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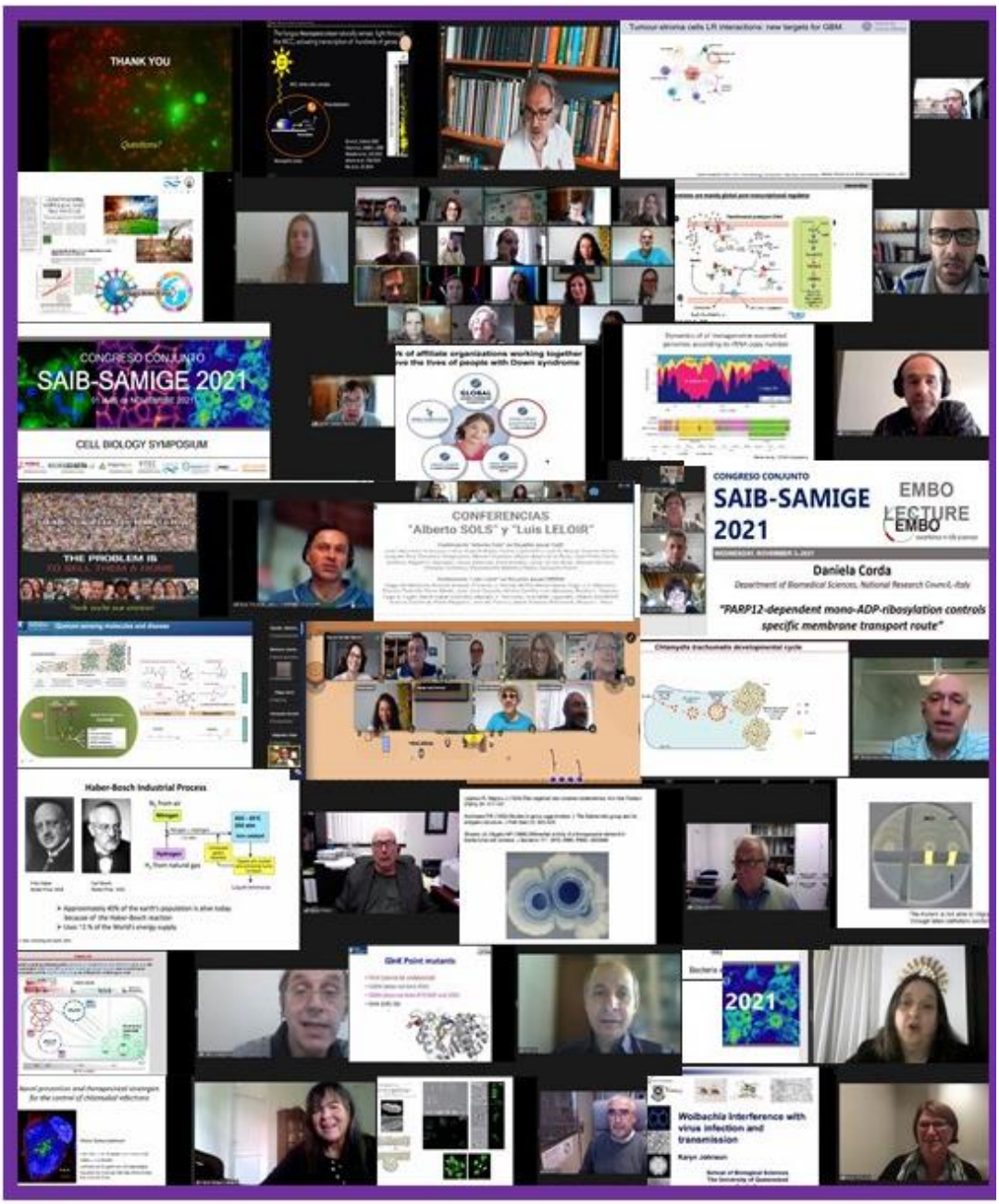
SAIB - SAMIGE Joint meeting
2021 *on line*



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development with appearance typical of *Botrytis* sp., and *Aspergillus* sp. respectively, while no fungal contaminants were observed in inoculated fruits under experimental conditions. In addition, the mean yeast population count in YPG-C increased 3 log cycles in control sample at 2 days at 30 ºC, while it was not detected in inoculated samples. Similar results were observed on Mac Conkey and SSA media at both 4º and 30 ºC as confirmed by electronic microcopy. Similarly, no *L. monocytogenes* count was detected at 24 h in fermented grape juice with Oo. In this condition TCP remained unchanged after 7 days incubation at 30 ºC while, the antioxidant activity increased 21% relative to control. Conclusions: Autochthonous *L. plantarum* and *O. oeni* strains exhibited strong antagonistic activities against pathogenic bacteria and spoilage microorganisms in MP strawberries and fermented grape juice respectively which is a great goal for their potential application as biocontrol agents. It should be noted that the study of *O. oeni* MS46 in SGJ stored at abusive temperature as an alternative to its use in winemaking is reported here for the first time.

MI-P141-309
UTILIZATION OF AUTOCHTHONOUS STRAINS FROM WINERY WASTE AND GRAPE MUST AS STARTER CULTURES FOR WINEMAKING IN NORTHERN ARGENTINA

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Malolactic fermentation (MLF) occurs during the winemaking of red wines to improve their quality and organoleptic attributes. Nowadays, MLF in the Argentine wineries is mainly produced by commercial lactic acid bacteria (LAB). In the present study, we propose using native lactic acid bacteria isolated from wine waste and red grape must, which were selected for their relevant malolactic activity in *in vitro* assay, high ethanol tolerance, and inability for producing biogenic amines. First, their esterase activity were evaluated to select the strains with the higher aromatic potential for vinification assays. High esterase activity was found in CE of *Oenococcus oeni* strains such as MS46 and B18 strains (from must and Malbec wine lees, respectively), but not in CS or SN. SDS-PAGE of these CE fractions revealed bands with a 38 KDa estimated size. Esterase activity assays were performed in triplicate in 3 cell fractions: culture supernatant (SN), cell suspension (CS), and cell-free extract (CE) using p-nitrophenyl acetate as substrate. The final reaction mixture contained Citrate-Phosphate buffer (pH 5.0), substrate solution (1 mM), and the sample (reaching a final OD_{600} of 0.5 for CS). After incubation at 37°C for 2 h, 0.5 M sodium hydroxide were added to stop the reaction. Absorbance at 410 nm was compared with a p-nitrophenol standard curve. The winemaking process was carried out on Malbec type must (density, 1.115 g/cm3; initial pH, 3.68) and Cabernet Sauvignon must (density, 1.115 g/cm3; initial pH, 3.68) from a winery located in Colalao del Valle (Tucumán, Argentina). For the alcoholic fermentation (AF), both must types were inoculated in duplicate with the *Saccharomyces cerevisiae* strain mc2. Musts incubation lasted 10 days and the volumetric mass was monitored at 20 °C. At the end of AF process, wines with the following values were obtained: ethanol 14.5% v/v, pH 3.72, residual sugars <2.00 g/L, and L-malic acid 2.87 g/L (Cabernet Sauvignon), and 2.50 g/L (Malbec). For the MLF, *O. oeni* MS46 and B18 strains were grown until end of growth exponential phase in adaptation medium (In g/L: MRS 50, Fructose 40, Glucose 20, L-malic acid 4, Tween 80 1, Pyridoxine 0.1 mg/L, Ethanol 7%). After centrifugation, they were inoculated in duplicate at 10^7 UFC/mL. A control assay without inoculation was included. MLF was controlled by L-malic acid consumption (R-Biopharm enzymatic kit). In addition, viable cells counts in MRS medium supplemented with Fructose (5 g/L) and L-malic acid (4 g/L) and pH variation were determined. A major goal here was that the *O. oeni* strains B18 and MS46 demonstrated high esterase activity in CE. In addition, SDS-PAGE of these CE fractions revealed bands with a 38 KDa estimated size. So, these strains were selected to inoculate in fermented musts. In Malbec wine, the malic acid concentration reached levels < to 0.02 g/L after 21 days with both strains tested. Similar values were obtained for the Cabernet Sauvignon after 28 days while in the control assay, L-malic acid slightly changed. Both MS46 and B18 strains showed a great capacity to complete MLF, not presenting marked differences in their behaviors and showing a count of 10^3 UFC/mL at the MLF process end.

PLANTS BIOCHEMISTRY and MOLECULAR BIOLOGY

PL-P01-09
CONTRIBUTION OF LIMYB IN *Arabidopsis thaliana* UV-B RESPONSE

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LIMYB is a transcription factor involved in *Arabidopsis thaliana* plant defense against viral infection. In this signaling pathway, LIMYB interacts with the ribosomal protein RPL10A in the nuclei to downregulate the translational machinery. Thus, *A. thaliana* plants overexpressing LIMYB show lower protein synthesis, less association of viral mRNA with polisomes and higher tolerance to viral infection. Although *LIMYB* expression is not regulated by UV-B radiation, our aim is to elucidate whether LIMYB, in cooperation or not with RPL10A, is involved in UV-B responses. For this purpose, we investigated the effect of UV-B in Arabidopsis *limyb* mutants and overexpressing plants. First, we analyzed transcript levels of previously

described *LIMYB* target genes such as *RPL4*, *RPL13*, *RPS25*, *RPL28e* and *RPS13a* after UV-B exposure. Both the mutation and the overexpression of *LIMYB* does not affect the expression by UV-B radiation of these genes. However, *LIMYB*-overexpressing lines show less inhibition of primary root elongation after UV-B treatment with respect to WT plants, while the opposite is observed in *limyb* mutants. In addition, *LIMYB*-overexpressing plants exhibit decreased membrane damage, not change in the chlorophyll content and increased levels of UV-absorbing phenolic compounds after UV-B exposure in comparison to WT and mutant plants. Our results suggest that LIMYB could participate in UV-B responses and its overexpression could improve UV-B tolerance in Arabidopsis.

PL-P02-24
METABOLIC CHANGES IN LEAVES OF *Prunus persica* INOCULATED WITH *Taphrina deformans*

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Leaf peach curl is a disease affecting *Prunus persica* trees around the world. The causal of the disease is the dimorphic fungus *Taphrina deformans*. In addition to leaf hypertrophy and reddish coloration, the disease is characterized by a decrease in photosynthesis. In order to identify early defense responses of *Prunus persica* against *Taphrina deformans* infection, in a previous work we analyzed differentially expressed genes (DEGs) by RNA-seq in leaves from a susceptible (DS) and a resistant (DR) genotype after 12 and 96 hours of fungal inoculation. Fold change was calculated as the relation between normalized gene counts at 12 or 96 hpi with respect to 0 hpi for each genotype. Functional classification of DEGs revealed that photosynthesis was among the ten most enriched categories in both genotypes. In this way, to get insight into the effects of the pathogen in plant photosynthesis and carbohydrate metabolism in asymptomatic leaves challenged with the fungus, we explored the levels of chlorophylls (Chls), sugars such as sucrose, glucose and starch, the alcohol sugar sorbitol which is the major photosynthetic product, and the content of Rubisco and sorbitol dehydrogenase. Two genotypes with contrasting sensitivity (DS and DR) were analyzed after 12 and 96 hours post inoculation with *T. deformans* and compared to the control at 0 hpi. Chla and -b decreased at 12 and 96 hpi with respect to 0 hpi in DS, while slightly decrease in Chlb were observed at 96 hpi in DR. In both genotypes, Rubisco content decreased at 96 hpi with respect to 0 hpi. It is interesting to note that DS0 exhibited greater levels of sucrose, sorbitol and starch than DR0. Starch content decreased in both genotypes at 12 and 96 hpi with respect to 0 hpi; however, the reduction was greater in DS than in DR. Moreover, starch content tended to be restored at 96 hpi in DR. Sucrose levels also decreased in both genotypes after inoculation. With respect to glucose, while it decreased in DR over time after inoculation, glucose content increased in DS, with maximum levels at 12 hpi. Sorbitol levels decreased at 96 hpi in both genotypes (four-times and two-times in DS96 with respect to DS0 and in DR96 with respect to DR0, respectively). These findings, together with transcriptomic data suggests a decrease in photosynthesis and accumulation of photosynthates in infected leaves. However, the impact on these processes is stronger in the susceptible genotype. In symptomatic leaves, a change to a type of metabolism similar to that of sink tissues has been described. The results presented here suggest that the effects on carbon metabolism start to occur very early after inoculation when symptoms are not yet developed.

PL-P03-58
GENOMIC STABILITY IS ALTERED IN SALT-TREATED ATMSH7 MUTANTS

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DNA mismatch repair (MMR) is a highly conserved biological pathway that improves the fidelity of DNA by correcting single base-base mismatches and unpaired nucleotides that arise through replication errors. Plants encode MutS protein homologs (MSH) conserved among other eukaryotic organisms, but also contain an extra MSH polypeptide (MSH7). The *Arabidopsis thaliana* MutSγ (heterodimer of MSH2-MSH7) preferentially recognizes some base–base mismatches. Considering that soil salinity is one of the main causes of abiotic stress that can threaten genome integrity, we studied the effect of salt on the tenth generation (G10) of *msh7* T-DNA insertional mutant and wild type *A. thaliana* plants. Seeds were sown on agar plates containing 0.5X Murashige and Skoog medium (MS) and grown for 10 days at 22°C under a 16/8 light/dark photoperiod. Seedlings were then transferred to agar plates containing MS supplemented with 100 mM NaCl and grown for 48 hours. DNA of each plant was isolated before and after treatment. High Resolution Melting (HRM) and Inter Simple Sequence Repeats (ISSR) molecular markers were chosen to determine genome stability. HRM analysis was performed with specific primers designed for reported regions with frequent SNPs and COLD-PCR for mutant enrichment. We found that wild type plants under control and salt-treated conditions conserved the same melting curve pattern, while mutant plants under salt conditions showed a shift in the melting curve pattern with respect to the control. As for ISSRs, no polymorphisms were observed in wild type plants under control and treated conditions. However, the treated mutant genotype showed ISSR band loss compared with control plants, which indicates the presence of genomic mismatches that prevent ISSR primers annealing. Taken together, our results suggest that MSH7 is involved in salt stress-induced DNA damage response.