SELECTED LACTIC ACID BACTERIA

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Chickpea (*Cicer arietinum L.*) is an important pulse crop used in human nutrition with potential application to the development of novel functional and gluten-free foods. Like other legumes, it is a good source of high-quality proteins, dietary fiber, low glycemic index carbohydrates, unsaturated fatty acids, vitamins and minerals and many bioactive phytochemicals associated with positive effects on human health such as a decreased risk of cardiovascular disease, diabetes and metabolic syndrome, among others. Therefore, research on novel applications and development of legumes derived products has raised significantly. However, beside their benefits, legume plants synthesize antinutritional factors (ANF) as defense against predators that cause adverse physiological effects to humans and animals. These substances include enzyme inhibitors, phytic acid, tannins, lectins and α-galactosides which affect the digestibility and bioavailability of nutrients and cause gastrointestinal discomfort. Fermentation has been proposed as an effective technological strategy for improving nutritional and nutraceutical properties of legumes as it has proven to remove ANF with the simultaneous release of bioactive compounds. Since fermentation performed with an autochthonous starter culture would be better than a spontaneous uncontrolled one, the aim of this work was to improve the technofunctional quality of chickpea flour by fermentation with selected LAB isolated from legumes cultivated and consumed in northwestern Argentina. For this purpose, a Randomized Complete Block Design was carried out to assess the influence of some fermentation variables such as the addition of *Lactiplantibacillus plantarum* CRL 2211 and/or

Weissella paramesenteroides CRL 2182 (0-7 Log CFU/g), temperature (30-37 ºC), time (8-24 h) and dough yield (160-200) on LAB population, acidification, ANF and total phenolic contents (TPC). To explain LAB enzymes behaviour during fermentation, a modelling approach including molecular docking and dynamics simulations of tannase-phenols (gallocatechin) and protease-inhibitor (Bowman-Birk and Kunitz type) complexes were performed. Fermentation of chickpea flour with both strains for 24 h at 37ºC led to an increase in LAB, acidity, TPC and contributed to tannins and trypsin inhibitors removal. Tannases from LAB present in chickpea showed a relevant affinity for gallocatechin (-5.4 to -8.9 Kcal/mol) and their interaction mechanism involves polar contacts between catalytic residues GLU, ASP, HIS, and LYS from the active sites with oxygen atoms from hydroxyl groups of catechin, epicatechin and procyanidins. Regarding interactions between LAB proteases and trypsin inhibitors higher relative affinity and binding energy values (-40.4 kcal/mol) were observed for *L. plantarum* endopeptidases. The results suggest that the combination of experimental and simulation data may lead to a better understanding of food fermentation to enhance nutrifunctional properties.

MICROBIOLOGY – EDUCATION in MICROBIOLOGY

MI-P041-287

MICROBIOLOGY LABORATORY CLASSES DURING THE PANDEMIC CONTEXT

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Most of the subjects of the Microbiology Career have a large hourly load of laboratory classes. In the context of pandemic, practical classes were redefined. Although laboratory classes provide undergraduate students with hand experience and with the opportunity to explore methods, during the present period the students had little contact with the laboratory classes. Therefore, based on the preventive and mandatory social restrictions of the year 2020, we revised the subject to a virtual format and adapted its content to the ongoing COVID-19 pandemic. The activities in the laboratory were reformulated including the technologies from the point of view of critical pedagogy. Classes were carried out by videoconference platforms contemplating the inclusion of all students. The virtual classroom is a tool that offers the possibilities of teaching online, but it is more than a virtual environment, since it is made up of 6 elements: the teacher, the student, the context, the time, the contents, and the didactic proposal. To promote the development of learning activities in this period, work was done in the virtual classroom, innovating with different digital resources. These resources had rarely been used in-person classes, although we consider that in the present context, they contributed to improving the pedagogical option, since they were used to support the construction of knowledge in the undergraduate students. We worked with diagrams, photos, and videos to visualize what the work to be carried out in the laboratory would be like. Discussion of the possible results to be obtained and how they could be solved in the laboratory was encouraged. As professors we understood that mediation of educational proposals with digital technologies must be accompanied by new ways of planning, interpreting, and understanding the teaching role and the class itself. Technologies only allow a pedagogical transformation if we think them as attractive, challenging, and critical projects.

MICROBIOLOGY – MICROBIAL PHYSIOLOGY

MI-P042-13

HOMEOPHASIC ADAPTATION IN RESPONSE TO UVA RADIATION IN *Pseudomonas aeruginosa*: CHANGES OF MEMBRANE FATTY ACIDS COMPOSITION AND INDUCTION OF *desA* AND *desB* EXPRESSION

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In bacteria, exposure to changes in environmental conditions can alter the membrane fluidity, affecting the essential functions of this structure in the cell physiology. To adapt to these changes, bacteria keep the correct fluidity by varying the length, the saturation degree, the *cis/trans* monounsaturated ratio, and the branching of phospholipids acyl chains, as well as the proportion of cyclopropane fatty acids. This phenomenon, known as homeoviscous or homeophasic adaptation, involves activation of gene expression and/or protein activity in order to maintain an optimal cell viability. In *Pseudomonas aeruginosa*, this response is realized mainly by two mechanisms of fatty acids desaturation, the FabA-FabB and DesA-DesB systems. The main synthesis pathway of unsaturated fatty acid is through FabA and FabB enzymes, which introduce double bonds in nascent acyl chains. On the other hand, the two oxygen-dependent Δ9 desaturases, DesA and DesB, collaborate in the unsaturated fatty acid synthesis with the Fab system. DesB was also involved in adaptation to osmotic stress and in pathogenic processes. In the present work, we studied the effect of ultraviolet-A (UVA) radiation on the homeophasic process in *P. aeruginosa*, by analyzing the changes produced on the fatty acid composition of the cell membrane and the associated genetic response. UVA is the major fraction of solar ultraviolet radiation reaching the Earth´s surface and exerts its lethal effects mainly due to oxidative damage of the bacterial membrane. The prototypical strain PAO1 was grown under sublethal UVA doses or in the