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SAIB - SAMIGE Joint meeting
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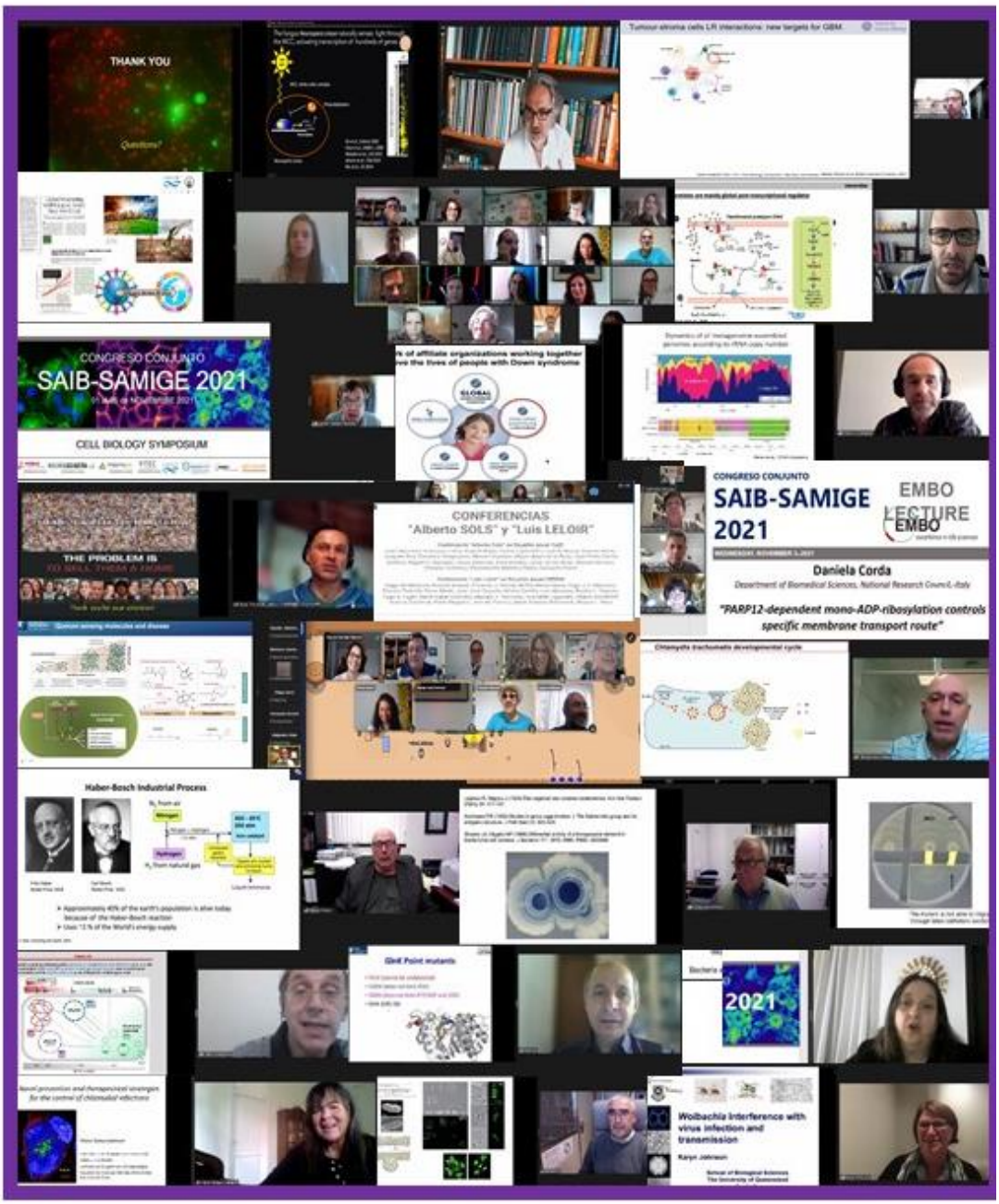

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MI-P024-68
INFLUENCE OF THE PROCESSING METHOD ON THE ANTINUTRITIONAL CONTENT AND FUNCTIONAL PROPERTIES OF CHICKPEA (*Cicer arietinum*) FLOUR

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The development of novel functional foods is a major challenge for the food industry due to growing consumer's demand of healthy products. Legumes, such as chickpea, represent an attractive alternative for these food formulations due to their nutritional value and gluten free nature. However, legumes derived flours require complementary processing for reducing their antinutritional content (ANF) and the increasing of bioactive compounds and technological quality. The aim of this work was to assess the effect of different processing methods on the concentration of ANF, bioactive compounds and technological properties of chickpea flour. For this purpose, kabuli chickpeas produced in the Northwestern region of Argentina were subjected to soaking, cooking, microwaving, germination or a controlled fermentation with a co-culture of selected lactic acid bacteria (LAB): *Lactiplantibacillus plantarum* CRL 2211 and *Weissella paramesenteroides* CRL 2182. After processing, the grains were milled to obtain flours and their ANF concentrations: trypsin and α-chymotrypsin inhibitors, α-amylase inhibitors and tannins were determined by spectrophotometric methods. Bioactive compounds like total polyphenols and their antioxidant activity were assessed by Folin-Ciocalteu reagent and DPPH radical scavenging activity, respectively, whereas the amino acid profile was determined by HPLC. As technological parameters, the water and oil retention capacity, gelation and emulsification of each flour were evaluated. Regarding the removal of ANF, traditional cooking was the most efficient treatment for the elimination of protease and α-amylases inhibitors leading to minimal concentrations, whereas biological methods such as fermentation and germination removed 65% and 50%, respectively. However, fermentation produced a decrease of tannins content greater than 80% (4.29±0.0 to 0.85±0.3 mg EAG/100g) whereas the other treatments did not produce significant changes. Regarding the incidence of treatments on bioactive compounds, fermentation and germination increased the concentration of phenolic compounds from 647±26 to 1017±50 and 929±53 mg EAG/100g respectively, and enhanced the antioxidant activity from 50% in untreated flours to 82% in fermented flours and 72% in germinated flours. Free amino acid contents were also increased after fermentation, being Glu, Arg, Tyr and Lys the predominant. Finally, traditional cooking and microwave treatments decreased the water and oil retention capacity of flours, whereas soaking and biological treatments increase the oil retention capacity. Fermentation was also better than the other treatments for improving gels and emulsions formation. Our research demonstrates that fermentation of chickpea flours with selected LAB is an efficient strategy for the removal of ANF, the increase of bioactive compounds and the improvement of technological properties relevant for the formulation of functional foods.

MI-P025-79
EFFECT OF ORAL ADMINISTRATION OF *Lactobacillus johnsonii* CRL1231 ON ADIPOSITY AND INFLAMMATORY STATUS OF MICE WITH METABOLIC SYNDROME

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Metabolic syndrome (MS) is one of the most relevant health problems in the world due to increased consumption of high-fat diets and the consequent obesity. MS is a cluster of cardio-metabolic risk factors and comorbidities conveying high risk of both cardiovascular disease and type 2 diabetes. Comorbidities associated with MS include proinflammatory state, prothrombotic state, non-alcoholic fatty liver disease. *Lactobacillus johnsonii* CRL1231 (Lj) is a strain with feruloyl esterase activity which increases the release of ferulic acid (FA) in the intestine and improves the biomarkers of MS. When the AF esterified in bran fibers is released, it can exert its lipid-lowering effect. The objective of this work was to evaluate the effect of oral administration of Lj on accumulation of abdominal and hepatic fat, and inflammatory state of mice with MS induced by a high-fat diet supplemented with wheat bran (HFD+WB). Male six-week-old Swiss albino mice (n = 24) were fed for 14 weeks; they were divided into 3 groups: Control group: mice received water and normal diet; MS group: mice received water and HFD+WB; MS+Lj group: mice received suspension of Lj (dose: 10^8 CFU / day / mouse) and HFD+WB. The adiposity index (AI) was calculated: AI = [Fat weight / Body weight] x 100. Histopathological analysis of liver and epididymal adipose tissue (evaluation of adipocyte area) was performed. Plasma levels of AST and ALT transaminases were measured by enzymatic methods and leptin levels by immunoassay. Cytokine levels (TNF-α, IFN-γ, IL-6 and IL-10) were determined by flow cytometry. The AI was 2 times higher in MS group compared to Control group, and decreased 30% in MS+Lj group compared to MS group. Abundance of large adipocytes (4000-8000 μm^2) was 9% in Control group, 57% in MS group, and it was reduced to 20% in MS+Lj group. Plasma leptin levels were 7 times higher in MS group than in Control group, and 2 times lower in MS+Lj group with respect to MS group. The levels of pro-inflammatory cytokines (TNF-α, IFN-γ, IL-6) increased in MS group compared to Control group, and decreased in MS+Lj group. The levels of anti-inflammatory IL-10 were reduced 3 times in MS group compared to Control group, but an increase of 2 times was evidenced in the MS+Lj group. Liver histology revealed steatosis in the MS group and showed a reduction in fatty infiltration in hepatocytes of the MS+Lj group. Increased levels of ALT and AST are often associated with liver damage resulting from unhealthy habits, such as a high-fat diet. Results showed that ALT and AST levels increased 2 times in MS group with respect to Control group, while MS+Lj group did not

show significant differences with the Control group. According to the results obtained in this work, oral administration of Lj reduces AI, prevents hypertrophy of adipose tissue, decreases hyperleptinemia, and improves the inflammatory profile and steatosis in mice with MS fed HFD+WB.

MI-P026-86
BACTERIAL COMMUNITY STRUCTURE OF WINES FROM A NON-TRADITIONAL WINE REGION OF ARGENTINA

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Argentina is ranked as the fifth wine world producer after Italy, France, Spain, and the United States. Although most of the traditional wine-producing regions are located along the Andes Mountains range, new vineyards have been recently established in the southwest of Buenos Aires Province, and it is a thriving activity of great cultural and economic value. The malolactic fermentation (MLF) is responsible for the conversion of L-malic acid from grapes to L-lactic acid and CO_2, causing a reduction in the total acidity of the wine, and modifying its flavor. It occurs during or after alcoholic fermentation and is carried out mostly by Lactic Acid Bacteria (LAB) species. In the present work we studied the variations in wine bacterial diversity through three consecutive vintages (2017, 2018, and 2019), and how climatic conditions affected said diversity. NGS technique (amplicon sequencing) was used to identify partial sequences (V3-V4 region) of the 16S rRNA gene. Climatic data was obtained from the "Sistema de Información y Gestión Agrometeorológica", INTA database. Grape must and wine of the Malbec variety, at different fermentation stages, were studied. Additionally, pH and L-malic acid were evaluated for each sample studied. For the 2018 vintage, the winemakers reported a great loss in productivity during the months prior to harvest, resulting in an insufficient yield to produce wines of each variety. Consequently, only one grape must sample could be obtained, comprised of a mixture of the varieties Pinot Noir, Chardonnay, Sauvignon, and Malbec. During the years of our study, there was an unseasonable spring frost in 2017. Our results showed that the wine bacterial microbiota became less diverse over the years. Also, a core of microorganisms belonging to different phyla was conserved across the vintage years. *Proteobacteria* and *Actinobacteria* were the most abundant groups. A high relative abundance of the *Acetobacteraceae* family and a scarcity of LAB were detected, which could be related to a slowdown in the malolactic fermentation throughout the years, reported by winemakers. We believe that the results obtained contribute to a better understanding of the bacterial microbiota in these wines and could provide valuable knowledge that could improve the winemaking production. In fact, the winemakers have eliminated a cold soaking process prior to the fermentation to shorten it and prevent the proliferation of AAB.

MI-P027-91
EXPRESSION OPTIMIZATION OF RECOMBINANT XYLANASE IN *Lactococcus lactis* NZ9000 TO ENHANCE SILAGE FERMENTATION

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Cellulose, lignin, and hemicellulose (formed mainly by xylan) are among the main constituents of the cell wall of plant cells that make up the basic forages of bovine feed. Xylan, consisting of β-1,4-linked xylopyranosyl residues, is the second most abundant polysaccharide; it is hydrolyzed by Xylanases (EC 3.2.1.8) that are present in many fungi, yeasts as well as bacteria. The ability of ruminants to convert plant biomass unsuitable for human consumption into meat and milk is of great social and agricultural importance. However, the efficiency of this process is highly dependent on the digestibility of plant cell walls. The use of enzymes in the silage contributes to this process in several ways: produces an improvement in fermentation, improves digestibility, increases metabolizable energy, and produces a change in structural carbohydrates, which is beneficial when the silage reaches the rumen. *Lactococcus lactis* is one of the most commonly used lactic acid bacteria in fermented food production. Because it is considered Generally Recognized As Safe (GRAS), the implementation of this strain in biotechnological processes and industrial enzymes production could simplify the downstream processing and diminish contamination risks. The aim of this work was the over-expression of the XynA xylanase in *L. lactis* NZ9000 strain. The *xynA* gene from *Bacillus subtilis* was codon-optimized, synthesized, and cloned in the pNZ8048 plasmid under the control of the *Pnis* promoter. Expression and activity were assessed by growing the strain 48 hours in M17-agar plates with 1% xylan and 0, 10, or 50 ng/ml of nisin as inducer. Congo Red stain was used to observe xylan degradation halo, under these conditions both inducer concentrations gave similar results. Then, expression was optimized using M17 liquid medium, for *L. lactis* the best conditions for protein overexpression were 50 ng/ml nisin and 24 h of induction at 30ºC. Protein over-expression was detected, with the expected molecular weight, in medium supernatant after precipitation with TCA and Coomassie Blue staining on SDS-PAGE gels. No intracellular expression of XynA could be observed, indicating that the signal peptide encoded by *xynA* is functional in *L. lactis*. Protein presence in medium supernatant was also observed 48 h after induction suggesting good stability of the protein. Further characterization of enzymatic activity *in vitro* and *in vivo* will help to determine potential biotechnological applications.