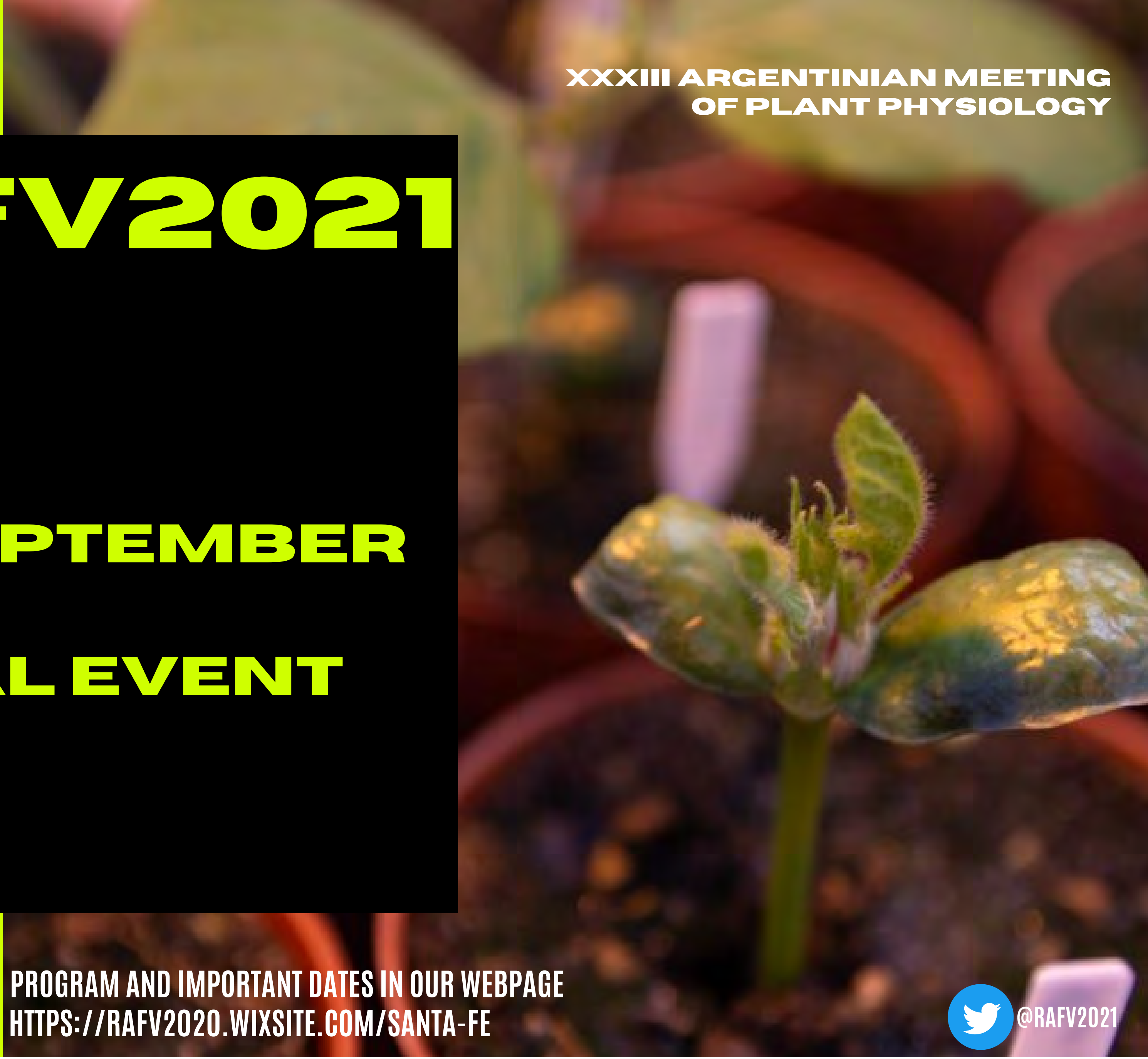
XXXIII ARGENTINIAN MEETING
OF PLANT PHYSIOLOGY

RAFV2021



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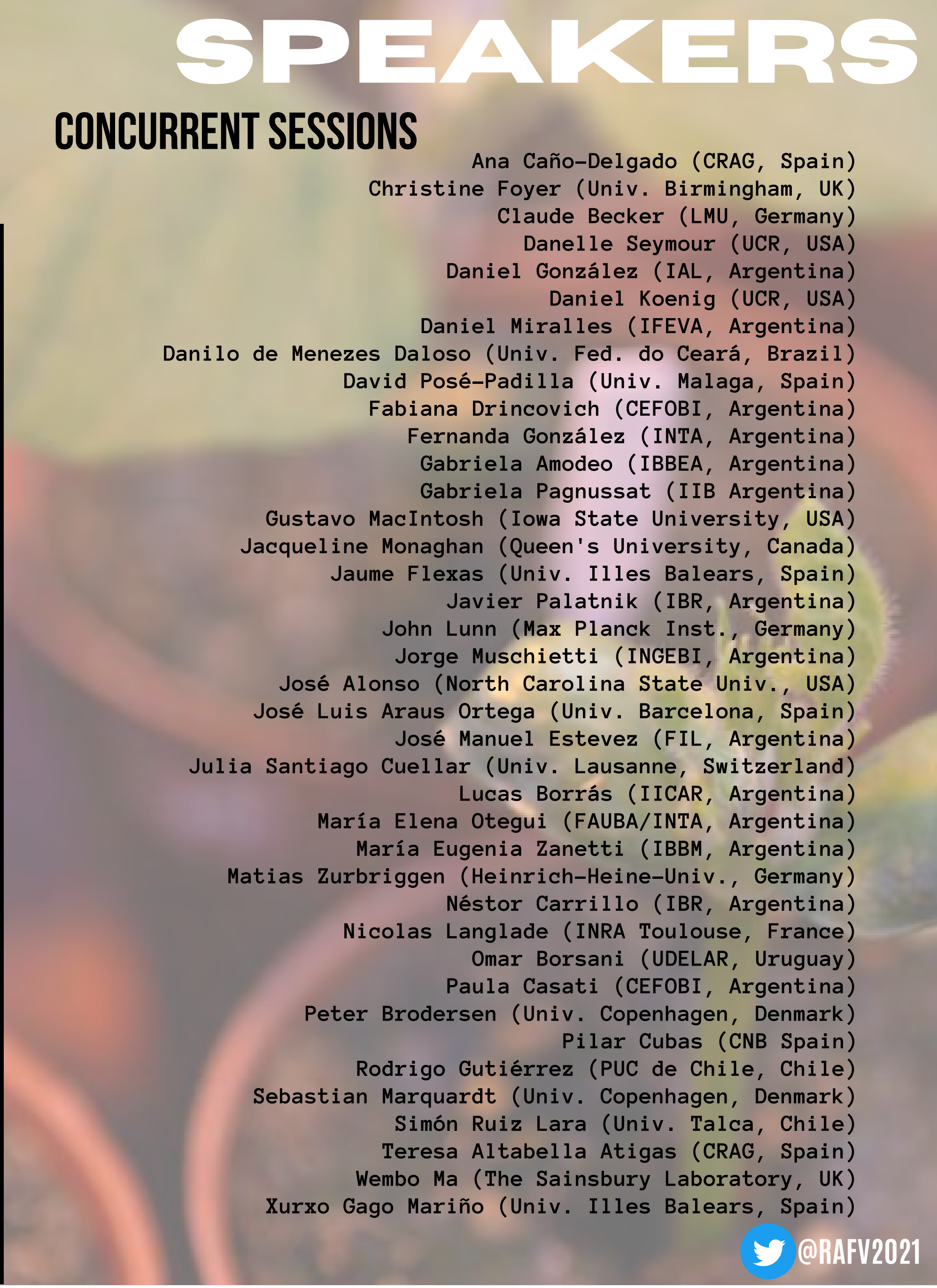
SPEAKERS

KEYNOTE SPEAKERS

Blake Meyers
Danforth Centrer, USA
Ueli Grossniklaus
Univ. Zürich, Switzerland

PLENARY LECTURES

Francois Tardieu
INRA Montpellier, France
Jorge Casal
IFEVA/FIL, Argentina
José María Paruelo
IFEVA, Argentina / INIA, Uruguay
Julia Bailey-Serres
UCR, USA
Mark Stitt
Max Planck Inst., Germany
Xiuren Zhang
Texas A&M Univ., USA



CONCURRENT SESSIONS

Ana Caño-Delgado (CRAG, Spain)
Christine Foyer (Univ. Birmingham, UK)
Claude Becker (LMU, Germany)
Danelle Seymour (UCR, USA)
Daniel González (IAL, Argentina)
Daniel Koenig (UCR, USA)
Daniel Miralles (IFEVA, Argentina)
Danilo de Menezes Daloso (Univ. Fed. do Ceará, Brazil)
David Posé-Padilla (Univ. Malaga, Spain)
Fabiana Drincovich (CEFOBI, Argentina)
Fernanda González (INTA, Argentina)
Gabriela Amodeo (IBBEA, Argentina)
Gabriela Pagnussat (IIB Argentina)
Gustavo MacIntosh (Iowa State University, USA)
Jacqueline Monaghan (Queen's University, Canada)
Jaume Flexas (Univ. Illes Balears, Spain)
Javier Palatnik (IBR, Argentina)
John Lunn (Max Planck Inst., Germany)
Jorge Muschietti (INGEBI, Argentina)
José Alonso (North Carolina State Univ., USA)
José Luis Araus Ortega (Univ. Barcelona, Spain)
José Manuel Estevez (FIL, Argentina)
Julia Santiago Cuellar (Univ. Lausanne, Switzerland)
Lucas Borrás (IICAR, Argentina)
María Elena Otegui (FAUBA/INTA, Argentina)
María Eugenia Zanetti (IBBM, Argentina)
Matias Zurbriggen (Heinrich-Heine-Univ., Germany)
Néstor Carrillo (IBR, Argentina)
Nicolas Langlade (INRA Toulouse, France)
Omar Borsani (UDELAR, Uruguay)
Paula Casati (CEFOBI, Argentina)
Peter Brodersen (Univ. Copenhagen, Denmark)
Pilar Cubas (CNB Spain)
Rodrigo Gutiérrez (PUC de Chile, Chile)
Sebastian Marquardt (Univ. Copenhagen, Denmark)
Simón Ruiz Lara (Univ. Talca, Chile)
Teresa Altabella Atigas (CRAG, Spain)
Wembo Ma (The Sainsbury Laboratory, UK)
Xurxo Gago Mariño (Univ. Illes Balears, Spain)

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MONDAY 13 **SATELITE ACTIVITIES**	
9:00-10:30	Workshop on Scientific graphic presentations (by Arg. Plant Women, Chair: Veronica Arana)
10:30-11:00	break
11:00-12:30	Will the Nagoya protocol change how we deal with digital sequence information in plant research? Research and Law perspectives (by the Global Plant Council, Chair: Fernanda Gonzalez)
12:30-13:30	break
13:30-15:00	Meet the editors Chairs: Ana Laxalt, Carlos Garcia-Mata, Humberto Debat Joint activity by New Phytol., Nature P., Plant Cell, FEBS eLife, JXB, Plant Direct, Plant J., Plant Phys., CoB
15:00-15:30	break
15:30-17:00	SAFV General Assembly

TUESDAY 14	
9:00-9:30	Open and Keynote speaker
9:30-10:30	**Keynote Lecture - Wenbo Ma** (Chair: Pablo Manavella:
10:30-11:00	break
11:00-13:00	**Concurrent Session 1** (Chair: Elina Welchen)
11:00-11:40	David Posé-Padilla
11:40-12:20	Xurxo Gago Mariño
12:20-13:00	Erwan Michard
11:00-13:00	**Concurrent Session 2** (Chair: José Manuel Estevez)
11:00-11:40	Ana Caño-Delgado
11:40-12:20	Nicolas Langlade
12:20-13:00	Daniel González
13:00-14:00	break
14:00-16:00	**Concurrent Session 3** (Chair: Javier Botto)
14:00-14:40	Rodrigo Gutiérrez
14:40-15:20	Daniel Koenig
15:20-16:00	Fabiana Drincovich
14:00-16:00	**Concurrent Session 4** (Chair: Marcelo Helguera)
14:00-14:40	Daniel Miralles
14:40-15:20	Lucas Borrás
15:20-16:00	Fernanda González
16:00-16:30	break
16:30-17:30	**Plenary Lecture 1 - Julia Bailey-Serres** (Chair: M. Eugenia Zanetti)
17:45-19:00	Posters and video presentations 1

WEDNESDAY 15	
9:00-11:00	**Concurrent Session 5** (Chair: Carlos Figueroa)
9:00-9:40	John Lunn
9:40-10:20	Teresa Altabella Atigas
10:20:11:00	Danilo de Menezes Daloso
9:00-11:00	**Concurrent Sessions 6** (Chair: Fernanda Gonzalez)
9:00-9:40	José Luis Araus Ortega
9:40-10:20	Jaume Flexas
10:20:11:00	María Elena Otegui
11:00-11:30	break
11:30-12:30	**Plenary Lecture 2 - José María Paruelo** (Chair: Daniel Miralles)
12:30-13:30	break
13:30-15:30	**Concurrent Sessions 7** (Chair: Daniel Gonzalez)
13:30-14:10	Jacqueline Monaghan
14:10-14:50	Gustavo MacIntosh
14:50-15:30	María Eugenia Zanetti
13:30-15:30	**Concurrent Session 8** (Chair: Ana Laxalt)
13:30-14:10	Néstor Carrillo
14:10-14:50	Jorge Muschietti
14:50-15:30	Gabriela Pagnussat
15:30-16:00	break
16:00-17:00	**Plenary Lecture 3 - Jorge Casal** (Chair: Paula Casati)
17:15-19:00	Posters and short comunications 2

THURSDAY 16	
9:00-11:00	**Concurrent Session 9** (Chair: Néstor Carrillo)
9:00-9:40	Christine Foyer
9:40-10:20	Pilar Cubas
10:20-11:00	Matias Zurbriggen
9:00-11:00	**Concurrent Session 10** (Chair: Georgina Fabro)
9:00-9:40	Rosa Lozano-Dúran
9:40-10:20	Claude Becker
10:20-11:00	Julia Santiago
11:00-11:30	break
11:30-12:30	**Plenary Lecture 4 - Francois Tardieu** (Chair: M. Elena Otegui)
12:30-13:30	break
13:30-15:30	**Concurrent Session 11** (Chair: Jorge Muschietti)
13:30-14:10	Omar Borsani
14:10-14:50	Gabriela Amodeo
14:50-15:30	José Manuel Estevez
13:30-15:30	**Concurrent Session 12** (Chair: Juan Carlos Diaz)
13:30-14:10	José Alonso
14:10-14:50	Paula Casati
14:50-15:30	Danelle Seymour
15:30-16:00	break
16:00-17:00	**Plenary Lecture 5 - Xiuren Zhang** (Chair: Javier Palatnik)
17:15-19:00	Posters and short comunications 3

FRIDAY 17	
9:00-10:00	**Plenary Lecture 6 - Mark Stitt** (Chair: Carlos Figueroa)
10:00-10:30	break
10:30-12:30	**Session 13** (Chair: Federico Ariel)
10:30-11:10	Sebastian Marquardt
11:10-11:50	Javier Palatnik
11:50-12:30	Peter Brodersen
12:30-13:30	break
13:30-14:30	**Keynote Speaker 2 - Blake Meyers** (Chair: Pablo Manavella)
14:30	Closing remarks

ABSTRACTS

3
DT166BD
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Mariana Abrile

Nicotiana alata L. growth in soils amended with leachate sludge under different heavy metal loads

Mariana Guadalupe Abrile[1], María Laura Fiasconaro[1], Daiana Soledad Orecchia[1], María Eugenia Lovato[1]
(1) Instituto de Desarrollo Tecnológico para la Industria Química, Consejo Nacional de Investigaciones Científicas y Técnicas, Universidad Nacional del Litoral, Colectora Ruta Nacional Nº 168 km 0 (Paraje El Pozo), Santa Fe, Argentina.

The shortage of organic matter (OM) and the presence of pollutants -such as heavy metals (HM) - hinder plant growth in cover soils of sanitary landfills. Use of alternative fertilizers sources such as sludge, seems to be an adequate solution to the lack of OM in the soils. However, HM presence still appears as a problem. Our objective was to evaluate the growth of *Nicotiana alata* L. in soils amended with leachate sludge, under different HM loads.

The soil was amended with sludge derived from the treatment of leachate from a sanitary landfill. In addition, it was contaminated under different concentrations of Ni, Pb and Cr applying a Box–Behnken experimental design with three numerical factors. The plants grew in the substrate and were harvested once the flowering stage began. Different responses were determined such as: stem height, root length, aerial and root dry weight. They were evaluated using the Response Surface Methodology.

Preliminary results suggest that *Nicotiana alata* L. exhibits a favorable response to medium levels of contamination. Nevertheless, plant growth was affected when the concentration of the different metals increased after a certain value. Particularly, Ni content had a strong influence on root and aerial parts dry weight.

It could be suggested that *Nicotiana* sp. would be suitable for growth in substrates with moderate levels of heavy metals contamination and not only in soils amended with sludge. However, it is necessary to exert a broad control over the levels of contamination to which plants are exposed.

PP247TG

Area: Plant breeding

Tipo de presentación: Poster en formato PDF

Enviado por: Ana Laura Achilli

Genetic gains in grain yield and yield-related traits of durum wheat in Argentina (1934 – 2015)

Ana Laura Achilli[1], Pablo Federico Roncallo[1], Maria Sofia Grande[1], Juan Manuel Calfuquir[1], Viviana Echenique[1]
(1) Centro de Recursos Naturales Renovables de la Zona Semiárida (CERZOS-CONICET), Departamento de Agronomía, Universidad Nacional del Sur (UNS), Camino La Carrindanga km 7, Bahía Blanca, Argentina

Knowing the genetic gains in grain yield and yield-related traits is essential to design future breeding strategies that allow the development of higher-yielding wheat cultivars. The objective of this study was to determine the genetic changes in grain yield made by durum wheat breeding in Argentina, identifying the yield components responsible for such changes. For this, a wide set of durum wheat cultivars released in Argentina was analyzed in three field trials. A significant linear trend ($R^2 = 0.55$) was observed between the year of released and grain yield of cultivars, with an increase of 26.94 kg ha^{-1} yr^{-1} (0.81% yr^{-1}) from 1934 to 2015. Grain yield showed an increase of 51% when comparing the old cultivars (<1980) with the intermediate ones (1980-1999), while between the intermediate and modern cultivars (> 2000) the increase was only 16%. Harvest index was the variable that best explained the changes in grain yield, not finding an association between grain yield and aerial biomass. Grain number per plant increased 13% from old to modern cultivars, while thousand kernel weight did not show differences. Increases in the number of grains per plant could be attributed to two main components, the number of spikes per plant and the number of grains per spike. An in-depth analyses of the components of the number of grains per spike showed that it was the number of grains per spikelet ($R^2 = 0.73$) not the number of spikelets per spike that explained most of the variation.

Financing: This research was funded by the Agencia Nacional de Promoción Científica y Tecnológica (ANPCYT-PICT 2015-N°1401), Universidad Nacional del Sur (UNS), Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET) and the European Union's Horizon 2020 (MSCA-RISE-2015-N°691109 EXPOSEED).

5
JT344JL
Area: Epigenetics, Chromatin, non-coding RNAs, RNA biology
Tipo de presentación: Poster en formato PDF
Enviado por: Natalia Achkar

Phosphorylation of HYL1 C-terminal domain has regulatory roles on HYL1 activity

Natalia Achkar[1], Axel Giudicatti[1], Pablo Manavella[1]
(1) Instituto de Agrobiotecnología del Litoral (CONICET-UNL-FBCB), Paraje El Pozo, Santa Fe, Argentina.

Gene-silencing, mediated by micro RNAs (miRNAs), is one of the most important mechanisms of post-transcriptional gene regulation. To balance gene expression/silencing, miRNA abundance is tightly regulated. In plants, the endonuclease DICER LIKE 1 (DCL1) converts the primary miRNA into mature miRNAs. To achieve a precise excision of the miRNA, DCL1 requires the assistance of HYPONASTIC LEAVES 1 (HYL1) and SERRATE. HYL1 comprises two double-stranded RNA-binding domains, which mediate interactions with miRNA precursors and partner proteins, a nuclear localization signal, and a C-terminal domain constituted of six tandem repetitions of a highly conserved 28 amino acids motif with unknown function. As we previously demonstrated, phosphorylation in two serines, located in each RNA-binding domain, regulates HYL1 activity and controls its stability in response to light conditions. However, a mass-spectrometry analysis revealed that serines located in each repetition at its C-terminal region are also phosphorylated. Furthermore, the 1001 genomes project revealed that the number of repetitions in HYL1 changes among different *Arabidopsis thaliana* ecotypes. Here, we report that phosphorylation of the C-terminal region of HYL1 also appears to have regulatory roles on the protein activity. Using mutant phosphomimetic versions of HYL1, we found that modifications in the C-terminal repeats impact the affinity of HYL1 with interacting partners, the number of D-bodies per cell and plant development. The number of repetitions in the C-terminal domain also affects the subcellular protein localization. To date, the HYL1 C-terminal domain was thought to be dispensable for the protein activity, a premise that we challenged in this study.

6
TF874QG
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Humberto Fabio Causin

Germination responses and antioxidant metabolism in Zephyrantes tubispatha seeds exposed to different thermal conditions

María Cecilia Acosta[2], Vilma Teresa Manfreda[2], María Luciana Alcaraz[2], Humberto Fabio Causin[1]
(1) Universidad de Buenos Aires. CONICET, Departamento de Biodiversidad y Biologia Experimental (DBBE), Instituto de Biodiversidad y Biología Experimental y Aplicada (IBBEA), Facultad de Ciencias Exactas y Naturales., Int. Güiraldes y Av. Cantilo. Ciudad Universitaria, Ciudad Autónoma de Buenos Aires, Argentina.
(2) Universidad Nacional del Centro de la Provincia de Buenos Aires (UNCPBA), Facultad de Agronomía, República de Italia 780, Azul, Argentina

Zephyranthes tubispatha is a species distributed along several countries of South America, whose flowers are of great ornamental interest. Although it can be multiplied through bulbs or scales, the germination of its seeds is simpler and cost-effective. Temperature is an important environmental cue that controls germination, however its effect on *Z. tubispatha* has been scarcely investigated. Previous results of our group showed that its seeds have an optimal temperature range for germination between 14 and 25 °C, with higher temperatures (HTs) being progressively inhibitory. The main objectives of the present work were to study the germination responses of *Z. tubispatha* seeds to different temperature treatments, with special emphasis on the role of the antioxidant metabolism, given the importance of reactive oxygen species (ROS) in the control of this process and dormancy release. The involvement of abscisic acid (ABA) in the inhibition of germination by HT was also evaluated. Our results show that while germination was almost nil above 28°C, maximum percentages could be recovered after transferring the seeds to 20 °C, suggesting that thermoinhibition rather than thermodormancy was the underlying phenomenon. This effect was associated with changes in the generation of superoxide anions in specific embryonic regions. Interestingly, some response traits differed depending on the length of the HT (33°C) pretreatment, probably reflecting strategies aimed to discriminate between transient and seasonal (long-lasting) increments in temperature. Germination responses are discussed in terms of the effect of HT on ABA metabolism, lipid peroxidation, and on key components of the antioxidant metabolism.

Financing: El presente trabajo fue financiado con fondos provenientes de la Universidad de Buenos Aires y la Universidad Nacional del Centro de la Provincia de Buenos Aires

7
SR842FL
Area: Plant Physiology and Ecophysiology
Tipo de presentación: video presentacion
Enviado por: Martín Acreche

Oil and protein concentrations and fatty acid composition of chia (Salvia hispanica L.) grains as affected by variations in environmental conditions

Jimena Pérez Brandán[1], Natalia G. Izquierdo[2], **Martín Acreche**[1]
(1) INTA EEA SALTA-CONICET, Ruta 68, km 72, 4107, Cerrillos, Salta, Argentina
(2) CONICET-IIDEAGROS, Facultad de Ciencias Agrarias, Universidad Nacional de Mar del Plata, Mar del Plata, Argentina

Chia has strengthened it consumption because its grains have the highest content of omega-3 acid in grain crops. The objective was to determine the effect of variations of environmental conditions on oil and protein concentrations and fatty acid profile of chia grains. Treatments consisted of two chia populations (white-seeds and mixed-seeds) and different sowing dates that generated variations in temperature and radiation during grain filling. Oil concentration decreased and protein concentration increased with the delay in sowing date. There were significant and positive associations of oil concentration with day and night temperatures and accumulated intercepted radiation, whereas protein concentration showed, in general, significant and negative associations with those environmental variables. This behavior led to a negative association between this two quality components ($R^2= 0.54$; $p< 0.001$; n=24). Palmitic and linoleic acids decreased, whereas stearic and linolenic acids increased, as day and night temperatures increased. In addition, there was a decrease of palmitic acid and an increase of oleic acid as accumulated intercepted radiation increased. An increase of the concentration of oleic acid was associated with an increase of the concentration of stearic acid and decreases of the concentrations of palmitic and linoleic acids; while the concentration of linoleic acid was negative associated with the concentration of linolenic acid. Although both chia populations responded similarly to environmental conditions, the white-seeds population showed higher concentration of palmitic and linolenic acids, whereas the mixed-seeds population showed higher linoleic acid concentration. Summarizing, changes in environmental conditions modified the quality of chia grains.

Financing: The study was partially funded by grants from INTA (PNIND 2013-2018 N° 1108064) and Ministry of Science and Technology of Argentina (PICT 2015 N° 875). JPB had a doctoral scholarship from CONICET.

8
FP716JK
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: María Agostina Affinito

Expression of a vacuolar Na+/H+ antiporter from Lotus tenuis improved salt tolerance of transgenic Arabidopsis thaliana at germination stage

María Agostina Affinito[1], María Aurora Maciel[1,2], María Lorena Roldán[3], Julieta Aguilá[1], Mariana del Vas[4], Antonio Díaz Paleo[3]
(1) Universidad Nacional del Noroeste de la provincia de Buenos Aires, Monteagudo 2772, Pergamino, Argentina
(2) Centro de Investigaciones y Transferencia del Noroeste de la Provincia de Buenos Aires (CIT NOBA, CONICET-UNNOBA-UNSAdA), Monteagudo 2772, Pergamino, Argentina
(3) INTA EEA Pergamino, Ruta 32 Km 4.5, Pergamino, Argentina
(4) Instituto de Agrobiotecnología y Biología Molecular (IABiMo), CICVyA, INTA, CONICET, Nicolas Repetto y de los Reseros s/n, Hurlingham, Argentina

Lotus tenuis is a perennial forage legume that is naturalized in the Flooding Pampa region of Argentina. Even when it is considered a salt-tolerant species, the mechanisms underlying this trait are not fully understood. Intracellular compartmentation of Na^+ into vacuoles by NHX antiporters is an important and well-known strategy to reduce ion toxicity during salt stress. To study the contribution of *Lotus tenuis* NHX1 antiporter to salinity tolerance, the *LtNHX1* coding region was cloned into pEarleyGate203 vector downstream of the CaMV35S promoter. The recombinant plasmid was introduced into *Agrobacterium tumefaciens* GV3101, and a transgenic *Arabidopsis thaliana* line was obtained by *Agrobacterium*-mediated transformation using the floral dip method. The expression of the transgene was confirmed by RT-PCR analysis. Seeds of wild-type (Col-0) and T3 generation of the transgenic line (P8-68) were sown on MS media containing 0 (control), 50, 100 and 150 mM NaCl. Germination speed was estimated by using a modification of the Timson Index: $GI = \Sigma G/t$ where G is the percentage of seeds germinated at 5-day intervals and t is the total germination period (25 days). Two-way ANOVA and DGC multiple-comparisons method were performed. Compared to wild-type, P8-68 displayed less sensitivity under salt stress, with higher index of germination speed and a higher percentage of seed germination after 25 days. In addition, under 50 and 100 mM NaCl, GI of P8-68 was not significantly reduced compared to control conditions. These results suggest that the constitutive expression of *LtNHX1* contributes to enhance salt tolerance at germination stage.

9
SC352JJ
Area: Plant Physiology and Ecophysiology
Tipo de presentación: video presentacion
Enviado por: Juan José Agüero

Improving yields through triple genotype by environment by management interaction in North Western Argentina quinoa systems.

Improving yields through triple genotype by environment by management interaction in North Western Argentina quinoa systems.

Juan José Agüero[1], Martín Moisés Acreche[2], Héctor Daniel Bertero[3], Ramiro Néstor Curti[4]
(1) Universidad Nacional de Jujuy, General Manuel Belgrano, Facultad de Ciencias Agrarias, Alberdi 47, San Salvador de Jujuy, Argentina
(2) Instituto Nacional de Tecnología Agropecuaria, Cerrillos, EEA Salta, Ruta Nacional N° 68 km 172, Cerrillos, Argentina
(3) Universidad Nacional de Buenos Aires, CABA, Facultad de Agronomía, Avda San Martín 4453, CABA, Argentina
(4) Universidad Nacional de Salta, Salta, Facultad de Ciencias Naturales, Avda Bolivia 5150, Salta, Argentina

The aim of this experiment was to understand the physiological basis of genotype by environment by management interaction in quinoa. Experiments were carried out at four environments combining two locations (Valleys and Puna) and two years (2017 and 2019 for Valleys, 2018 and 2019 for Puna). Local genotypes (RQ252 from Valley and RQ420 from Puna) plus Sea Level cultivars (Titicaca and Puno, adapted to low altitude and high latitude environments) were compared under plant densities of 7 and 14 pl m^{-2} evaluating yield, biomass accumulation and harvest index. Despite of the changes in plant density, the correlations between yield and biomass in Valleys (R^2= 0.70, p<0.0001) and yield and harvest index in Puna (R^2= 0.52, p<0.0001) were consistent. The triple genotype by environment by management interaction was significant for yield, biomass accumulation and harvest index. Local genotypes showed higher yields at the high plant density in Puna, but no differences in the Valleys, while sea level cultivars showed less variability between plant densities or environments. In Puna, differences between plant densities were associated to biomass accumulation in RQ252 and to harvest index in RQ420, respectively. In conclusion, plant density effects vary with environment and genotype, and the yield components which are affected also vary between genotypes.

Financing: This studied was founded by National Institute of Agricultural Technology.

10
RL524MJ
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Gastón Ahumada

Effect of pruning levels on Yield, Fruit Maturity and Reserves in Malbec vineyards trellised to single high wire system

Gastón E. Ahumada[1], Miguel A. Pirrone[1], Diana Segura[2], Marcelo J. Belmonte[1], Carla V. Giordano[3], Carina V. Gonzalez[2]
(1) Grupo Peñaflor S.A.
(2) Instituto de Biología Agrícola de Mendoza
(3) Instituto Argentino de Investigaciones en Zonas Áridas, CONICET-UNCuyo-Gobierno de Mendoza

The main objective of winter pruning of grapevines is to regulate vegetative and reproductive growth. Pruning level (number of buds per meter of productive cordon) affects budbreak, leaf area development, maturity, yield and reserve levels . In this work, we evaluated for the first time in Argentina, the effect of different pruning levels on leaf area development, yield, grape maturity and reserve levels of Malbec vineyards trellised to a SHW system in Mendoza. We imposed different winter pruning levels during three growing seasons 2017, 2018 and 2019: 16, 24, 32 and > 32 buds per meter of productive cordon (buds m^{-1}). We measured total leaf area (TLA) at veraison, yield and fruit composition at harvest and structural reserves in trunk at leaf fall. Soluble solid concentration (°Brix) in berries was similar among treatments with the exception of 2018 where 16 buds m^{-1} that presented highest values. In general terms, we found that the interannual variation of reserves (starch) in trunk was inversely correlated with yield interannual variation. 24 and >32 buds m^{-1} presented high yield and high levels of reserves, 16 buds m^{-1} presented high levels of reserves, but lower yields. Meanwhile 32 buds m^{-1} presented high yield but it was not sustainable over time due to their decrease in reserve levels in the third year. > 32 buds m^{-1} reached its highest TLA and reserve levels in the third year, indicating that this is the minimum period necessary to stabilize its yield and reserves at sustainable levels over time.

11
QQ262QP
Area: Developmental Biology
Tipo de presentación: video presentacion
Enviado por: Ana Alarcia García

THE ROLE OF DEVIL PEPTIDES IN CONTROLLING CELLULAR PROLIFERATION AND PLANT MORPHOGENESIS

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DEVIL (DVL) genes have been identified in Arabidopsis and other plant species. They encode small size peptides of unknown function, belonging to a gene family of 24 members in Arabidopsis, and are associated to plasma membrane. *DVL* genes were characterized by their overexpression phenotypes, which affect fruit morphology. Loss-of-function mutants do not have any morphological phenotype, so their biological function is unknown.

We carried out studies to characterize how DVL peptides interact with plasma membrane, how they are expressed and accumulate, to identify other proteins that interact physically with them, and to study whether the combination of multiple loss-of-function mutants affects development. Our preliminary results suggest that DVL peptides appear to be mobile signals not integrated in plasma membrane, that participate in the control of cell cycle and cell division processes. We are currently generating combinations of multiple T-DNA and CRISPR/Cas9 mutants in different *DVL* genes. These combinations do not show obvious loss-of-function phenotypes, suggesting a high functional redundancy among members of *DVL* family.

Due to the lack of a visible phenotype, we performed a transcriptomic analysis of a quintuple *DVL* mutant. RNA-seq results showed pollen tube development-related genes significantly altered.

To confirm and better understand the differences in spatial distribution of mRNA and peptides for DVL1 and DVL8, we have generated reporter lines to try to determine whether this differential distribution is due to peptide active transport. We are functionally validating the possible protein interactions uncovered in a yeast-2-hybrid screening. These and other preliminary results will be presented.

Financing: This work has been supported by “Subvenciones para la contratación de personal investigador de carácter predoctoral-ACIF2018”. Funded by “Generalitat Valenciana - Conselleria de Educación, Investigación, Cultura y Deporte” and “Programa Operativo del Fondo Social Europeo 2014-2020 de la Comunitat Valenciana”

12
RN549DL
Area: Biochemistry and Metabolism
Tipo de presentación: Poster en formato PDF
Enviado por: Carlos Guillermo Bartoli

Effect of GDP-L-galactose phosphorylase deficiency in the expression of ascorbic acid biosynthetic and ethylene signaling genes in tomato leaves and fruits

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Ascorbic acid (AA) plays several functions in plants. The Smirnoff-Wheeler pathway or galactose pathway is the main AA synthesis pathway both in tomato fruits and leaves. Besides, there is evidence indicating that AA may be synthesized in fruits from metabolites derived from the degradation of pectin during ripening. This work explores the effect of the deficiency in GDP-L-galactose phosphorylase (GGP, the enzyme catalyzing the key regulatory reaction and the first exclusively dedicated to AA synthesis) in the expression of genes associated with AA biosynthesis and ethylene signaling. The study was performed with two Micro-Tom deficient lines in GGP1 (*slggp1*). Plants were grown hydroponically inside a greenhouse during spring-summer seasons under an irradiance of 700 μmol photons m^{-2} s^{-1} at midday and a temperature of 25±2 ºC. Leaf and fruit samples were collected and stored at -80 °C until gene expression was analyzed by RT-PCR. The expression of genes encoding enzymes upstream and downstream GGP-catalyzed reaction for AA synthesis and recycling ascorbic acid from oxidized forms in leaves and in fruits along ripening in wild type and both *slggp1* was studied. In addition the synthesis of other genes associated with the AA biosynthetic pathway such as those leading to the formation of components of cell wall or pectin degradation and ethylene signalling was also analysed. The results presented here show alterations in the expression of genes involved in AA and cell wall metabolism and ethylene perception as a consequence of GGP1 deficiency that would explain modifications observed in *slggp1* plants.

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13
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Area: Developmental Biology
Tipo de presentación: Poster en formato PDF
Enviado por: Antonela Alem

ROLE OF TCP TRANSCRIPTION FACTORS IN COTYLEDON OPENING AND EXPANSION IN RESPONSE TO LIGHT

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After germination, exposure to light promotes the opening and expansion of the cotyledons and the development of the photosynthetic apparatus in a process called de-etiolation. This process is crucial for seedling establishment and photoautotrophic growth. TEOSINTE BRANCHED 1, CYCLOIDEA, and PROLIFERATING CELL FACTORS transcription factors (TCPs) proteins constitute a family of plant-specific transcription factors that control various processes of plant development such as embryogenesis, germination, and the morphogenesis of leaves and flowers. They also participate in the modulation of hormone signaling pathways, thus adjusting cellular processes to internal growth demands and signals received from the environment, as light and temperature. TCP proteins are divided into two classes, I and II. The TCP family contains 24 members in *Arabidopsis*, many of which have been shown to interact with transcription factors from other families. In this study, we identified GOLDEN2-LIKE 1 (GLK1), a key transcriptional regulator of photomorphogenesis, as a protein partner class I TCPs from Arabidopsis. We found that the class I protein TCP15 and GLK1 are jointly required for cotyledon opening and the induction of cell expansion and photosynthesis associated genes during de-etiolation of Arabidopsis seedlings. Our results suggest that the functional interaction between these transcription factors may serve to coordinate the execution of two distinct processes required for correct de-etiolation, i.e. cell expansion and the biogenesis of the photosynthetic apparatus.

14
QD298LS
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Héctor Daniel Bertero

Contrasting developmental responses to high temperatures in a quinoa RIL population

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Quinoa has been promoted as a crop for marginal environments. Because of this and high international prices its cultivation was expanded to more than 100 countries in the last decades, and some of these new environments face high temperatures. This is accentuated by temperature increase as a consequence of climate change, making high temperatures a risk even in the high Andes. High temperature reduces plant productivity by affecting reproductive and vegetative growth. Knowledge about quinoa responses to temperature stress is scarce and there is a need to identify tolerant genotypes. To do this, a RIL population comprising ~ 290 genotypes was developed at BYU University (Provo, Utah) by crossing two parents regarded as contrasting for their responses to temperature: Ollagüe from the Chilean Highlands (sensitive) and G-205, from the Chilean lowlands (tolerant). Plants of this population were grown in two glasshouses under two temperatures: LT (temperatures cycled between 10 and 20 °C during the night/day) and HT (20 to 35 °C) at a facility associated to the Plant Stress Center, Shanghai, China. One 10 l pot was used per plant and there were three replicates by temperature treatment. Several nonlinear models were fitted to the Dev. Stage vs. time relationship. Complex responses to temperature were detected, with some genotypes showing a general increase or decrease in developmental rate with temperature, while others differed in their temperature responses only at the late reproductive stages. These responses could be exploited by breeders and agronomist to improve quinoa adaptation to specific environments.

Financing: Chinese Academy of Sciences (CAS)

15
DD782QQ
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Vitor Amorim-Silva

TTL Proteins are Safeguards of the Cellulose Synthase Complex during Abiotic Stress

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As sessile organisms, plants require mechanisms to detect and respond to adverse conditions, balancing growth and defense responses. Recent studies have shown that plant cell wall remodeling is essential for plants adaptation to environmental stress. Cellulose is the main component of the primary plant cell wall and is synthesized by the plasma-membrane localized cellulose synthesis complexes (CSCs). In Arabidopsis, the *TETRATRICOPEPTIDE THIOREDOXIN-LIKE (TTL)* gene family is composed by four members (*TTL1* to *TTL4*). Mutations in *TTL1*, *TTL3*, and *TTL4* genes cause impaired brassinosteroid signalling (Amorim-Silva, 2019) but also reduced growth under salt and osmotic stress due to defects in plant cell wall integrity, which are particularly visible in the presence of agents known to inhibit cellulose biosynthesis. Genetic and microscopy analyses indicate that *TTL* genes are essential in sustaining the stability of CSCs during salt stress at the plasma membrane. Due to the utmost importance of maintaining cellulose biosynthesis during stress conditions, we are aiming to uncover the mechanisms that TTL proteins play in this process.

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16
FJ722KP
Area: Plant Physiology and Ecophysiology
Tipo de presentación: video presentacion
Enviado por: Martín Acreche

Row spacing and sowing density as management strategies to improve radiation capture, radiation use efficiency and grain yield in chia (Salvia hispanica L.)

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Sowing density (SD) and row spacing (RS) are management strategies that modify crop canopy, radiation capture, radiation use efficiency (RUE) and grain yield. The objective was to determine the combined effects of SD and RS on radiation interception, RUE and grain yield generation in chia. Two experiments were conducted during 2017 and 2018 using a factorial design. In both years, the RS were 0.26 and 0.52 m, whereas the SD were 5, 9, 13 plants m^{-2} in 2017 and 9, 13, 17 y 21 plants m^{-2} in 2018. RS or the interaction between SD and RS did not affect grain yield and yield components. At higher SD, increases in grain yield were associated with increases in total dry matter without modification in harvest index. Grain number m^{-2}, grains per verticillaster and verticillaster m^{-2} also increased with SD. In the SD5 treatment, the increase of 1000-grain weight partially offseted the low grain number m^{-2}. The intercepted photosynthetically active radiation (PAR), adjusted by a logistic model, revealed that SD5 was the only treatment which did not reached maximum PAR interception (78%) leading to the lowest accumulated intercepted PAR and RUE. The treatment RS26 needed less thermal time to reach maximum interception and had higher accumulated intercepted PAR than RS52 according to the logistic model. Summarysing, the increase in SD generated increases in accumulated PAR and RUE that lead to higher growth and grain yield.

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17
KF695HJ
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: MARIA VERONICA ARANA

Cryptochromes are the dominant photoreceptors mediating heliotropic responses of Arabidopsis inflorescences

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Inflorescence movements in response to natural gradients of sunlight are frequently observed in the plant kingdom and are suggested to contribute to reproductive success. Although the physiological and molecular bases of light-mediated tropisms in vegetative organs have been thoroughly investigated, the mechanisms that control inflorescence orientation in response to light gradients under natural conditions are not well understood. In this work, we have used a combination of laboratory and field experiments to investigate light-mediated re-orientation of *Arabidopsis thaliana* inflorescences. We show that inflorescence phototropism is promoted by photons in the UV and blue spectral range (≤500 nm) and depends on multiple photoreceptor families. Experiments under controlled conditions show that UVR8 is the main photoreceptor mediating the phototropic response to narrowband UV-B radiation, and phototropins and cryptochromes control the response to narrowband blue light. Interestingly, whereas phototropins mediate bending in response to low irradiances of blue, cryptochromes are the principal photoreceptors acting at high irradiances. Moreover, phototropins negatively regulate the action of cryptochromes at high irradiances of blue light. Experiments under natural field conditions demonstrate that cryptochromes are the principal photoreceptors acting in the promotion of the heliotropic response of inflorescences under full sunlight.

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18
LG854QB
Area: Epigenetics, Chromatin, non-coding RNAs, RNA biology
Tipo de presentación: video presentacion
Enviado por: Agustín Lucas Arce

Transposonic siRNA-producing Inverted Repeats as regulators of gene expression through chromatin looping in Arabidopsis thaliana

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Transposons are known as genomic parasites and can account for more than 80% of plant genomes. However, there are several reported cases in which their effects, mainly on gene expression, have an adaptive or agronomic value. A transposon in the promoter of the sunflower HaWRKY6 gene is involved in a complex regulatory mechanism. It is an element with an inverted repeat (IR) which is transcribed and generates 24 nt siRNAs. These siRNAs target the IR region triggering DNA methylation and serving as an anchoring point for two short range chromatin loops. These loops regulate HaWRKY6 expression in a dynamic and tissue specific mode. We decided to explore similar mechanisms of gene regulation in the *Arabidopsis thaliana* genome. We found approximately 1200 genes near IRs, of which we focused on 350 presenting natural variation in transposonic IRs. We selected for the study Col-0 plants, mutants defective in DNA methylation and siRNA production, and two accessions with variation in IRs. On these plants we performed a CaptureC assay (a targeted HiC) to investigate the chromatin topology in these loci and the potential role of the IRs in the regulation of the genes. We further explored the mechanism by simultaneously analyzing gene expression (RNA-Seq), siRNAs molecules (sRNA-Seq) and DNA methylation (BS-seq). Our results show that a proportion of the selected genes are potentially regulated at the chromatin level by the IR near them.

19
BB535FF
Area: Systems, Synthetic, and Computational Biology
Tipo de presentación: Poster en formato PDF
Enviado por: Valentina Goytia Bertero

Transcriptome and proteome meta-analysis of tomato chaperone network during ripening

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Heat Shock Proteins (HSPs) are a super family of chaperones that have been characterized in different organisms. In plants, HSPs participate in the refolding of denatured proteins during physiological processes such as developmental changes and abiotic stress response. The aim of this work was to perform an integrative analysis from a bioinformatic and inferential approach based on protein-protein interaction (PPI) network building in *S. lycopersicum* cv. Micro-tom during fruit ripening. Expression data publicly available from two independent experiments at transcriptome and proteome levels were included. PPI networks were built using Cytoscape and the MCODE algorithm was applied to identify clusters. Each output cluster was further analyzed with the gene enrichment analysis tool, Fisher's exact test, $p \leq 0,05$ and Benjamini-Hochberg method. GO term enrichment analysis was conducted by the PlanRegMap tool. Our interatomic study allowed us to identify specific networks for each ripening stage of fruit development, evidencing that two clusters during advanced stages were over-represented by HSP families (HSP70 and HSP20), chaperones (Proteasome assembly chaperone) and common protein interactors associated with protein folding, protein synthesis and degradation, and response to stress (GST, ER auxin binding protein, TRP ripening regulated protein). These findings were detected for both levels of analysis: transcriptomic and proteomic, from two independent datasets. Finally, we found that some of these up-regulated chaperones show the presence of HSE motifs in their 5´UTRs. Our combined and inferential bioinformatics approach allowed us to integrate RNA, protein expression and co-expression levels of chaperones involved in cv. Micro-tom during fruit ripening.

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20
NM393TF
Area: Biotic Interactions
Tipo de presentación: video presentacion
Enviado por: Rocío Cecilia Arce

The role of chloroplast redox state in plant-pathogen interactions and its dependence on light

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Chloroplasts represent a central hub in plant metabolism as they are not only the major source of energy in the light, but also environmental sensors that communicate with the nucleus via a diversity of retrograde signals such as secondary metabolites and reactive oxygen species (ROS). These signals can modulate nuclear gene expression to regulate plant immune responses. Light also provides signals to deploy successful defensive responses against environmental stresses including pathogens. To unravel the role of chloroplast redox state and the influence of light in biotic interactions, we studied the response of tobacco plants expressing plastid-targeted cyanobacterial flavodoxin (Fld) facing diverse types of plant-pathogen interactions under photoperiod and darkness. Fld is an electron shuttle which decreases ROS accumulation when expressed in plastids, behaving as a general chloroplast antioxidant, and prevents over-reduction of the photosynthetic electron transport chain. In the light, transgenic plants exhibited a delay of symptoms under infection with different *Pseudomonas syringae* pathovars, relative to wild-type siblings. They showed lower ROS levels when challenged with the microorganisms, which correlated with a reduced occurrence of stromules and a decreased production of phytoalexins. Inoculated wild-type plants displayed a reprogramming of central metabolism under the biotic interactions that was ameliorated by Fld expression. No differences between lines were observed in the dark, indicating that the Fld effect was light-dependent. Our results suggest that ROS generated by illuminated chloroplasts have a significant role in the defensive strategies of plants against biotic stress.

21
FN452KM
Area: Abiotic Stress
Tipo de presentación: video presentacion
Enviado por: Josiane Argenta

Identifying Molecular Markers Associated with Tolerance to 2,4-D Drift Rate in Cotton Chromosome Substitution Lines

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The off-site movement of 2,4-D herbicide to adjacent non-target crops and other plants is a concern worldwide. The introduction of herbicide drift-tolerant cotton chromosome substitution lines (CS lines) into the cropping systems will allow farmers to have the option to plant a cultivar tolerant to possible 2,4-D drifts that could damage non-transgenic cotton and reduce its yield. In our previous study, we identified three cotton CS lines tolerant to the field rate of 2,4-D. The objective was to identify molecular markers associated with tolerance to 2,4-D drift rate in selected cotton CS lines. Six different cotton CS lines/varieties were applied at the 2-3 leaf stage with five different rates of 2,4-D (0, 5, 25, 50, and 75% of the recommended dose of 1,120 g a.i. ha^{-1}). Ten days after application, leaves of each treatment were collected, and DNA extraction was performed. DNA was subjected to PCR using ten microsatellite markers, visualized in 1.5% agarose gel, and DNA bands were scored using CrossChecker. Results show that line CS-45 presented amplification of a band in the range of 200-300 base pairs in the presence of primer BNL3255, whereas the other lines/varieties did not. Studies conducted in the greenhouse show that CS-45 is highly susceptible to the drift rate of 2,4-D, presenting approximately 45% herbicide injury. More research is needed to identify additional markers and possible genes related to 2,4-D tolerance. This information can be used as a genetic resource in cotton breeding programs to develop 2,4-D drift tolerant varieties.

Financing: Mississippi State University Cotton Incorporated

22
LT317FH
Area: Signal Transduction
Tipo de presentación: video presentacion
Enviado por: Denise Arico

TOWARDS CONSOLIDATING A MECHANISM WHEREBY CIP7, A MICROTUBULE ASSOCIATED PROTEIN, REGULATES HYPOCOTYL ELONGATION.

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Phosphorylation events provide a powerful mechanism of transducing light signals. In an early light-induced phosphoproteome study in *Arabidopsis thaliana*, we identified a protein that presents light-responsive dephosphorylation in the presence of photoactivated photoreceptors. This protein was previously reported to interact with the key repressor of photomorphogenesis COP1 and thus, it is potentially involved in early photomorphogenesis events. *In vivo* assays with transcriptional reporters presented the expression pattern in dark-grown seedlings; comprising cotyledons, upper hypocotyl and roots. GUS assays, RT-qPCR and translational reporters with native promoter revealed that light downregulates its expression. Several confocal microscopy assays with stably transgenic over-expressing lines showed localization to cortical microtubules. Indeed, the C-terminal domain containing the light-regulated phosphosite is necessary for microtubule association. We are studying the biological implications of this phosphosite by generating phospho-mimic/dead transgenic lines. Going further in post-translational regulation, treatments with MG132 suggested some partitioning between microtubules and nucleus when blocking proteasome activity in the light. To confirm this, we are currently generating the over-expressing lines in background *cop1-6*. Finally, it is known that photomorphogenic inhibition of growth is stronger in the upper one-half of the *Arabidopsis* hypocotyl, which is where light-signalling mutant hypocotyls are found to continue to elongate. As microtubules are key regulators of cell expansion and the upper hypocotyl is the more light-sensitive region of this embryonic shoot; we are evaluating phenotypes of CRISPR-CAS9 mutated lines regarding growth and microtubule dynamics. All these results lead to a hypothetical model that links the light-signalling pathway to microtubules regulation.

23
MS166FC
Area: Plant breeding
Tipo de presentación: Poster en formato PDF
Enviado por: Ana Arruabarrena Pascovich

Genome editing to break genetic linkage in tomato: high lycopene content and indeterminate growth

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In red tomatoes, fruit lycopene content is controlled, among other factors, by the decrease in *Lycopene Beta Cyclase* (*CYC-B*) gene expression. Spontaneous mutations like *old gold* (*og*) and *old gold crimsom* (og^c) generate non-functional CYC-B enzymes. Although these variants are used in breeding programs to increase red color and lycopene content, the mutations underlying this phenotype are only present naturally in genotypes carrying an additional mutation, *sp*, which is responsible for the tomato determinate growth habit. Since *CYB-B* and *SP* genes are closely linked and co-segregate, tomato cultivars that bare *og* or og^c mutations have also determinate growth. In Uruguay, most tomato cultivars used have indeterminate growth.
The goal of this work is to generate novel mutations in the *CYC-B* gene directly into indeterminate growth tomato lines using CRIPR/Cas9. Novel edited alleles were generated and characterized and E0 and E1 plants were phenotyped. Results suggest that plants carrying the novel mutations accumulate more lycopene in their fruit than the wild type. Foreign DNA-free plants were detected in E2 progeny and will be further genotyped for identification of possible off target mutations. Selected plants will be assessed for lycopene content and antioxidant capacity. These novel elite breeding lines will be readily available for INIA´s tomato breeding program to generate indeterminate cultivars with high lycopene content.

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24
MQ269LK
Area: Epigenetics, Chromatin, non-coding RNAs, RNA biology
Tipo de presentación: Poster en formato PDF
Enviado por: Jennifer Artunian

Bioinformatic analysis of het-siRNAs and phasiRNAs in the symbiotic interaction between Phaseolus vulgaris and Rhizobium etli

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Small RNAs (sRNAs) act as regulators of gene expression at transcriptional and post-transcripcional levels. One of the most important and characterized group of sRNAs are small interference RNAs (siRNAs), which are processed from double stranded RNA precursors to produce mature RNAs of 20-24 nucleotides that play different regulatory functions. In particular, heterochromatic siRNAs (het-siRNAs) are 23-24 siRNAs that mediate *de novo* DNA methylation and chromatin accessibility. In this work, we characterized het-siRNAs differentially regulated in the nitrogen-fixing symbiosis between common bean (*Phaseolus vulgaris*) and its symbiont *Rhizobium etli*. sRNA libraries from plants inoculated with the efficient strain of *R. etli* SC15, the less efficient strain 55N1 or mock-inoculated were sequenced and analyzed. We identify 236 het-siRNAs differentially accumulated in all pairwise comparisons. Twenty-five of these het-siRNA peaks are located near differentially regulated genes, which encode proteins with unknown functions (44%), transcription factors (16%) or non-coding RNAs (12%). The production of phased secondary small interfering RNAs (phasiRNAs) is triggered by the endonucleolytic cleavage of a miRNAs, leading to the regulation of target transcripts in *cis* or *trans*. Eighteen phasiRNAs were differentially regulated, whose putative targets include receptors, transcription factors and cytoskeleton components. Our results identified het-siRNAs and phasiRNAs, which might regulate the expression of genes that influence the outcome of the nitrogen–fixing symbiosis.

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25
PR378QC
Area: Epigenetics, Chromatin, non-coding RNAs, RNA biology
Tipo de presentación: Poster en formato PDF
Enviado por: Mishaneh Asgari

Flowering time regulation by the miRNA156 in the beet (Beta vulgaris ssp. maritima)

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Successful reproduction of the plants is assumed as a crucial challenge for meeting nutritional needs of growing human population. One of the significant changes in the plant's life cycle is its transition from vegetative to reproductive phase. Obviously, the flowering and bolting processes are influenced by many genetic and physiological factors. In this way, several main regulatory pathways and effective genes have been identified, so far. The age-dependent phenomenon as an effective pathway of reproductive transition phase is influenced by the miR172 and miR156 genes. In the present study, the miR156 sequence was identified in the sugar beet genome. First, the *miR156* gene was cloned into the over-expression construct from the *Beta vulgaris* genome and, then, was transferred to the beet explants. After the confirmation of transgenic plants, the transcript level of *miR156* gene, and its target genes (*SPL4* and *SPL9*) were evaluated in transgenic plants related to the control plants. Also, transgenic plants were studied in terms of flower phenotypic development, and root growth characteristics. By evidence evaluation, the research revealed that over-expression of *miR156* played an effective role in reduction of *SPL4* and *SPL9* genes' expression that resulted in flowering suppression in the Sea beet. According to the findings, it had also a suppression effect on the root growth in transgenic beets.

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26
KP515DN
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Priscila Ariane Auler

Global methylation in Oryza sativa (L) under recurrent and non-recurrent drought stress

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Drought stress is one of the major environmental challenges for plants especially under climate change, characterized by extreme events such as drought period alternates to intensive raining. The effects of drought vary depending on the plant growth phase and the occurrence of a previous stress, which can leave a memory of the stress. There are two main mechanisms for memory formation, that is, metabolic memory and epigenetic memory. Beside that, rice is one of the most important crops as the primary food source for more than half of the world's population and the drought may occur at any time of rice growth from vegetative stage to grain filling, and the reproductive stage is the most susceptible one. In this work, 5 – methylcytosine (%) analysis were used to elucidate the effects of drought in single stress event at vegetative or reproductive stage or recurrent at both stages in rice plants. Drought stress increased the total DNA methylation when applied at vegetative stage in single (32.98%) and recurrent event (25.91%) and decreased it in plants stressed only at reproductive stage (17.61%), respect to the levels measured in well-watered ones (21.54%). In conclusion, the greater genomic stability (higher levels of 5mC) is clearly evident in plants under drought only in the vegetative stage (V). In addition, it is clear that part of this stability remains when the plants were subjected to recurrent stress (V+R) because the methylation levels were higher than those of plants exposed to drought only at reproductive stage (R).

Financing: Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - Brazil (CAPES), Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) and the Fundação de Amparo à Pesquisa do Estado do Rio Grande do Sul – (FAPERGS).

32
HM619SG
Area: Developmental Biology
Tipo de presentación: video presentacion
Enviado por: Anna Backhaus

What determines the shape of the wheat spike?

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Grain-bearing spikelets are attached along the inflorescence of wheat (*Triticum aestivum*) in a distichous manner. But not all spikelets are equal: central spikelets produce more and larger grains than spikelets at the apical and basal end of the spike, resulting in a lanceolate shape (Bonnett, 1966). Various hypotheses exist for why apical spikelets gradually become smaller, for example, the reduced availability of resources (Whingweri, 1981). But thus far it remains a mystery why the most basal spikelets are rudimentary (i.e. of small size and failing to produce grain).

We found that this bi-directional gradient in spikelet productivity is established very early in development. Using novel low-input RNA-sequencing we found that, transcriptionally, larger differences exist across a spike than between the same sections from different developmental timepoints. Among the differentially expressed genes we identified the MADS-box transcription factor *VEGETATIVE TO REPRODUCTIVE TRANSITION 2* (*VRT2*) to be significantly upregulated in the basal sections compared to the apical sections at all timepoints. Furthermore, ectopic expression of *VRT2* in *T. polonicum* (Adamski, 2020) lead to the development of larger bract anlagen at floral transition and increased the number of rudimentary basal spikelets significantly in both field and glasshouse. The number of rudimentary spikelets however was affected by the environment, so we investigated the effect of sowing date, shading, and nitrogen on basal spikelet survival in the field. We hypothesise that failure to downregulate *VRT2* delays the transition from vegetative to floral development in basal spikelets, which in turn negatively affects spikelet ridge development.

33
MK137QM
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Sandra Baioni

Panicum coloratum seed priming (I): germination and seedling growth improvement.

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Panicum coloratum (perennial millet), forage with excellent aptitudes for Buenos Aires Southwest, still has low adoption by farmers due to the difficulties of its very small, with scarce reserves and dormant seeds. Seed priming could improve germination and establishment problems by a simple prehydration treatment before sowing, because priming triggers early events causing seed invigoration. The aim of this work was to evaluate priming effect on seed and seedling performance of *Panicum coloratum* var. *coloratum*. Priming treatments were: hydropriming (distilled water, 12 h at 25 °C); matripriming (Whatman N° 41 filter paper, 12 h at 25 °C) and osmopriming (2% $CaCl_2$ solution, 24 h at 30 °C). Seeds were air-dried for at least 1 weak and used for perform trails in a controlled temperature (25 °C/ 30 °C) and photoperiod (12 h) chamber. Germination percentage (GP), mean germination time (MGT) and seedlings growth were evaluated. It was observed that matripriming was the most effective treatment to increase GP (340 % than fresh seeds) and reduced MGT by a third. Seedling weight and length were 2,25 and 2 times greater, respectively. Hydro and osmopriming were slightly less efficient, GP was 5 and 10 percentage points lower, MGT was 10-30% higher and seedling growth was 50% in average lower than matripriming.

Financing: La financiación provino de los fondos otorgados por la Universidad Nacional del Sur, Secretaría General de Ciencia y Tecnología, mediante un Proyecto de Grupos de Investigación (PGI)

34
FJ235FJ
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Sandra Baioni

Panicum coloratum seed priming (II): establishment improvement and stress tolerance.

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Panicum coloratum have a poor field establishment and priming, a controlled pre-germination hydration, can solve this problem. During priming, considered a stresfull event, seeds acquire stress memory and cross tolerance. Seed vigour increase, and subsequently, seedlings and plants have a higher growth and stress tolerance. The objective of this work was to evaluate priming effect on seedling growth under water and saline stress during establishment. Priming treatments were: hydropriming (distilled water, 12 h at 25 °C); matripriming (Whatman N° 41 filter paper, 12 h at 25 °C) and osmopriming (2% $CaCl_2$ solution, 24 h at 30 °C). Seeds were air-dried and used for perform greenhouse establishment essays. Seeds were sown in containers with soil; watered treatments were Control (without water stress), 50% and 25% field capacity (FC). Saline treatments were: 3; 6; 9 and 12 dS m^{-1} (NaCl solutions). Hydro and matripriming were the most effective treatments on seedling growth: seedling root length was 100 % higher, even under stress conditions; seedling dry weight was significantly higher in primed treatments without stress (50 to 120% higher), and under stress had higher growth performance (up to 300%). Seedling survival was 100% in priming treatments, while in unpriming treatment was 15% lower. Osmopriming was little less efficient, 10-25% lower. Water potential decrease was significant in unprimed treatment while in priming treatments the decrease was only significant with 25% FC and salinity greater than 9 dS m^{-1}. *P. coloratum* showed greater tolerance to salinity than to water deficit.

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FB455MF
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Mercedes Barat Carnino

Sowing date affects soybean N fixation because of soil nitrate changes.

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In many soybean production systems sowing date expands for several months. In the Argentinean central region early sowing dates are showing maximum yields, but their consequences for crop N uptake and biological nitrogen fixation (BNF) are not known. High BNF rates are necessary to improve soil N balances, and our general objective is to identify management options for maximizing BNF and yield. We hypothesize that BNF is maximum at intermediate sowings because BNF in early and late sowings is limited by early low soil temperatures or high soil nitrate concentrations, respectively. Four genotypes (maturity groups (MG) IV and V) were tested under September to December sowing dates in Santa Fe, and a N fertilizer treatment at sowing was added in all sowing date x genotype combinations (100 kg N ha^{-1}). Seed yield and total N uptake were affected by sowing date and genotype, but not by the N treatment. Both variables followed similar quadratic responses; MG V genotypes showed maximum yields and N uptake in the earliest sowings, while MG IV cultivars reached maximum values in intermediate sowings. However, delaying sowing date always decreased BNF (average 0.22% day^{-1}). Nitrogen fertilization reduced BNF 15% across sowing dates and genotypes. Results highlighted that yield and total N uptake responded similarly to sowing date, and not to N fertilization. The linear decline in BNF with delayed sowing dates, instead of an optimum response, support the concept that soil nitrates are the main driver of soybean BNF instead of temperature in these sowing dates.

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36
JM898FC
Area: Biotechnology, Research Tools, Resources
Tipo de presentación: Poster en formato PDF
Enviado por: Anabel Maria Ines Barbosa

Effect of storage on the viability of tree tomato seeds detected by Tetrazolium assay.

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The Tetrazolium test is a destructive test that allows us to differentiate viable and non-viable seeds because the salt is reduced by taking electrons from the respiratory chain of living tissues. Mature fruits of *Solanum betaceum* Cav. were collected in April of 2021 and were stored in paper bags at room temperature. The objective of this work was to determine the percentage of viability of the seed lot of *Solanum betaceum* Cav. The seeds were placed for 24 hours in a beaker with water at room temperature, then a cut of approximately ¼ of its length, after that the seeds were placed in 0.1% tetrazolium solution, and incubated for 24 h at room temperature in the dark. The seeds were then rinsed with water, opened in half, and observations made with the use of a stereomicroscope (Zeiss Stemi 1000). Five replications of 10 seeds each were performed. Those that were fully stained were considered viable seeds, and those that were not stained or partially stained as non-viable. Eighty-six percent of the sample were viable seeds. Therefore the seeds of *Solanum betaceum* conserve high viability at three months of harvesting at stored conditions described.

37
NL493KJ
Area: Biotechnology, Research Tools, Resources
Tipo de presentación: Poster en formato PDF
Enviado por: Anabel Maria Ines Barbosa

Comparison of the effect of gibberellic acid on Solanum betaceum seeds in two different culture media.

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The tomato tree *Solanum betaceum* (*S. betaceum*), is species whose fruit has a high potential for genetic improvement, also provides a high concentration of ascorbic acid and antioxidants. The objective of this work was to determine the viability of the seeds in different culture media and the effect of gibberellic acid on it. Fruits of *S. betaceum* were collected in April 2021 in San Lorenzo, Salta, Argentina. The seeds were washed for 10 minutes with running tap water and detergent, using a magnetic shaker, then rinsed three times. In a laminar flow chamber, the seeds were disinfected with 70% alcohol for 1 minute, followed by 5% NaOCl for 5 minutes, and rinsed three times with sterile distilled water. Subsequently, one seed per culture tube was sown with MS or GD medium with gibberellic acid (GA) in the following concentrations: 0, 0.15, 0.2, 0.25, 0.3, 0.4, 0.5 ppm. Each treatment had 12 experimental units. The tubes were taken to the growth chamber, with a photoperiod of 12 h and a temperature of 27º C, the tests remained for 30 days. Germination data were taken every 7 days. The variables analyzed were germination start time and germination percentage. Statistically significant differences were found between the treatments for the germination percentage ($H = 30.67$; $p = 0.0008$). Treatments with GD medium had a germination start time of 14 days, while MS treatments started germination 22 days after sowing. The GD medium decreases the germination start time.

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MF785SD
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Karolaynny Barbosa

Plant growth and starch mobilization in Citrus sinensis under magnesium deficiency

Plant growth and starch mobilization in Citrus sinensis under magnesium deficiency

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Photosynthetic processes within chloroplasts require substantial amounts of magnesium (Mg) and which role is crucial for citrus fruit yield and quality, related to sugar transport in trees. The characterization of nutritional and biochemical statuses were evaluated in Valencia Americana sweet orange branches [C. sinensis (L.) Osbeck], with the following characteristics: symptomatic branch (vegetative branch with visual symptoms of Mg deficiency) and asymptomatic branch (vegetative branch without symptoms of Mg deficiency). Such characteristics were evaluated in trees exhibiting three flushes of growth (assessed individually) with 5 replications of two branches per tree. Our results demonstrate that the effects of Mg deficiency negatively influenced the development of new growth flushes. Mg deficiency was not evenly distributed in the canopy, with branches demonstrating different levels of Mg on the same tree. The Mg content in leaves of symptomatic branches was 35% lower than in asymptomatic branches. Branches with Mg deficiency symptoms exhibited a reduction in leaf area of the 3rd flush of growth (youngest), when compared to the same of asymptomatic branches. The leaves of the 1st growth flush (oldest) of the symptomatic branch (leaves with visual symptoms) exhibited a higher concentration of starch than the leaves of the others flushes. Unlike the leaves, the woody part of the asymptomatic branches exhibited higher starch contents than the symptomatic branches. Leaves with symptoms of Mg deficiency demonstrated a protective mechanism in relation to photosynthetic energy dissipation as well a low efficiency of photosystem II.

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39
MH924MF
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Catalina Barbot Perera

Characterization of a soybean aminotransferase and it's potential role in molecular breeding to enhance drought stress

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Soybean is one of the most important crops worldwide in terms of productivity and relevance in the international market. Water deficit is one of the major stress factors that determine grain production.

Tolerance to water deficit is a complex feature, which has had limited success in soybean breeding programs. Numerous genes have been identified whose overexpression increases tolerance to this stress condition.

Faced with water stress, plants may display an array of responses, which allow them to cope with adverse environmental conditions. Metabolic reprogramming is one of the most general responses to abiotic stress. Various studies show the importance of the accumulation of amino acids such as proline and branched chain amino acids (BCAA), in tolerance response to abiotic stress in different plant species.

Changes in the concentration of BCAAs appears to be determined by the expression of branched-chain amino acid transferases (BCAT) that participate in their synthesis and degradation.

Our work focused on the functional characterization of a soybean BCAT, and it´s role in BCAA metabolism and abiotic stress tolerace. We have generated Arabidopsis lines overexpressing BCAA fused to GFP, in order to determine the subcellular localization of the enzyme. To elucidate the biological role of BCAT in responses to water deficit, we generated Arabidopsis lines overexpressing BCAT. The resulting overexpressing lines will be evaluated phenotypically under stress and optimal growth conditions.BCAA content will be analyzed in the transgenic overexpressing lines in order to assess the role of BCAT in the metabolism of this type of amino acids.

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40
CB476QN
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Pamela Barengo

EFFECTS OF Bacillus Safensis S9 ON SOYBEAN PLANTS (Glycine max L. Merrill) UNDER SALINITY

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The increase in soils salinity causes important losses in crops yields. Plant growth-promoting bacteria (PGPB) are alternative treatments to alleviate this abiotic stress. In this work, we evaluate the effects of *Bacillus safensis* S9 on soybean plants grown under salinity. Nidera® seeds genotype were treated with S9 grown in Lysogeny Broth medium (LB), overnight (ON), diluted to optical density (OD) of 1 during 5 minutes. Control plants were treated with LB only. Plants were grown in 5 L pots with sand and irrigated with NaCl solution from stage V2 (only salt treated plants) in a greenhouse. Water Potential (WP, upper and lower canopy) and Water Use Efficiency (WUE) were measured in R2.5 stage and membrane stability (*Ion Leakage*) in R5 stage. Statistical analysis was performed using Infostat® Software. Salinity decreased WP in order of 60 % and increased WUE in 52.8%. Plants under 0 mM increased WUE in 132% by effect of bacterial treatment . An increase of cell membranes damage was observed in presence of 75 mM NaCl related to 0 mM in both bacterial treatment (92%). In conclusion, the treatment with S9 had a negative effect on WP both control and stressed plants. Bacterial treatment increased WUE in control plants, while there were no changes under salinity. No differences in cell membrane stability was observed in the 4 treatments. *Bacillus safensis* S9 inoculation did not help plants to recover from saline negative effects. New approaches will be necessary to propose *Bacillus safensis S9* as an effective inoculant.

Financing: ASACTEI, ANPCyT, CAI+D

41
FN375QN
Area: Plant Hormones
Tipo de presentación: Poster en formato PDF
Enviado por: Javier Orlando Barone

Salicylic and jasmonic acid-mediated defence genes regulation in leaves of flooded tomato plants

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Given the increase in flooding events and the fact that multiple stresses generally occur simultaneously, it is crucial to understand how partially submerged plants respond to biotic stresses. Flooding causes changes in hormonal interaction during adaptive responses. The objective of this study was to assess flooded tomato plant responses to biotic stress. For this, 30 days old tomato plants were subjected to flooding for 6 days and the concentration of salicylic (SA) and jasmonic acid (JA) was determined in leaves. In addition, the expression of SA responsive genes induced by pathogens such as *NONEXPRESSOR OF PATHOGENESIS-RELATED GENES 1* (*NPR1*), *PATHOGENESIS-RELATED GENES* (*PR1a* and *PR2a*), and the expression of JA responsive genes, induced by herbivores, such as *PROTEINASE INHIBITOR* (*PI-I* and *PI-II*) was analysed. The expression of the *ALLENE OXIDE SYNTHASE* (*AOS*) gene, involved in JA biosynthesis, was also measured. Flooding increased SA concentration along with the upregulation of *NPR1*, *PR1a* and *PR2a* whereas a decrease in JA content was observed. Consistently, *PI-I* and *AOS* expression levels were reduced while the expression of *PI-II* did not change in leaves of flooded plants. These data suggest that flooding may prepare plants to pathogen resistance at the expense of increased susceptibility to herbivores.

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TQ233NN
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Claudio Baroni

Effect of selenite on growth and water status in broccoli seedlings transplanted under saline stress

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Salinity has negative effects on horticultural crops; affecting growth, development and quality. On the other hand, it is known that selenium is beneficial for certain plant species; since it provides protection under stress conditions such as salinity. Previously, we have been able to determine that the application of 12 μM of sodium selenite improves the quality of broccoli seedlings by increasing root activity. The objective of the work was to evaluate the effect of selenite on growth and water status in broccoli seedlings transplanted under saline stress. The trial was conducted in a plant chamber and treatments consisted of continuous irrigation with 12 μM selenite in 50% Hoagland, from sowing and for 21 days. Subsequently, the seedlings were transplanted into 1 L pots containing inert substrate and were watered with nutrient solution plus the addition of NaCl (0 and 100 mM). After 30 days of saline treatment, the aerial part of the plants was collected to analyse growth and water status. The results showed that salinity significantly reduced the height and number of leaves; however, no effect of selenium was observed ($p>0.05$). Both salinity and selenium treatment did not modify the chlorophyll index. In contrast, only saline treatment increased electrolyte leakage ($p<0.05$). Regarding the water status, the treatment with selenium increased both the water potential and the leaf relative water content under saline stress situation, compared to controls ($p<0.05$).Therefore, the application of selenite during the production of broccoli seedlings could be useful to increase the tolerance to saline stress.

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43
TS835FG
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Alejandra Tamara Barraza

Evaluation of emergency of Paulownia fortunei var. Mikado from seed submitted to pre-germinative treatments

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Paulownia fortunei is a highly heliophyte species, it does not germinate in dark conditions (Hartmann & Kester, 2014), and the emergency varies from 15 to 60 days in seedling nursery (Zevallos Fernández, 2018). The objective was to evaluate the emergence of seedlings, whose seeds were subjected to different pre-germinative treatments. The pre-germinative treatments involve imbibition of seeds (48h) at different temperatures: 4°C (c) and 24°C (e). The sowing was carried out in a substrate composed of mulch:vermiculite (3:1). The photoperiodic conditions for storage were: (d) dark (24h) or (l) light (13,35h) at 24ºC and 53%HR. Four treatments resulted: T1 (cd), T2 (cl), T3 (ed) y T4 (el). The fungicide Almacigol was applied as a palliative treatment. The test lasted 21 days and every 3 days data were taken to evaluate the emergence percentage (%E), seedling length (Sl), contamination percentage (%C) and time necessary for first seedling emergence (TNES). The %E, Sl, %C and TNES were analyzed with the Kruskall Wallis test (%5) using Infostat. T3 reached higher %E (34.62%) followed by T4 (26.92%) and showed statistically significant differences (H=11.40; p=0.0001). The highest Sl was presented by T1 (h=3.16 cm/seedling) followed by T4 (h=1.57 cm/seedling) (H=67.37; p<0.0001). The lowest TNES was 7 days for T2 and T4 with 10 days (H=0.11; p=0.54). At the end of the experience, a 0.38%C was obtained. The results differ from those expressed by Hartmann and Kester and Zevallos Fernández for the photoperiodic conditions in germination and onset of emergence, respectively.

44
PK711GG
Area: Developmental Biology
Tipo de presentación: Poster en formato PDF
Enviado por: Virginia Barrera

SCL28 promotes endoreplication and cell expansion in Arabidopsis by activating a group of SIAMESE-RELATED cyclin-dependent kinase inhibitors.

SCL28 promotes endoreplication and cell expansion in Arabidopsis by activating a group of SIAMESE-RELATED cyclin-dependent kinase inhibitors.

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Plant organ growth initiates with proliferating cells generated by the mitotic cell cycle (MCC). Then, cells enter a expansion and differentiation program. During the later stage, cells often switch to an alternative cell cycle named endoreplication (ER), in which cells replicate their DNA without progressing through mitosis nor cytokinesis.

The transition from MCC to ER involves regulatory mechanisms that specifically inhibit mitotic cyclin/cyclin-dependent kinase (CDKs) complexes causing cells to oscillate between S and G1 phases for a defined period. One of these regulatory mechanisms involves a family of CDKs inhibitors named *SIAMESE-RELATED (SMR).* These proteins have been reported to trigger the transition from the MCC to ER by its association with specific CDKs.

SCL28 is a transcription factor that is expressed preferentially in G2/M cells in the root meristem and promotes progression through these phases of the cell cycle. From a transcriptome analysis of *SCL28* mutants we found that several *SMRs* genes were downregulated in the mutant. In this work we characterize the regulation of *SMRs* by SCL28 and its role in promoting MCC to ER transition, cell expansion and differentiation.

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SS142GP
Area: Developmental Biology
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Enviado por: Virginia Barrera

SCL28 promotes endoreplication and cell expansion in Arabidopsis by activating a group of SIAMESE-RELATED cyclin-dependent kinase inhibitors.

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Plant organ growth initiates with proliferating cells generated by the mitotic cell cycle (MCC). Then, cells enter a expansion and differentiation program. During the later stage, cells often switch to an alternative cell cycle named endoreplication (ER), in which cells replicate their DNA without progressing through mitosis nor cytokinesis.

The transition from MCC to ER involves regulatory mechanisms that specifically inhibit mitotic cyclin/cyclin-dependent kinase (CDKs) complexes causing cells to oscillate between S and G1 phases for a defined period. One of these regulatory mechanisms involves a family of CDKs inhibitors named *SIAMESE-RELATED (SMR).* These proteins have been reported to trigger the transition from the MCC to ER by its association with specific CDKs.

SCL28 is a transcription factor that is expressed preferentially in G2/M cells in the root meristem and promotes progression through these phases of the cell cycle. From a transcriptome analysis of *SCL28* mutants we found that several *SMRs* genes were downregulated in the mutant. In this work we characterize the regulation of *SMRs* by SCL28 and its role in promoting MCC to ER transition, cell expansion and differentiation.

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46
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Tipo de presentación: Poster en formato PDF
Enviado por: Andana Barrios

Long noncoding RNAs: a role in modulating the activity of partner transcription factors in Arabidopsis thaliana?

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Plants survival relies on their fascinating capacity for adaptation to the changing environment. Plant developmental plasticity relies on transcriptional reprogramming, which largely depends on the activity of transcription factors (TFs). In this project, we aim at determining the role of the *Arabidopsis thaliana* TF NF-YA2 (Nuclear Factor A 2) in root development in response to external stimuli. To this end, the combination of RNA-seq and ChIP-seq approaches revealed that NF-YA2 directly regulates key genes involved in water deprivation and lateral root development.

Considering that the binding affinity of the mammalian TF NF-YA to its apoptosis-related targets is modulated by a long noncoding RNA (lncRNA) called *PANDA*, we searched for NF-YA2-associated lncRNAs in Arabidopsis. RNA-IP-seq allowed us to identify a subset of lncRNAs that could bind to NF-YA2, which we named *AtBAMBOOs* after their counterpart in mammals. *AtBAMBOOs* appeared as regulated by environmental stresses and differentially regulated during lateral root development, underlying their role in the plant capacity to integrate environmental cues. Ongoing experiments will allow us to decipher the molecular basis of NF-YA2-*AtBAMBOOs* interaction and the related developmental outputs.

47
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Area: Evolution, Ecology, or Genetics
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Enviado por: Gian Barros

Quillaja saponaria plastome revisited: sequence update and re-annotation

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Quillaja saponaria is an important South American woody species in the production of vaccine adjuvants, from triterpene saponins produced by its specialized metabolism. Few genomic resources are available for this species. Among them is the assembly of its chloroplast genome (published in 2019;NCBI accession MH880827), showing an estimated size of 132,854 bp, considerably smaller than that identified in species of the same order, such as *Suriana maritima* (163.747 bp) and *Polygala japonica* (165,439 bp). The reduced size might indicate assembling errors due to the use of inappropriate genome assembling tools. To test our misassembly hypothesis, the objective of this study was to re-assemble and re-annotate the *Q. saponaria* chloroplast using assemblers and strategies specially developed for the recovery of plastid genomes. Illumina MiSeq sequencing data was assembled using a *de novo* approach in NOVOPlasty v4.3 and by mapping against reference genomes in the Geneious software. We obtained a complete chloroplast sequence of 160,393 bp, with 86 genes, of which 37 are tRNAs (33 in the original assembly) and eight are rRNAs (four in the original assembly). Our version is highly similar to NCBI accession NC_047356.1, which corresponds to an unannotated chloroplast assembly deposit from another specimen of *Q. saponaria*. Our study highlights the importance of the correct selection of tools and strategies for assembly and sequence annotation using small reads and demonstrates that mixed assembling strategies can improve the assembly and annotation of the *Q. saponaria* chloroplast genome.

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48
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Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Carlos Guillermo Bartoli

Influence of incident irradiance on the growth of patagonian cypress seedlings in nursery

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Patagonian cypress (*Austrocedrus chilensis (D. Don) Pic. Serm. et Bizzarri*) is a native conifer of the sub-antarctic forest, which is considered an isohydric species with a strong stomatal control. This characteristic might be the cause of the low rate of its initial growth, even in the nursery under optimal conditions of irrigation, fertilization and temperature control. Seeking to understand the effect of irradiance on this behavior, the objective of this work was to determine how different shading dynamics through gaps, strips or diffuse light treatments influence the development of Patagonian cypress seedlings in the nursery. We worked under two specific hypotheses: (1) High levels of irradiance cause damage of photosystems producing an inhibition of photosynthetic activity; (2) High levels of irradiance decrease photosynthesis indirectly through stomata closure. Patagonian cypress seedlings, were grown at three shading dynamics (gaps, striped, and diffuse) and contrasted with full incident light, evaluating the effect of these treatments on morphological variables and allometric relationships. Higher growth was observed in plants under the gaps and the strips irradiance treatments, maintaining good allometric relationships in both cases. In addition, photosynthesis was analyzed through the measurement of modulated fluorescence of chlorophyll and photosynthetic oxygen evolution in a CO_2 saturated atmosphere. No differences were observed in this complementary analysis, suggesting that the light environment does not restrict plant growth through increased photoinhibition or decreased potential photosynthesis. To further test the stomatal limitation induced by light treatments, the measurement of ^{13}C concentration in leaf tissues is now in progress.

49
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Area: Developmental Biology
Tipo de presentación: Poster en formato PDF
Enviado por: Sandy Bastos Martins

Pollination type does not influence seed germination rates in Cleomaceae species

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Members of Cleomaceae have been studied mainly regarding its transitional C_3-C_4 photosynthetic metabolism and floral characteristics. Nonetheless, little is known about pollination types and its influence on seed germination. In this sense, the aim of this work was to verify the influence of pollination type on the rate of seeds germination. For this, 20 specimens of Brazilian Cleomaceae were used. Both herbaceous and shrubby individuals, belonging to the genera *Cleoserrata*, *Gynandropsis* and *Tarenaya* (series: Spinosa I/II; Aculeatae; Paviflorae and Rosea) were studied. The studied species are self-compatible, and various types of pollination may occur. Accordingly, five pollination tests were carried out. Mature fruits from each tagged flower were harvested and seeds placed to germinate in a growth chamber (25°C day/19°C night, relative humidity of 60%). Interestingly, the type of pollination had no effects on seeds germination. Members of *Tarenaya* serie Spinosa I exhibited higher germination rates (~65%), followed by *Gynandropsis* and *Cleoserrata* (38%), Spinosa II (35%) and Aculeatae (25%). This results can be explained since many mature seeds enter a period of inactivity, or extremely low metabolic activity (dormancy). Accordingly, this study revealed that Cleomaceae fresh seeds exhibited a physiological dormancy. However, further experiments using greater number of taxa and longer time intervals of storage, as well others treatments (alternative temperatures, GA_3, KNO_3, leaching, pre-chilling and soaking) are required to an in deep understanding of the variability in germination rates observed in Cleomaceae species.

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50
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Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Marina E. Battaglia

Developmental plasticity in Arabidopsis thaliana under combined cold and water deficit stresses during flowering stage

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In nature, plants are exposed to multiple and simultaneous abiotic stresses that influence their growth, development, and reproduction. In the last years, the study of combined stresses has aroused the interest to know the physiological and molecular responses, because these new stress conditions are probed to be different from the sum of the individual stress. We are interested in the study of the acclimation of plants growing under the combination of cold and water deficit stresses prevalent in cold-arid or semi-arid climates worldwide. We hypothesized that the reproduction of the acclimated plants will be compromised and affected. *Arabidopsis* plants were submitted to long-term combined stress from the beginning to the reproductive stage, when floral bud was visible, until the silique development.

Our results demonstrate severe morpho-anatomical changes after acclimation to combined stress. Inflorescence stem morphology was altered having a delayed bolting and a limited growth. Flowering and silique formation were delayed, and a higher size in the corolla and the petals was observed. Flower and silique number were severely diminished as a result of combined stress, unlike acclimated plants to individual cold stress. These traits were recovered after deacclimation to optimal conditions and plants achieved similar silique production as control plants. The long-term stress results suggest that there is not a single dominant stress, but there is an alternating dominance depending on the structure or the plant stage development evaluated.

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51
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Enviado por: Victoria Bauer

Participation of glutathione peroxidases in ferroptotic cell death in Arabidopsis thaliana.

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Recently, we described an oxidative and iron dependent mechanism of regulated cell death in Arabidopsis which we referred to as ferroptosis, due to its similarities to a mechanism previously described in animals. Specifically, we found that a 10-minute heat shock (HS) treatment induces cell death in *Arabidopsis thaliana* root hairs, which is inhibited by pre-incubation with the canonical ferroptosis inhibitors Fer-1 (a lipophilic antioxidant) and CPX (an iron-chelating agent). The cellular death induced by HS is characterized by depletion of intracellular glutathione and ascorbic acid, accumulation of cytosolic and lipid reactive oxygen species (ROS), cytoplasmic retraction and mitochondrial shrinkage. Here, we studied the participation and regulation of glutathione peroxidases (GPXs), which are able to detoxify lipid peroxides and have a central role in animal ferroptosis. Our studies showed that HS results in a reduction of GPX activity and in lower levels of *GPX5* and *GPX6* mRNAs, which are the two prevalent isoforms present in roots. These results are similar to what was observed in animal ferroptosis. To determine if *GPX* mutants showed increased ferroptosis sensitivity, we performed a thermotolerance essay in four T-DNA-insertion mutant lines for *GPX* (*gpx2, gpx3, gpx4* and *gpx8*). However, no significant differences between mutants and wild type plants were observed. The analysis of putative post-translational modification (PTM) motifs in GPX6 revealed the existence of diverse potential sites of phosphorylation, glycosylation and myristylation, which might be potential targets for regulation.

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52
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Area: Abiotic Stress
Tipo de presentación: video presentacion
Enviado por: Melike Busra Bayramoglu Karsi

A PERSPECTIVE ON THE DISTRIBUTION OF LEAD IN THE ENVIRONMENT AND THE DYNAMIC ROLE OF MEMBRANE TRANSPORTERS FOR PHYTO-REMEDIATION

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Due to fast pace urbanization, mechanization, and industrial activities, heavy metals are accumulating in our environment at accelerated rate. Lead has a range of pollution sources to the environment, both spatially and temporally, based on a variety of environmental media, including peat, lake sediments, ice and snow cores, forest mosses and herbarium archives, as well as atmospheric aerosols. The Pb (lead) is the second most harmful pollutant as a heavy meatal after arsenic which poses high risk to plant, animal and human health. Since Pb is non-biodegradable and it can persist in our eco-systems. Root growth inhibition, stunted plant growth, blackening of root system and degradation of chloroplast thereby interrupting photosynthesis leads to poor plant productivity in terms of biomass or yield. Plant have developed strategies at molecular, biochemical level which can cope to hazardous material like Pb. The insight into such molecular mechanisms can facilitate to reduce the risk of such notorious heavy metal by phytoremediation or bioremediation strategy. Excess emissions of trace metals in the form of particulates pollute the surface environment and also contribute to air pollution as they enter the air or may be carried into rivers and the sea via urban runoff. That is why urban runoffs degrade the quality of environmental aquatic systems at the same time lead to increasing contaminants in aquatic organisms through bioaccumulation and bio-magnification, potentially causing elevated trace metal concentration in the food chain.

Keywords: Membrane transporters, phytoremediation, metal transport, heavy metal pollution, lead, Pb contamination

53
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Area: Developmental Biology
Tipo de presentación: Poster en formato PDF
Enviado por: Carolina Bellino

FUNCTIONAL CHARACTERIZATION OF GZF1 DURING BRANCHED INFLORESCENCE DEVELOPMENT

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The grass family is characterized by their inflorescence architecture, which final form is the result of a balance between the ability of the axillary meristems to form branches or terminate in spikelets. GRASS ZINC FINGER 1 (GZF1) is a *Cys2-His2-type zinc finger* transcription factor that seems to influence the fate of axillary meristems at early stages of inflorescence development. The aim of this work is to explore the molecular and functional divergence of GZF1 grass homologs. By comparison of *C2H2 zinc finger* peptide sequences available on databases, we observed a partial conservation of the sequences towards the C-terminal. As a result of phylogenetic analysis, we identified two successive duplications of GZF1 at the grass family origin which generated three unique grass sequences lineages. In order to generate knowledge on GZF1 expression patterns and its biological role, we performed experiments with GZF1 homologs of three PACMAD species (*Zea mays, Setaria viridis, and Cenchrus echinatus*). Expression experiments showed that GZF1 homologs are preferentially expressed in inflorescence with developing branches and their expression decays at late stages of inflorescence development. Transgenic *Arabidopsis thaliana* plants that overexpress GZF1 homologs showed a highly branched phenotype in comparison with wild type plants. We observed the presence of sterile branches similar to bristles of the Setaria inflorescence. These results suggest that homologs of GZF1 may regulate the fate of apical and axillary meristems in transgenic Arabidopsis plants.

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Area: Cell Biology
Tipo de presentación: Poster en formato PDF
Enviado por: Francisco Benitez

IDENTIFICATION OF SYT1 INTERACTORS CONNECTS CALCIUM SIGNALING, ENDOPLASMIC RETICULUM BENDING, PLASMODESMATA AND MEMBRANE CONTACT SITES

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Synaptotagmin1 (SYT1) is an *Arabidopsis thaliana* protein essential for tolerance to abiotic stress (Schapire et al., 2008; Pérez-Sancho et al., 2015; Ruiz-Lopez et al., 2020). SYT1 forms endoplasmic reticulum-plasma membrane contact sites (ER-PM CS), microdomains conserved across eukaryotes where protein tethers maintain the membranes of these organelles in close apposition without fusing. The short distance between membranes facilitates processes such as ion and lipid transport (Pérez-Sancho et al., 2016). Thus, SYT1 transports diacylglycerol from the PM to the ER during abiotic stress to assure PM integrity (Ruiz-Lopez et al., 2020). Usually, protein complexes form the core of contact sites. In particular, SYT1 forms dimers with SYT1, SYT3, SYT5 and CLB1, all members of the SYT family and EPCS tethers (Lee et al., 2020; Ruiz-Lopez et al., 2020). We found that SYT1 interacts with proteins involved in different cellular processes by non-targeted proteomic approaches. SYT1 interacts with reticulons, ER-resident proteins responsible for ER curvature, crucial for ER morphology and lipid transport at ER-PM CS (Collado et al., 2019). Additionally, SYT1 interacts with ECAs, Ca^{2+}-ATPases located at the ER membrane. SYT1 also interacts with sterol methyltransferases, key enzymes in the route of sitosterol and stigmasterol biosynthesis. The homeostasis of the sitosterol and stigmasterol is crucial for the tolerance to wound, heat and bacterial stress presumably by affecting PM fluidity. MCTPs, plasmodesmata-exclusive proteins are also SYT1 interactors (Brault et al., 2019). We are now investigating the role of SYT1 in these processes using biochemical, genetic and cellular biology approaches.

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55
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Area: Signal Transduction
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Enviado por: Ignacio Beramendi
Phospholipase C role in stomatal development.

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Stomata consist of two guard cells (GC) around a pore and act as turgor-operated valves for gas exchange and transpiration in plants through the formation and regulation of stomatal pore.
Phosphoinositide-specific phospholipases C (PI-PLC) is a gene family with 9 members (*PLC1*-*PLC9*) in *Arabidopsis thaliana*. PLCs are known to participate in diverse signaling processes in plants, embryogenesis, root development and plant pathogen interaction. In Arabidopsis, PLCs 3, 5 and 7 were reported to modulate stomatal movement, however there is no information about PLC role in stomatal development.
Stomata are formed by asymmetric divisions of meristemoid stem cells forming meristemoid (M), and then meristemoids forming guard cell mother (GMC). Finally, the GMC are divided symmetrically to generate two GC. These processes of stomatal differentiation are regulated by different transcription factors, including SPEECHLESS, MUTE, FAMA, etc.
In the present work we evaluate the role of *PLC5* in stomatal development. We analyzed the variations in the key stages, M, GMC and GC among Arabidopsis wild type (wt), *PLC5* knockdown mutant (*plc5*), and *PLC5* overexpressing lines (OE-*PLC5*) plants. We have also analyzed the expression pattern of PLC5 in the different development stages, and we compare it with the expression levels of the key transcription factors controlling stomatal development. The presented data indicate that OE-*PLC5* has alteration in stomatal pattern at the GC stage, suggesting that PLC5 might be involved in the process of stomatal development.

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JC464DH
Area: Plant breeding
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Enviado por: Rick Berentsen

VERNALIZATION REQUIREMENT IN GLOBE ARTICHOKE

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Early production is an important breeding objective for globe artichoke (*Cynara cardunculus* var. *scolymus*). Previous studies indicate that the early-bolting trait in artichoke is largely related to a vernalization requirement. However, most studies have been performed in the field, under non-controlled conditions, or by applying a vernalization treatment only during part of the growing cycle. To determine the effect of vernalization on bolting time under controlled conditions during the whole vegetative stage, we performed two experiments in which genotypes with different degrees of earliness were subjected to the presence or absence of vernalizing temperatures (<10°C). In the first experiment, using an early, an intermediate and a late bolting line, non-vernalised plants of the late genotype bolted about 50 days (or 21%) later than vernalized ones, which experienced 698 hours at <10ºC. However, the effect of vernalization was not significant in the early and intermediate lines. In an identical experiment with four clones, one early, one intermediate and two late bolting, the effect of vernalization was measured by scoring the developmental stage of the shoot apical meristem (SAM). The absence of vernalization, as compared to the control (715 hours < 10°C), delayed the transition to a pointed meristem by 8 days (or 5%) in the late and intermediate bolting clones while having no effect on the early clone. These results indicate the presence of a vernalization requirement specifically in the late bolting genotypes. Samples have been taken for a subsequent RNA-seq study to identify genes involved in vernalization perception.

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RH654NB
Area: Biotic Interactions
Tipo de presentación: Poster en formato PDF
Enviado por: Valeria Bernardo

Antagonistic activity of rhizobacteria against Nacobbus aberrans in pepper plants.

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Nacobbus aberrans is a phytoparasitic nematode that affects several horticultural crops grown undercover. Since chemical nematicides cause severe adverse effects on the environment and human health, it is priority to develop sustainable alternatives, such as the use of biological control agents. Rhizobacteria are promising microorganisms to control nematodes due to their ability to suppress the reproduction, the egg hatching and the development of juvenile states via to the synthesis of antibiotics and enzymes such as chitinases and proteases. It was evaluated the effect of two rhizobacteria isolates on the nematode population and the physiological and biochemical responses of infected pepper plants. The experiment was carried out in a greenhouse under controlled conditions, in pots. The plants were inoculated with formulations containing *Bacillus subtilis* (BS) and *Bacillus thuringiensis* (BT) at transplantation and then every 15 days. Three days after transplantation (DDT), half of the pots were inoculated with 5000 eggs of the nematode. At 120 DDT, the number of total eggs recovered from each pot was reduced by 90% and 93% in plants treated with BS and BT, respectively, compared to a control treatment without rhizobacteria application. An increase in the content of soluble proteins (54%) and chlorophyll level (18%), as well as on net photosynthesis, transpiration, stomatal conductance and efficiency in the use of water was also found in plants exposed to rhizobacteria. This was also associated to a lower accumulation of proline and sugars in plants, which are two metabolites involved as osmoregulators in situations of water stress.

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PK699DR
Area: Plant breeding
Tipo de presentación: Poster en formato PDF
Enviado por: Julieta Sofía Bianchi

INTROGRESSION OF THE FOUR-SEEDED PODS TRAIT TO INCREASE SOYBEAN YIELD POTENCIAL

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Soybean yield depends on seed number (SN) and seed weight (SW). In turn, SN is the result of pod number (PN) times seeds per pod (SPP). To enhance SPP we developed lines with high percentage (>60%) of four-seeded pods (4SP). However, its use with breeding purposes required first to know its heritability (h^2). Besides, possible interactions between SPP and the other yield components must be considered. Individual plants of recombinant inbreed lines (RILs) and field plots of near isogenic lines (NILs) with different SPP and SW, were used for testing the impact of introgressing the 4SP trait into elite soybean germplasm. The h^2 of SPP, PN, and SW was: 0.96, 0.18 and 0.65, respectively, for the NILs, and 0.97, 0.06 and 0.79, respectively, for the RILs. For NILs, high positive correlation with SN (0.89, $P<0.0001$) and no correlation with SW (-0.15, ns) was observed for yield. SN correlated positively with SPP and PN (0.48 and 0.84, respectively, $P<0.001$) but not significant correlation between SPP and PN was observed ($r=0.17$, ns). For RILs, correlation between SPP with PN was low ($r=-0.21$; $P<0.0001$) and not significant with SW ($r=-0.01$, ns). The high h^2 of SPP found in NILs as well as in RILs indicate that this trait is under strong genetic control, making it especially suitable for breeding. Results also suggest that the impact of increasing SPP on SN is independent of variations in PN or SW.

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59
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Area: Epigenetics, Chromatin, non-coding RNAs, RNA biology
Tipo de presentación: Poster en formato PDF
Enviado por: Carlos Esteban Hernando

Getting out of the shade: characterization of the transcriptional network that modulates shade avoidance responses in soybean.

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Plants grown at high crop densities receive reduced light irradiance as a result of mutual shading. Some plants have developed the ability to avoid shade by readjusting phenotypic traits such as growth rates of the stems, internodes and petioles. Collectively, these responses are known as the Shade Avoidance Syndrome (SAS). Whereas these responses may be useful in the wild to improve photosynthetic efficiency, in agronomical practices they are detrimental because resources that should be used for the filling of the harvested organs are diverted to sustain elongation. In order to unveil the molecular mechanisms behind the SAS in the agronomical relevant legume *Glycine max*, plants were grown in a variety of conditions, from contrasting densities in the field to different shade simulations in the laboratory. We perform a high throughput transcriptome analysis of petioles and leaves that allowed us to develop a tissue-specific shade avoidance gene expression and alternative splicing network. Here we describe the different phases of the response from light perception and signaling, to hormone-mediated cell elongation in these tissues. Our work is the first that describes the molecular orchestration behind the soybean shade avoidance responses, as a starting point to introduce novel approaches for crop improvement.

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Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Aldana Boero

MORPHO-PHYSIOLOGICAL AND BIOCHEMICAL RESPONSES OF DIFFERENT SUNFLOWER INBRED LINES (Helianthus annuus L.) SUBJECT TO WATER STRESS

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In sunflower plants, water stress modifies various processes involved in their growth and development. Our aim was to evaluate the morpho-physiological and biochemical responses of seedlings of four sunflower inbred lines (B59, B71, C803 and R461-4) exposed to water stress during the early vegetative growth (V2). Seedlings were grown in pots with sand inside Conviron PR48 Environmental Rooms. At 4th day after sowing, and subsequently each 3 days, irrigations were carried out at field capacity with Hoagland solution 50% ionic strength (control) and 400 mM mannitol solution (water stress). When the seedlings reached the V2 growth stage, they were harvested, sectioned in aerial and radical part and the different parameters were evaluated. All the morpho-physiological and biochemical parameters analyzed were altered by water stress. The leaf area showed a significant decrease in all lines. Stomatal conductance and osmotic potential decreased significantly in B59 and B71 lines. Regarding the hormonal content, ABA and SA increased in aerial part of seedlings of the four inbred lines in response to water stress. In radical part of B59 and C803 water stressed-seedlings ABA was the most abundant phytohormone whereas in B71 and R461-4 its content decreased. JA increased in C803 water stressed-seedlings. The total carbohydrates content significantly increased in C803 and R461-4 lines under water stress. The obtained results demonstrated that the inbred lines showed different adaptation strategies as a consequence of imposed water stress. Furthermore, this response was closely related to the sensitivity of each line to stress.

NS335MP
Area: Biotic Interactions
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Enviado por: María Florencia Bogino

An oomycete effector manipulates Arabidopsis Auxin and Brassinosteroid signaling pathways.

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Effectors are molecules secreted by pathogens that alter host defense responses and metabolic processes. HaRxL106 is an effector protein from *Hyaloperonospora arabidopsidis* (Hpa)*,* an obligated biotrophic oomycete pathogen of the plant *Arabidopsis thaliana*. When HaRxL106 is constitutively expressed *in planta* (Col-0/35S:YFP-106 lines), plants become more susceptible to Hpa and to *Pseudomonas syringae* (Pst) and phenocopy the Shade Avoidance Syndrome (SAS) even though they are grown in normal light conditions. Assays in yeast (Y2H) and *in planta* (BiFC and CoIP) demonstrated HaRxL106 interaction with Arabidopsis proteins IAA11 and BIM1. The first is a negative regulator of Auxin signaling, while BIM1 activates BR-responsive gene expression.

We performed Hpa and Pst infection assays in *iaa11* and *bim1* mutants in order to asses if these proteins are necessary for the enhanced susceptibility observed in Col-0/35S:YFP-106 plants. Interestingly, *bim1* mutants showed reduced bacterial and Hpa growth compared to wild type plants, while *iaa11* mutants were more susceptible. To evaluate BR-, Auxin- and defense-related gene expression we performed qPCR-assays in the formerly described genotypes before and after infection with Hpa.

We also expressed HaRxL106 into *iaa11* and *bim1* mutant backgrounds. Surprisingly, only *iaa11*/35S:YFP-106 plants reproduced the SAS-like phenotype. In addition, when HaRxL106 was expressed in an estradiol inducible way (Col0/pER8:HA-106 lines), a slight promotion of hypocotyl elongation was observed. Currently, we are developing qPCR-assays to evaluate BRs- Auxin- and defense-gene expression in Col0/pER8:HA-106 lines and generating *iaa11* and *bim1*/pER8:HA-106 lines.

NQ699QF
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Marcela Borda

Flowering patterns in young pecan trees

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Pecan [*Carya illinoinensis* (Wangenh.) K. Koch] is a wind-pollinated, monoecious tree-nut crop exhibiting heterodichogamy; hence, complementarity of pollination and receptivity periods is generally required for high yield. Pollination and receptivity windows were identifies and compares in young trees (7 years old) of 2 pecan cultivars grown in the north-center Buenos Aires province. This experiment was conducted at a commercial pecan orchard in Navarro (Buenos Aires province), in 2019 flowering period. Ten trees of “Pawnee” (protandrous) and “Shoshoni” (protogynous) cultivars were evaluated from October 20 up to November 20. Catkins were sampled and evaluated with a stereo microscope to observe the area of dehiscence and pollen presence. Stigma receptivity was evaluated with the H_2O_2 method. Bubbles around the stigmatic surface, once female flower is submerged in H_2O_2, indicates positive receptivity. To indicate the evolution of the two evaluated parameters, a 5-stage ordinal scale was used and the median was subsequently calculated; where “0” represents process not initiated in both organs, “4” necrotic catkins and stigma, and “2” maximum pollen shed and stigmatic receptivity. In base to this scale we observed that “Pawnee” was the first cultivar to shed pollen, from 25/10 to 10/11, while “Shoshoni” did it five days later (30/10) and finished by 15/11. Conversely, “Shoshoni” showed stigma receptivity earlier (25/10 to 15/11) than “Pawnee” (30/10 to 15/11). Preliminary results could indicate that both cultivars are complementary in pollination. This information is important to select pecan cultivars for nut production.

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65
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Area: Plant Physiology and Ecophysiology
Tipo de presentación: video presentacion
Enviado por: Ilara Budzinski

Transcriptomic and GC-MS metabolomic analysis reveals molecular changes in leaves of two contrasting Coffea arabica cultivars after hexanoic acid priming

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Priming is a mechanism which leads to a physiological state enabling plants to respond more rapidly/robustly to biotic or abiotic stress. Many natural compounds act as plant defence elicitors and have been related to priming, hexanoic acid (Hx) is one of them. Coffee (*Coffea* spp.) is one of the most important commodity in the international market. Despite its economic importance, analysis of physiological changes taking account molecular responses are still scarce. We aimed to investigate to which extension Hx could modulate *C. arabica* metabolism, being a potential eliciting agent. So, we applied Hx in roots of two *C. arabica* cultivars (Catuai Vermelho and Obatã) and performed transcriptome and metabolome analysis of leaves. Up to 94% of reads were mapped to the *C. arabica* public genome. Differentially expressed genes (DEGs) were identified based on FPKM ratio and statistical analyses. A total of 57 and 63 DEGs were found in Catuai and Obatã, respectively. Most DEGs correspond to upregulated genes in response to Hx, in both cultivars. DEGs were functionally annotated through Blast2GO and revealed that oxidation-reduction, organic substance and primary metabolic process might play a dominant role in the leaf response to priming. By GC-MS we identified 70 metabolites with known structure (e.g. amino acids, carbohydrates, lipids, organic acids) of which 80% were found in both cultivars. By combining PLS-DA and ANOVA we found that different metabolites were modulated after priming. These data contribute to identify key molecules responsive to Hx as well as indicate pathways modulated by this eliciting agent.

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Enviado por: Agustina Buet

Effect of pre-storage treatment with a nitric oxide donor on the postharvest quality of cherry fruits

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It has been reported that nitric oxide (NO) has a positive effect on fruit quality during postharvest storage. In this work, we analyzed the effect of pre-storage treatment with S-nitrosoglutathione (GSNO), a NO donor, on the quality of cherry fruit (*Prunus avium*) var. Lapins during postharvest storage at two different conditions. Cherry fruits were treated by immersion in deionized water solution of 0, 0.1 and 0.5 mM GSNO for 5 min and then kept in cold chamber (0.5°C) or in fridge (4-8°C) for fifty days. Fruit samples were collected every ten days and quality parameters (fresh weight, fruit firmness, skin color, titratable acidity, pH and relative water content of peduncle) were analyzed. After thirty days of storage in fridge, treatment with 0.1 mM GSNO led to a retention of fruit firmness (20% higher than control fruits) and reduced the trend to darken of the skin color (HUE angle and chroma) respect to control fruits. When kept in cold chamber, GSNO treated fruits showed slightly higher fruit firmness (7%) than control fruits. Overall, the results show that exogenous NO led to a lesser loss of fruit firmness and had a positive effect on skin color changes, being more relevant in fruits stored in the fridge. These results suggest that exogenous NO treatment could protect cherry fruits facing a challenging environment, in sub-optimal storage conditions (such as fruits kept al 4-8°C).

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Area: Plant Physiology and Ecophysiology
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Enviado por: Nardia Bulfe

Differential growth of hybrid pine families in Misiones, Argentina, is not linked to their stomatal behavior

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INTA-PINDO hybrid pine is the result of the crossing between *Pinus elliottii* var. *elliottii* and *Pinus caribaea* var. *hondurensis*. The aim of this study was to analize variables that can explain the differential growth between two hybrid pine families. Plants of the families F12 and F28 were established under field conditions in July 2020, with periodic measurements until April 2021 of Total Height (TH, cm). Since October, maximum stomatal conductance (g_{smax}, mmol m^2 s^{-1}) and leaf water potential (Ψ_l, MPa) were measured at 10 a.m. In dry and wet periods, daily curves of g_s and Ψ_l were traced. Initial TH was different between F12 and F28 (30.1 ± 3.8 and 20.8 ± 2.5 cm respectively; $p = 0.007$). The accumulated increment in TH was different between families since September, being final increment in TH (April 2021) of F28 (71.4 ± 18.0 cm) higher than of F12 (33.3 ± 10.3 cm). The whole growing-season mean of g_{smax} and Ψ_l were similar between families (323.3 ± 150.4, 373.3 ± 103.1 mmol m^2 s^{-1}; -1.9 ± 0.57, -1.8 ± 0.52 MPa; $p > 0.05$). Daily g_s and Ψ_l were different comparing dry and wet periods (g_s: $p = 0.016$; Ψ_l: $p < 0.001$), but not between families ($p = 0.754$ and 0.315), without interaction between factors (period*family) ($p = 0.842$ and 0.646). Family stomatal behavior was not related to initial size and morphological dynamics, which could be related to a differential allocation to aboveground vs. belowground biomass or to differences in resource use efficiency.

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GR746GM
Area: Biotic Interactions
Tipo de presentación: Poster en formato PDF
Enviado por: Sebastián Pablo Rius

Epigenetic regulation associated with systemic resistance induced by Trichoderma in Zea mays leaves

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Trichoderma spp. are considered as promising biological control agents since, during its symbiosis with plants, they induce them a systemic priming state of defenses. Therefore, the primed plants are able to mount a quicker and robust immune response to effectively ward off a broad spectrum of pathogens.

Priming of plant defenses is marked by changes at transcriptional, metabolic, and epigenetic level. Epigenetic regulation involves the restructuring of chromatin through covalent modifications of DNA and histones that modulate its accessibility.

Here we investigate the epigenetic reprogramming in leaves from maize plants inoculated with *T. atrovidire* and infected with *Colletotrichum graminicola*. The hemibiotrophic fungal pathogen, *C. graminicola* causes anthracnose in maize (corn) and is a major problem of maize susceptible to infection resulting in increasing economic concerns.

We have previously selected the group of maize genes whose expression is modulated in priming state induced by *T. atroviride* (Agostini et al., 2019). The aim of this research is to determine the changes in the structure of chromatine of promoters of some selected priming genes, trough FAIRE-qPCR (chromatin compaction/relaxation state) and ChIP-qPCR (histone post-translational modifications).

In conclusion, the systemic resistance induced by *T. atroviride* in maize plant leaves generates an open chromatin state in the promoters of relevant genes linked to hormone defense and signaling. Furthermore, it increases the acetylation of H3K9 and decreases the triple methylation of H3K27. This would indicate that these promoters are transcriptionally active to respond to a stress situation such a pathogen attack.

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69
RK251LP
Area: Biotechnology, Research Tools, Resources
Tipo de presentación: Poster en formato PDF
Enviado por: Oscar A. Ruiz

Biological Nitrogen Fixation, Carbon assimilation and plant performance of Lotus tenuis, contribute to define a strategic role in the lowlands in the Salado River Basin (Argentina)

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Forage production constitutes a great challenge for the Salado River Basin (Argentina), the major area devoted to livestock in the country. The successful naturalization of the European legume *Lotus tenuis* has a productive and environmental relevance for the region. This study aims to evaluate its strategic contribution to the Biological Nitrogen Fixation (BNF), reporting for the first time the B value for this species in these marginal environments for agriculture, necessary for future biotechnological applications. The ^{15}N natural abundance method was used to evaluate the BNF of *L. tenuis* at soil plots and non-leguminous weed species in the same plots were utilized as reference plants. The assays included determinations of the ^{13}C isotope, as well. Simultaneously, evaluations were carried out in the greenhouse for the determination of the B value of *L. tenuis* and the relative reproducibility of the field experiments. The results obtained demonstrated that the *L. tenuis* promotion is accompanied by an increase in forage quality, due to the predominance of this C3 legume species, over C4 species. Moreover, its contribution to N inputs to the system, through the BNF with native rhizobia demonstrated to be about 80%, a highly relevant percentage for these agroecosystems. This work supports the hypothesis that *L. tenuis* promotion plays a strategic role in the sustainability of the ecosystem, especially in soil constrained areas. Joined with data previously published, the results obtained contribute to support the criteria that define the naturalized legume playing a strategic role in the sustainability of agriculture marginal soils.

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Area: Biotic Interactions
Tipo de presentación: Poster en formato PDF
Enviado por: Pablo Daniel Caceres

TuMV infection in Arabidopsis: impact on root development and function

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Characterization of the morphological and physiological outcomes of viral infections is important to objectively quantify the damage caused by them, as well as to envision control strategies that can subsequently be objectively assessed. Due to the importance of water homeostasis and balance during stress, we focused on water management in Arabidopsis under viral infection, a topic that is still poorly understood. Taking into account the interconnectedness of plant tissues, and the spread of virus throughout the entire plant, we studied TuMV impact both at the rosette and root levels. A hydroponic-based system was optimized to gain access to intact root tissue. In this part of our work we show the main results that were found at the root level. Time-course analysis of root length showed that TuMV infection has a strong impact on root length, abruptly arresting growth and inducing curling of the root tissue, mimicking to some extent the phenotypes previously reported in aerial parts. Besides anatomical parameters, root functionality was assessed by measuring hydraulic conductivity (Lp), which was found to increase significantly under TuMV infection. Root hydraulic conductance (Lo) was also normalized by projected rosette area to estimate the capacity of the roots to provide water to leaves. Aquaporin expression was assessed by qPCR and clustering analysis revealed groups with different expression patterns in both root and rosette under TuMV infection. Finally, we show integrated results from rosette and root tissues obtained by means of multivariate analyses.

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71
QK985CC
Area: Plant Physiology and Ecophysiology
Tipo de presentación: video presentacion
Enviado por: Julieta Cagnacci

Deciphering tree responses to a changing climate: a case study in Southern beeches of Patagonia

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As a result of climate change, several forest biomes are facing increasing temperatures, extreme cold waves and/or severe droughts. Thus, it becomes essential to understand the way in which trees respond to changes in the environment. This work takes place in the Patagonian forests, the southernmost woody ecosystems of the world, where two *Nothofagus* species co-exist in non-overlapping thermal niches. While *N. obliqua* is predominant at lower and warmer environments around 650-850 meters above sea level (m), *N. pumilio* inhabits higher and colder montane environments, above 1000m. In this work, species' behavior was analyzed in three common gardens at 680, 930 and 1340m. Results showed that phenology of germination, which is environmentally regulated across altitude, contributes to the ability of survival of young *N. obliqua* and *N. pumilio* seedlings. Out of the species' natural range, phenology of germination was uncoupled from the favorable climatic window for seedling survival of *N. obliqua*. This behaviour was not observed in *N. pumilio*, for which survival was successful in all altitudes. Contrary, at later developmental stages, plants of *N. pumilio* presented signs of physiological stress in the lowest and warmest environments of the gradient, whereas *N. obliqua* showed equal performance along all altitudes. This suggests that, in *N. obliqua* and *N. pumilio*, small environmental changes such as those occurring along altitude constrain growth and/or survival, affecting different developmental stages. Overall, the results indicate different responses of these species to changes in climate and strategies aimed to explore its underlying genetic determinants will be presented.

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72
QJ955BJ
Area: Biochemistry and Metabolism
Tipo de presentación: Poster en formato PDF
Enviado por: Mariana Saigo

Application of a proteomic approach to decipher biological processes and functional organellar components for dual-cell photosynthesis in Setaria viridis

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The C_4 photosynthesis is typically characterized by the spatial compartmentation of the photosynthetic reactions into mesophyll (M) and bundle sheath (BS) cells. The initial carbon fixation gives rise to C_4 acids within M cells, which are transported to the BS cells. There, the C_4 acids are decarboxylated so that the resulting CO_2 is incorporated into the Calvin cycle. This work is focused on the study of *Setaria viridis*, a C_4 model close relative of several major feed and bioenergy grasses. According to the peptide identification and quantification by mass spectrometry, 1,376 proteins were identified in M and BS total protein samples. The statistical analysis showed that 489 proteins were more abundant in M and 336 in BS, which would support different metabolic scenarios. Gene ontology analysis and subcellular location prediction evidenced significantly different proteomes of chloroplasts, mitochondria and peroxisomes in M and BS. This can be related to the different functions of the organelles in M and BS compartments and also shows metabolic strategies to insulate the C_4 core to avoid the leakage of intermediates. In this presentation we describe a useful pipeline to manage proteomic data that uncovered novel lines to keep studying and expanding the knowledge on this topic.

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Area: Biochemistry and Metabolism
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Enviado por: Antonio Calderón

Impact of sound waves on accumulation of specialized metabolites in Stevia rebaudiana shoots

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There is increasing evidence that sound stimuli can affect plant metabolism and development. Although the underlying mechanisms involved in such effects are still far from being elucidated, this opens a new road to regulate plant behavior and performance. Plants are a vast source of compounds with industrial interest. The combination of *in vitro* culture techniques and physical elicitation could help achieve a cheaper and more sustainable, eco-friendly production of plant secondary metabolites (aka specialized metabolites), many of them with remarkable biological activity. This is the case for *Stevia rebaudiana* whose most characteristic specialized metabolites are steviol glycosides and phenolics (mainly hydroxycinnamic acids derivatives). In this work *in vitro* shoot cultures of *S. rebaudiana* were treated for two hours with audible sound waves at specific frequencies (100, 500, and 1000 Hz; 90 dB SPL) and the levels of stevioside, rebaudioside A, total soluble phenols, flavonoids, and hydroxycinnamic acids as well as the antioxidant capacity determined. Results obtained point to a promoting effect, especially of the 100 Hz treatment, on all the parameters assayed after 4 days. Curiously, when a booster treatment was applied on shoots three days after the first treatments only 100 Hz-treated shoots retained increased levels of all the metabolites analyzed, with the exception of hydroxycinnamic acids. In sum, these promising results encourage to carry out more in-depth studies aimed to understand the interactions between sound and plants. This will permit to take advantage of the huge potential benefits that can be derived from applying sound vibrations to plants.

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MP245DH
Area: Abiotic Stress
Tipo de presentación: video presentacion
Enviado por: Cristiane Paula Gomes Calixto Calixto

RNA-seq data reveals the alternative message of the plant transcriptome in response to temperature changes

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The future of food security is being threatened by climate change. To identify mechanistic solutions to improve plant tolerance under extreme temperatures, molecular responses to temperature changes must be understood. Transcriptional and post-transcriptional controls are involved in a wide range of plant environmental responses. Alternative splicing (AS), in particular, is a widespread mechanism impacting the stress defence in plants but it is often overlooked in plant genome-wide stress studies. In this context, we carried out a robust analysis of RNA-seq datasets to investigate the extension of cold- and heat-induced AS in Arabidopsis and rice, respectively. For this, datasets of interest were subjected to filtering and quality-control, followed by accurate transcript-specific quantifications. Powerful differential gene expression (DE) and differential AS (DAS) identified many novel temperature-regulated genes in both species. Detailed analysis of DAS genes coding for key regulators of gene expression suggests that AS helps shape transcriptome and proteome diversity in response to temperature changes. The knowledge resulting from this study confirmed a widespread transcriptional and post-transcriptional response to temperature stress in plants, and it provides novel candidates for rapidly advancing plant breeding in response to climate change.

75
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Enviado por: Damian Cambiagno

Repressive control of immune receptor genes by convergent epigenetic mechanisms

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Genes encoding PRR and NLR immune receptors determine the ability of a plant to resist microbial infections. Their repression is driven by diverse mechanisms avoiding there harmful hyperactivity. We studied the epigenetic control on their expression in *met1*, *cmt3*, *mom1*, *suvh4/5/6* and *ddm1* mutants, impaired in deposition of the repressive 5-methyl cytosine (5-mC) and histone 3 lysine 9 dimethylation (H3K9me2) marks. At optimal growth conditions, none of the mutants showed basal expression of the defense gene marker *PR1*, but all of them had greater resistance to *Pseudomonas syringae* pv. *tomato* than wild type plants. Moreover, *PR1* was induced in an earlier and/or stronger manner in these mutants, suggesting they are primed to stimulate immune cascades and defenses. The analysis of multiple available transcriptomes of each mutant, showed spontaneous activation of particular *PRR/NLR* gene subsets in uninfected conditions. We found 37 "mutant-specific" *PRR/NLR* genes likely activated at early infection stages. Specific epigenetic features at their promoters could explain their up-regulation in the mutants. As expected, *suvh4/5/6* and *ddm1* expressed *PRR/NLR* genes carrying 5-mC and H3K9me2 marks in uninfected wild type plants. Surprisingly, all mutants activated genes harboring the repressive H2A.Z/H3K27me3 marks at their promoters, which depend on the activity of REF6 demethylase and the chromatin remodeler PIE1, respectively. Therefore, MET1, CMT3, MOM1, SUVH4/5/6 and DDM1, together with REF6 and PIE1, would contribute to establish chromatin states that prevent constitutive *PRR/NLR* gene activation, but facilitate their priming by modulating epigenetic marks at their promoters.

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76
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Enviado por: María Victoria Canal

CYTOCHROME c AS A MITOCHONDRIAL REGULATOR OF ARABIDOPSIS DEVELOPMENT

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Mitochondrial respiration is essential for energy production in most living organisms. Cytochrome *c* (CYTc) is a soluble heme protein of the mitochondrial intermembrane space, delivering electrons to complex IV during the last step of aerobic cellular respiration. We previously reported that *Arabidopsis thaliana* plants with lower CYTc levels (*cytc* plants) exhibited decreased biomass and alterations in carbohydrate metabolism, explained in part by differential regulation in gibberellin (GA) homeostasis. Here, we used plants with changes in CYTc levels to explore possible connections between CYTc and the growth regulatory pathway represented by the Target of Rapamycin (TOR) kinase. Detailed analysis of *cytc* plants revealed phenotypic similarities with mutants in RAPTOR, a component of the TOR complex. These comprise delayed germination, decreased root and hypocotyl growth, and delayed vegetative development. Increasing CYTc levels in the *raptor* mutant partially restored root and hypocotyl growth. These observations suggest that CYTc is involved in the regulation of growth and development at these stages, either downstream or independently of the TOR pathway. In addition, autophagy, a process that is typically inhibited by the TOR pathway, is increased in *cytc* mutants compared to wild-type plants. Our results allowed us to speculate that, in addition to their central role in ATP production, plant mitochondria also act as signalling organelles, orchestrating growth and development through different regulatory pathways, in part represented by CYTc.

77
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Enviado por: Francisco Javier Cano Martin

Clonal variability of diploid and polyploid genotypes of Olea europaea in response to a CO2-enriched atmosphere

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The wild olive (*Olea europaea* L.) is an evergreen tree widely distributed across the Mediterranean Basin, and represents the ancestral form of the different varieties of the cultivated olive tree. We have characterized the functional and morphological response to an enriched CO_2 atmosphere of *O. europaea* genotypes belonging to three closely-related subspecies with different ploidy levels: the diploids ssp. *europaea* (southern Spain) and ssp. *guanchica* (Canary Islands), and the hexaploid ssp. *maroccana* (southwestern Morocco). Eleven genotypes (3 *maroccana*, 4 *europaea* and 4 *guanchica*) were propagated from *in-vitro* cultured plant material. Three micro-cuttings of each genotype were rooted and maintained *in-vitro* during two months before transplanting to pots of 7.5 l. Then, plants were grown for 3 months under well-watered conditions into walk-in growth chambers, and halved into two groups growing at ambient and enriched $[CO_2]$ atmospheres (400 and 800 ppm, respectively). All the clones showed an increased primary (stem height - SH) and secondary (base stem diameter - BSD) growth in $[CO_2]_{800}$, which was mirrored by an improvement in the leaf net photosynthesis (A_n). The three *maroccana* genotypes had lower SH and BSD than the genotypes of *europaea* and *guanchica*. Moreover, there was a high inter-clonal variability within the same subspecies in the response of functional and morphological variables (growth, leaf biometry and gas exchange) to CO_2. Though preliminary, our results point out to a high diversity of responses to CO_2 across genotypes of *O. europaea* from different genetic and ecological backgrounds.

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78
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Enviado por: Luciano Nicolás Caraballo Maillet

The sunflower gene HaHB11 confers waterlogging tolerance to maize hybrids

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HaHB11 is a sunflower transcription factor that belongs to the subfamily Homeodomain-leucine zipper I (HD-Zip I), whose members were associated to abiotic stress responses. HaHB11 has proved to be able to confer improved yield performance and flooding tolerance in Arabidopsis plants. Thus, it was accurate to assess the adaptation of such qualities to a crop in the attempt to analyze the biotechnological potential of this gene. This work aimed at studying the effect of ectopically expressing *HaHB11* in maize plants regarding its features. For this matter, two independent events carrying the *35S:HaHB11* construction in a hybrid B73 x Mo17 background were used to perform a waterlogging experiment in the greenhouse, and several traits were evaluated. Transgenic plants on control conditions had higher sucrose levels than controls. Subjected to the stress, they also exhibited higher levels of starch on roots, yet lower on leaves. On histological samples, HaHB11 plants' roots showed increased counts of protoxylem vessels. Towards stress recovery, HaHB11 plants grew taller, yielded greater biomass and exhibited higher nodal root counts than control plants. Regarding grain yield, the transgenic plants produced significantly more grains of a similar weight than the control plants, resulting in a greater seed yield. Transgenic plants also delayed their senescence several days in both waterlogging and control conditions. Altogether, these results indicated a greater tolerance to waterlogging in transgenic maize when compared to the control plants and suggest that HaHB11 is a very promising tool for improving crops' yields, especially in areas subject to flooding.

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79
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Enviado por: José Carballo

An epigenetic approach to disclose apomixis in Eragrostis curvula

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Apomixis is an asexual reproduction by seeds in which the progeny results genetically identical to the mother plant. Apomixis could revolutionise the agriculture as we know today since its transference to major crops could fix the hybrid vigour for more than one generation. Previous studies from our group suggest that epigenetic mechanisms such as **DNA methylation** could have a central role in the regulation of apomixis in ***Eragrostis curvula***. In order to probe this the methylation levels of sexual and apomictic plants of *E. curvula* were assessed using the MCSeEd technique, identifying the CG, CHG, CHH and A methylated contexts in DNA from inflorescences. Diferentially methylated positions (DMP) and regions were evaluated in sexual and full and facultative apomictic cultivars showing the **apomictic ones higher levels of DNA methylation**. In the differential analyses it was observed an increase of methylated positions mainly in regulatory regions. This behaviour was particularly clear in CG and A contexts and was associated to gene silencing in previous studies. Interestingly, **ROS1 and ROS4 genes**, responsible for the de-methylation in CG contexts, were found differentially methylated on regulatory regions when compared apomictic vs sexual genotypes. The silencing of ROS1 and ROS4 through methylation implies that other genes could not be expressed in apomictic genotypes, probably **de-regulating the sexual pathway and giving rise to the apomictic components**. This work also allowed us to identify other differentially methylated genes involved in different regulatory mechanisms, like **ubiquitin and auxin pathways**.

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80
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Area: Abiotic Stress
Tipo de presentación: video presentacion
Enviado por: Amanda A. Cardoso

Disconnection between cortex and vascular cylinder in stems of Selaginella during drought: damage or tolerance mechanism?

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Lycophytes are the earliest diverging, extant lineage of land plants to possess a vascular system, and thus a key group to understanding the evolution of water transport. Given that most lycophytes are adapted to ever-wet environments, it has long been hypothesized that these species, and by extension the common ancestor of all vascular plants, have few adaptations to drought. Here we investigated whether and how water transport (through hydraulic conductance (K) and xylem embolism) would be affected during drought in two species of *Selaginella*, the most ecologically diverse genus of lycophytes. For both *S. haematodes* and *S. pulcherrima*, declines in K of shoots were observed uncoupled from xylem embolism, which occurred at much lower water potentials (Ψ). Images of stems obtained *in vivo* through x-ray microcomputed tomography revealed that the decline K occurred with the formation of a large air-filled lacuna, disconnecting the central vascular cylinder from the cortex. This lacuna is the result of water loss and cell collapse in the cortex and likely a primary cause of declines in K. It could be hypothesized that this lacuna is drought-induced damage, however, our observations suggest that the large volume of water lost from cortical collapse plays a critical role during drought by supplying the remaining tissues with water. Consequently, we believe that recoverable cortical collapse and resistant xylem together provides *Selaginella* species with an efficient mechanism to survive diurnal excursions in vapor pressure deficit or even short periods of soil water deficit.

81
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Enviado por: Natalia Carrillo

Effects of shoot girdling on carbon partitioning and bud fertility of Vitis vinifera cv. Malbec

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Malbec is the most cultivated vine variety in Argentina. Although different selection processes have been carried out for many years and there are currently improved clones, many commercial Malbec vineyards present a marked instability of their productive potential. This is due to shatter, inflorescence necrosis, abscission of fruits and low fertility. It is known that carbohydrates are the major determinant of fruit set in grapes. Also, inflorescence or bunchstem necrosis is associated with a low supply of carbohydrates. Previous studies have demonstrated that redistribution of carbohydrates within the shoot could be performed by removing a portion of phloem tissue through an annular incision. The objective of this research was to evaluate the effect of girdling shoots in carbon partitioning and bud fertility. Three girdling treatments were applied to shoots at the beginning of bloom: a control without girdling; a girdle at the base of the shoot; and a girdle above the last cluster. The results showed that the girdling treatments increased node diameter, shoot fruitfulness and inflorescence dry weight. Total dry matter was similar for control and base girdled shoots, however, top girdled shoots reduced total dry matter significantly. A girdled at the base of the shoots altered the partitioning of carbon within the shoot, favoring the accumulation of carbohydrates towards clusters at expense of lateral shoots.

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Area: Plant breeding
Tipo de presentación: Poster en formato PDF
Enviado por: Pablo Federico Cavagnaro

Identification of candidate genes conditioning anthocyanin pigmentation in the phloem tissues of carrot (Daucus carota) roots

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Purple carrots can accumulate large quantities of anthocyanins in their roots, thereby providing color and antioxidant properties to this vegetable. Carrot anthocyanins are also used as food dyes. Thus, the concentration of these pigments in the carrot root is important for both purposes; increasing nutritional value and colorants production. Depending on the carrot genotype, anthocyanins can accumulate in the entire root, or they can be present in specific root tissues. Many purple carrot cultivars accumulate anthocyanins in the exterior of the root and in the root outer phloem (OP) tissues, (also called cortex), but not in the root inner phloem (IP). The genetic control of this tissue-specific pigmentation patter is not well understood. In this work, we investigated gene expression, by RT-qPCR analysis, of 19 anthocyanin-related genes, including transcription factors, anthocyanin structural genes, and genes involved in intracellular transport of anthocyanins, in purple OP (POP) *versus* non-purple IP (NPIP) tissues of two unrelated carrot backgrounds. Fifteen of the 19 genes were consistently upregulated in the POP in both genetic backgrounds, whereas two genes were upregulated in specific backgrounds. Altogether, our results suggest that two MYB transcription factors, *DcMYB7* and *DcMYB113*, are the main candidates conditioning anthocyanin pigmentation in the POP tissues in one of the two carrot lines analyzed, whereas only *DcMYB113* seem to control pigmentation in the other carrot line. These results increase our understanding on the complex genetic regulation underlying carrot tissue-specific anthocyanin pigmentation.

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83
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Area: Plant Physiology and Ecophysiology
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Enviado por: Isabella Carvalho

Growth and gas exchange of Canavalia ensiformis exposed to excess iron (Fe) in the soil

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The contamination of soils by heavy metals has been afflicting society for a long time due to human activities. Species tolerant to excess metals in the soil are promising for the phytoremediation strategy. Thus, the objective of this study is to characterize the growth capacity and iron tolerance of *Canavalia ensiformis*. The experiment was carried out in a greenhouse, with five treatments with five replications in a completely randomized design. The soil was contaminated with iron sulfate at the following concentrations: 0, 50, 150, 250 and 350 mg/dm^3 of soil. *Canavalia ensiformis* seeds were cultivated in pots for 45 days. Photosynthetic rate (A), transpiration (E), stomatal conductance (gs), number of leaves, length (cm) and fresh mass (g) of shoot and root were determined. As soil iron concentrations increased, A, E and gs decreased. Stem length decreased with increasing soil iron treatments. There was a gradual increase in fresh mass compared to the control treatment, 50 and 150 mg Fe/dm*3* and a decrease in a fresh mass in treatments 250 and 350 mg Fe/dm^3. On the other hand, in the root system, there was an increase in length and fresh mass throughout the treatments. It can be observed that at the concentration of 150 mg Fe/dm^3 there is an increase in biomass, and that from 250 mg Fe/dm^3 onwards there is a negative effect on biomass production. The root system seems to be one of the tolerance strategies of *Canavalia ensiformis* exposed to soil iron concentrations.

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84
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Enviado por: Daniel Carvalho Corrêa

Morphological aspects of cowpea treated with alternative inoculation in Brazilian Cerrado

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Alternative inoculation of Vigna unguiculata (cowpea) is a methodology that put in contact seeds of cowpea and rhizobium bacteria collected in loco in soils where planting will be performed to increase N absorption. In this methodology, we took nodules from thin roots extracted from cowpea, close the beginning of flowering, previously cultivated in the same area and we macerate them with water in a 3:1 proportion. After, we treated the cowpea seeds with this inoculant by 10 min. We evaluated how alternative inoculation affects cowpea growth in Brazilian Cerrado biome, a portion of Central Brazil characterized by high temperatures and poor nutrients soils. Seeds of cowpea, with and without treatment with alternative inoculants were planting in pots and in land to verify leaf N content, plant height, stem diameter, number of leaves, root length and number of nodules in roots. We do not find significant differences in these parameters analyzed between the inoculated and uninoculated plants, but results suggest an increase in root length and number of nodules. We could not exclude the hypothesis that inoculation was not responsible by morphological traits but can change internal N metabolism. Once we could not mensurated crop yield we do not have enough data to accept or discard it. Despite the methodology has showed insufficient in our study, it showed potential to increase growth and yield in cowpea in others Brazilian biomes, because of this more studies need to be performed in Cerrado conditions to optimize the understanding in alternative inoculation.

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85
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Enviado por: Milagros Cascallares

CYP77A7 is required for proper polar growth in Arabidopsis

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In plants, cytochromes P450 (CYPs) catalyze a variety of monooxygenation/hydroxylation reactions involved in the biosynthesis and degradation of a plethora of compounds implicated in diverse physiological responses, including growth and development. In this study, we explore the function of CYP77A7, a cytochrome P450 that belongs to the CYP77 family, with several members identified as putative fatty acid oxidases. A co-expression analysis determined that *CYP77A7* co-expresses with genes related to synthesis and modification of the cell wall, such as a pectinesterase and glycosyl hydrolases, all of them strongly expressed in pollen and pistils. Although a previous study with a transposon insertion mutant in this gene (*une9*) determined that the line had defects in female gametogenesis and pollen germination, we concluded that those defects were probably due to a mutation that, although probably tightly linked, was not in *CYP77A7*. We analyzed five mutants alleles with insertions in CYP77A7. In all cases we obtained homozygous mutants. No evident defects were observed in homozygous plants. However, mutant pollen tubes exhibited abnormal growth patterns, showing bifurcations and tip swelling. As the expression pattern of CYP77A7 showed expression not only in pollen tubes but also in other structures characterized by polar growth such as trichomes and roots, we closely looked at those organs in mutant lines. While trichomes did not show defects, root hairs showed more than one tip and aberrant tip shapes. These results support a role for CYP77A7 in the organization of the cell wall during polar growth, whose bases are currently under study.

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86
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Area: Plant breeding
Tipo de presentación: video presentacion
Enviado por: Cristina Castillejo Mangado

Identification of the Yellow Flesh locus uncovers natural variation in carotenoid concentration in strawberry fruit

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Natural variants in yellow/white fruit shades are documented in different strawberries, including *Fragaria chiloensis* and *F. vesca* as i.e. the *F. vesca* ‘Yellow Wonder’ cultivar. We have analyzed the genetic control of yellow/white flesh variation using an interspecific F_2 population (SSxFcL) of 105 lines derived from the cross of ‘Senga Sengana’ and *F. chiloensis* ssp. lucida. The yellow/white fruit color segregates quantitatively in these lines. Phenotypic data was qualitatively scored (presence/absence) and used with a linkage map of 2991 SNPs for quantitative trait loci (QTL) analysis. A single locus named ‘*Yellow Flesh’* controlled most of the observed variation. White flesh (absence of yellow pigments) was dominant over yellow flesh and fitted the 3:1 expected ratio (p=0.53). The ‘*Yellow Flesh*’ locus mapped to a reduced interval on linkage group 4-4, where one candidate gene, *FaCCD4-4*, has been detected. Carotenoid cleavage dioxygenase 4 (CCD4) cleaves carotenoids to yield apocarotenoids, which are subsequently converted into colorless compounds such as hormones or volatiles. We have identified a 432-bp deletion in the promoter of *FaCCD4-4* from yellow-fleshed accessions associated with a strong reduction in *FaCCD4-4* expression. As a result, SSxFcL yellow fleshed F_2 lines showed a significantly higher accumulation of a number of carotenoids, such as lutein, as well as a higher total carotenoid concentration. Lutein and zeaxanthin are important bioactive compounds that accumulate in the retina and have a protective role against age-related macular degeneration. A codominant high-resolution melting (HRM) marker able to accurately predict white/yellow flesh color in strawberry fruit has been developed.

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87
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Area: Biotic Interactions
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Enviado por: Beatriz Romero Rodríguez Rodríguez

Integrated transcriptome, smallRNA profile and methylome of the tomato-geminivirus interaction

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Geminiviruses constitute the largest family of plant-infecting viruses with small, single-stranded DNA genomes that replicate through double-stranded DNA intermediates. Because of their limited coding capacity, geminiviruses use plant nuclear machinery to amplify their genomes, which are packaged into nucleosomes forming chromatin as multiple circular minichromosomes. Thus, viral minichromosomes must encounter the nuclear pathways that regulate host gene expression and chromatin states. DNA methylation and post-transcriptional gene silencing play critical roles in controlling infection of geminiviruses and this pathogen can counteract these host defense mechanisms and promote its infectivity.

Tomato Yellow Leaf Curl Virus (TYLCV) belongs to the Begomovirus genus and is transmitted by the whitefly Bemisia tabaci. With only seven viral proteins, this geminivirus must create a proper environment for viral replication, transcription and propagation. Behind the apparent simplicity of geminiviruses lies a complex network of molecular interactions with their host and their natural vector, which induces a wide variety of transcriptional, post-transcriptional and chromatin changes in the host. To better understand this virus-host interaction at a genetic and epigenetic level we have analysed the transcriptome, sRNA profile and methylome of tomato plants (Moneymaker) infected with the geminivirus, TYLCV. Total RNA and DNA was extracted from tomato–infected plants (three biological replicates) and analysed at 2, 7, 14 and 21-day post-infection (dpi). Analysis of the changes in host transcription during the infection and its correlation with changes in sRNA profiles and DNA methylation will be presented and examined.

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88
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Area: Abiotic Stress
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Enviado por: Alexandra Castro

Identification and Functional Characterization of the BAG Protein Family in Physcomitrium patens

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The Bcl-2-associated athanogene (BAG) family is an evolutionarily conserved, multifunctional group of co-chaperones regulators that modulate a number of diverse processes. In plants, *BAG* genes were recently identified and play an important role in programmed cell death (PCD) mechanisms, involved in growth, development, and stress responses. Likewise, it has been reported that some members of this family are involved in the regulation of autophagy, for which they need to be cleaved. In this study, we identified *BAG* genes from different photosynthetic organisms in order to gather evolutionary insights on these proteins followed by an in silico characterization of the BAG family in the bryophyte *Physcomitrium patens*. Ten putative PpBAGs harbouring a characteristic BAG domain were grouped into two subfamilies based on the presence of additional conserved domains and phylogenetic distances. Caspase cleavage sites in PpBAG1, PpBAG3, PpBAG4-5, and PpBAG9 were predicted. In silico analysis of *BAG* genes revealed the presence of stress-responsive elements and a stress-regulated expression pattern that appears to be dependent on specifically organized promoter regulatory elements. Expression analysis of *PpBAGs* using qPCR showed that *PpBAG1-3* and *PpBAG8* gene expression increased significantly in response to heat stress. According to our analyses, the present data suggest that some members of P. patens BAG gene family may play a role in heat responses, autophagy, and pathogen immunity. Further research is therefore required for understanding their potential roles in stress responses.

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Area: Developmental Biology
Tipo de presentación: video presentacion
Enviado por: Luciana Castro

SC35 and EIF4A1 characterization in Arabidopsis

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Light is an environmental factor that regulates plant development. Light triggers different signaling cascade that activates genes during plant development, some of which are regulated by a process of phosphorylation-dephosphorylation. In a large scale-phosphoproteomic analysis we identified several proteins that changed their phosphorylation status independently of photoreceptors activation. One of these phosphoproteins is SC35 (Serine/arginine-rich splicing factor), which is an alternative splicing factor, and the other one is EIF4A1 (Eukaryotic translation initiation factor) which is involved in the initiation phase of translation. As a first step we characterize these proteins with mutants and transgenic plants of each gene, assessing their phenotype during plant development. Preliminary results show, that overexpression of SC35 can cause a pleiotropic change in Arabidopsis development when grown under continuous light condition, while under short day photoperiod, the pleiotropic effect is attenuated. Also, under 30°C and dark conditions, these transgenic plants present reduced hypocotyl elongation compared to the wild-type plants. On the other hand, *eif4a1* mutants, displayed a significant shorter hypocotyl compared to the wild-type plants, in part as result of retarded germination in the mutants. Our next step is to study the impact of the phosphorylation changes in these phenotypes to evaluate the biological function of phosphorylation.

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Enviado por: Antonella Catania

Beta vulgaris under salinity conditions: A modeling strategy to understand plant water management

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Abstract

Plant tolerance to salinity involves complex "decision making" for the plant to maintain turgor in an energy-efficient way without compromising metabolic activity. In the halotolerant *Beta vulgaris*, the capacity to surpass salinity implies a transition to a new steady-state that is characterized by only a 2% decline in water content and the change of the root hydraulic conductivity from high to low values after a threshold NaCl concentration value. In view of these findings, new hydraulic topologies of the water paths are necessary to explain and interpret the tolerance to salinity during the transition to the new steady state. Here we propose alternative topologies including new elements to the hydraulic circuit. Our objective is to explain the mechanisms of water movements on *Beta vulgaris* and its sensitivity to changes in the environment’s salinity in stress conditions. For this, we first work in model formulations as well as the identification of key components taking into account *Beta vulgaris* background and the electric circuit theory. Finally, we selected those topologies and elements which best adjusted to the recently published data. Our challenge is to integrate the information into a topological model that encompasses the dynamics of the water passage and the pathways involved in the root in terms of tolerance to saline stress concerning the control condition.

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Enviado por: Mariela Pontin

NITRIC OXIDE AND ABA INCREASED PROLINE, STOMATAL CONDUCTANCE, WATER STATUS AND ROOT GROWTH OF MICRO-TOM TOMATO PLANTS UNDER WATER STRESS

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This work aimed to evaluate the regulatory effects of nitric oxide (NO) and abscisic acid (ABA) on the proline content (PC), and physiological and morphological parameters in tomato plants (*Solanum lycopersicum* L.) cv. Micro-Tom subjected to water stress. From flowering to harvest, pot-grown plants in controlled conditions were exposed to the following treatments: water stress (WS, irrigation treatment, 50% of field capacity) versus non-stressed (WW, irrigated to field capacity), combined or not with sprays of 100 μM SNP (NO donor), 100 μM ABA and water. Proline contents (PC) were assessed in leaves and roots. The physiological parameters, stomatic conductance (*gs*), relative water content (RWC), and chlorophyll were determined. As well, the morphological parameters, leaf area (LA), root and stem lengths (RL, SL) and root/stem ratio were measured. The interaction between irrigation and chemical treatments (SNP and ABA) was significant for PC, RWC, *gs*, LA, SL, RL and RL/SL. Under irrigation, NO treated leaves increased the LA and *gs*, while root/stem ratio, RHC, *gs*, RL, RL/SL did it with ABA. Under WS NO and ABA stimulated PC, RHC, *gs* and SL, while root/stem ratio and LA were augmented only by ABA. These results suggest that ABA and NO act in a complementary way against drought stress.

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Enviado por: Agustin Francisco Caviglia

Deeping inside a plasma membrane strawberry aquaporin with high water capacity transport

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We have previously demonstrated in strawberry that FaPIP2;1, a plasma membrane intrinsic (PIP) aquaporin, is not only present but also shows an expression pattern that increases with ripening. The sequence of FaPIP2;1 presents motifs that are compatible with pH regulation, phosphorylation and methylation. Experiments in Xenopus oocytes demonstrated that FaPIP2;1 shows high water permeability (P_f) values that can be regulated by cellular acidification, phosphorylation and heteromerization events. Here we show that the transport capacity of FaPIP2,1 is higher than in other AQPs and that heteromerization modifies the sensitivity of FaPIP2;1 to membrane tension changes. This regulatory mechanism that has not been observed before in PIP members is characterized by non-linear relationships between water fluxes (J_w) and the applied osmotic gradients (?osm). Comparison to other mechanosensitive aquaporins shows that the P_f decrease in FaPIP2;1 is more sensitive to membrane tension changes associated with volume increments. Furthermore, since the high water-transport capacity of FaPIP2;1 is a feature that has not been addressed at molecular level we employ Molecular Dynamic (MD) simulations to predict how the water molecule moves through the permeable pathway. Here we show the results of 1 ?s simulations with a homology model of FaPIP2;1 developed with the crystal structure of SoPIP2;1 (PDB 2B5F). Our results indicate that in comparison to other aquaporins the water load capacity in the channel of FaPIP2;1 is high, which could explain its high transport rate.

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Area: Plant Physiology and Ecophysiology

Tipo de presentación: Poster en formato PDF

Enviado por: Florencia Luz Ceratto Fernandez

Effect of Bacillus safensis S9 on the development of broccoli (Brassica oleracea L. var. italica) seedlings

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Plant growth promoting rhizobacteria (PGPR) are microorganisms that colonise the rhizosphere of various plant species, benefiting the development of the host. It has previously been shown that *Bacillus safensis* S9 (S9) strain acts as PGPR in soybean; however, itsPGPR effect has never been studied on horticultural crops. The objective of this work was to evaluate the effect of *Bacillus* S9 on growth and root activity of broccoli seedlings. In order to evaluate PGPR ability, a short-term assay in growth chamber was performed. Broccoli seeds (cv. `Belstar`) were inoculated with *Bacillus* S9 suspension (LB, ON, OD=1)or witha culture media dilution (Control group). After 21 days of seeding, the aerial and root parts of the seedlings were collected to analyse growth parameters and root activity. The results showed that treatment with *Bacillus* S9 did not modify the height, leaves number, leaf area, chlorophyll index and dry weight of the aerial part (Fisher´s LSD test, $p>0.05$).However, both root dry weight and root activity increased significantly in the seedlings treated with *Bacillus* S9, compared to control (+57% and +53%, respectively,Fisher´s LSD test, $p<0.05$). These results suggest that the application of *Bacillus safensis*S9 during the production of broccoli seedlings would be useful to increase implantation when they are transplanted in the field.

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Area: Abiotic Stress
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Enviado por: Antonela E. Cereijo

Physiological and biochemical evaluations as indicators of abiotic stress tolerance in cotton

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Cotton is the most natural and textile fiber widely produced in the world, being approximately 95% produced by *Gossypium hirsutum* L. species. It is an essential economic crop since it not only produces raw materials for the textile industry, but it also generates valued raw material for food oils for human consumption and high protein feed for livestock. At present, there are few cotton genotypes adapted to the diverse climate conditions in Argentina, making it necessary to deepen local research to achieve improved materials. The present work aims to contribute to the cotton breeding program by establishing key physiological and biochemical stress tolerance indicators that may be useful in a selection process. In this context, Guazuncho-3 INTA seeds were sown in greenhouse pots and drought and salinity stress were applied in the vegetative developmental stage. Then, morpho-physiological and biochemical characteristics such as relative water content, hydric potential, SPAD, proline, K^+/Na^+, foliar temperature and biomass, were determined, as well as agronomic traits (net yield, fiber yield, harvest index, among others). The obtained results showed significant differences in most of the features evaluated in stressed plants compared to the control. In addition, direct relationships between certain characteristics evaluated in the vegetative stage and the final behavior of plants in maturity, such as proline vs. biomass, SPAD vs. fiber yield, K^+/Na^+ ratio vs. harvest index, among others, could be established. These associations would be important tools for the selection of cotton materials from traditional and mutation breeding programs with improved plasticity.

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95
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Area: Plant Physiology and Ecophysiology
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Enviado por: LUIS HERMINIO CHAIREZ TEJEDA

PRODUCTIVITY OF IRRIGATED RICE IN FUNCTION OF SHADE PERIOD

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The productive potential of irrigated rice crops is defined by the availability of solar radiation, especially in the reproductive stages, thus, light intensity is an important factor to obtain high yields. Thus, this study evaluates the productivity of irrigated rice, cultivar IRGA 424 RI produced in a greenhouse under 35% light restriction during the reproductive phase. The plants were shaded during two moments of the reproductive stages, R0-R4, R4-R9, and control conditions (ambient light). After harvesting, the components of grain yield were evaluated, including the number of panicles, the weight of grains per pot, the number of grains per panicle, spikelet sterility, and 1000-grain weight. Shading had a negative effect on productivity, causing greater sterility of spikelets in the treatment where light restriction occurred in the R4-R9 stages. The mil weight and grain weight per pot were lower than the control treatment, with lower values for the shaded treatment during the R0-R4 stages. The 1000-weight and the grain weight per pot were lower than the control treatment, with lower values for the shaded treatment during the R0-R4 stages. Understanding in which stages of crop development there is a greater loss in productivity due to light restriction can be a strategy to mitigate the effects of one year of El Niño on the irrigated rice crop since in the occurrence of this climatic phenomenon, the availability of solar radiation is lower enabling adequate sowing planning to minimize negative effects.

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96
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Area: Biotic Interactions
Tipo de presentación: Poster en formato PDF
Enviado por: José María Chaín

Arabidopsis thaliana as a facilitating model for the study of the plant-PGPB-drought interaction in forest crops

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Plant growth-promoting bacteria (PGPB) can improve nutrient absorption and tolerance to abiotic stresses in different plants. However, the study of the interaction between forest species and microorganisms is scarce due to the difficulty of experimenting with trees. By using the model plant *Arabidopsis thaliana* we can accelerate research times and increase the number of replicates and assays, gathering valuable information on the mechanisms of action of PGPBs. In this work, we evaluated the effect on the growth and drought tolerance of arabidopsis of two *Pseudomonas* strains recently characterized by our group as beneficial for the development and drought tolerance of *Eucalyptus grandis*. The inoculation of arabidopsis with both *Pseudomonas* strains reproduced the results observed in *E. grandis*, including an increase in leaf area and shoot biomass, as well as faster growth. It also stimulated the formation and elongation of root hairs and provided increased water stress tolerance. These effects occurred without evidence of internal colonization of the plants. We plan to evaluate whether these two bacterial strains exert their beneficial effect through the production of phytohormones (or by stimulating their production by the plant) and to use arabidopsis mutants and transgenic lines to elucidate the physiological pathways of their interaction. This translational, comparative research between *A. thaliana* and eucalypt in interaction with these PGPB will increase our understanding of this complex ecological process.

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Area: Biotic Interactions
Tipo de presentación: Poster en formato PDF
Enviado por: Amalia Chiesa

Genomic strategies for stacking resistance genes to Diaporthe aspalathi in soybean.

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Among the soybean [*Glycine max* (L.) Merr.] diseases that affect this crop, stem canker is of great importance. *Diaporthe aspalathi* is one of the causal agents and resistance to this pathogen has been documented, with five loci (*Rdm1* through *Rdm5*) conferring major resistance. The use of resistant varieties is the most effective and environmentally friendly strategy to reduce losses caused by biotic stresses. Once a resistance source is available, the analysis of the genetic control and mapping of the genomic regions associated with the resistance provide essential information. First, molecular markers (MM) can be used in breeding programs for the introgression and stacking of these loci in elite germplasm. Besides, fine mapping allows the identification of candidate genes responsible for the resistance. Thus, the objectives of this work are to map the *Rdm3* gene and identify MM tightly link, and then stack *Rdm3* with *Rdm4-5* loci, previously mapped by our group, in order to have an extensive and more durable resistance. Hence, a biparental population (160 $F_{2:3}$ families) from a cross between RA702 (susceptible) and Crockett (resistant) has been pheno- and genotypically analyzed by progeny tests with two different local isolates of the pathogen. The results fitted well with the expected segregation of a simple inherited and completely dominant gene. Furthermore, after a systematic search, polymorphic Single Simple Repeats (SSR)-MM were identified in each molecular linkage group of the soybean genetic map, which will be used in bulked segregant analysis for the identification of the genomic region associated with *Rdm3*.

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Tipo de presentación: video presentacion
Enviado por: Monika Chodasiewicz

Stress Granules – stress responsive membrane-less aggregates of protein, mRNA, and metabolites

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Stress granules (SGs) are evolutionary conserved aggregates of proteins and untranslated mRNAs formed in response to stress. Despite their importance for stress adaptation, the understanding of SGs in plants is still poor. In order to understand the mechanism of SGs assembly and its relevance for plants, identification of SGs stress-specific components is crucial. In our lab, we provide evidence that not only proteins and mRNA, but also metabolites can be sequestered into SGs, and composition of heat stress induced granules is quite diverse. A quarter of the identified proteins constituted known or predicted SG components in human cells. Intriguingly, the remaining proteins were enriched in key enzymes and regulators, such as cyclin-dependent kinase A (CDKA), that mediate plant responses to stress. In addition to proteins, nucleotides, amino acids, and phospholipids also accumulated in SGs. Recently we showed that SGs can be also formed in plastids, recruiting mRNA, proteins, and metabolites. Till today, our results indicated the presence of a preexisting SG protein interaction network and an evolutionary conservation of the proteins involved in SG assembly and dynamics. We also proved that SGs play important role in moderation of stress responses by selective storage of proteins and metabolites.

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Enviado por: Belén Ciacci

Contrasting changes of soil pH between urea and ammonium sulfate are reflected by the growth and nutrient status of Sorghum bicolor (L.) Moench in an alkaline saline-sodic soil: a greenhouse assessment.

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Alkaline saline-sodic (ASS) soils are restrictive for agriculture activity worldwide. In these soils, nitrogen fertilization can be used strategically. Ammonium sulfate (AS) and urea (U) fertilizers are widely used for crop production, differing in their effect on soil pH. Therefore, the aim of this work was to evaluate the changes in the rhizosphere pH and growth parameters of sorghum after the application of these two nitrogen fertilizers under greenhouse. For this trial, three sorghum hybrids, named here 163, 155 and SIP, were sown in 3L pots filled with two soil types: an alkaline saline-sodic (pH 9.14. and EC 4.68 µS/cm) and no-saline-sodic soil (pH o 5.69 and EC 0.73 µS/cm). U and AS (120 kg ha N^{-1}) were applied in two times (a half at sowing and the rest at the V5 stage). The rhizosphere pH, shoot dry weight, OJIP parameters, and leaf cations concentration were measured at the end of the trial (38 days after sowing). The results showed that, unlike U, the AS fertilization decreased rhizosphere pH (~0.6 units) and, depending on the hybrid, the shoot dry weight increased from 150% to 300% as well as the foliar concentrations of K^+ (14% - 112%), Mg^{2+} (55% - 252%) and Ca^{2+} (81% - 253%) with respects to the no-fertilized treatments. Moreover, AS-fertilized plants showed higher PI_{abs} and F_v/F_m values under AAS soil.We thus conclude that, the application of AS improves the sorghum nutrition and growth in AAS soil, representing a promising tool for sorghum production under saline-alkaline soils.

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100
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Area: Biochemistry and Metabolism
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Enviado por: Ana Paula Cislaghi

ROS-dependent signaling and redox subcellular changes triggered by flg22 in Arabidopsis

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In plants, perception of pathogen-associated molecular patterns (PAMPs) by surface-localized pattern recognition receptors (PRRs) activates the NADPH oxidase RBOHD that functions as an essential regulator of reactive oxygen species (ROS) levels. This biotic stress increases the generation of ROS that need to be detoxified to avoid deleterious effects. However, at the same time ROS are exploited for redox signaling to induce defences. In recent years it has become (increasingly) clear that oxidative and reductive modifications are confined in a spatio-temporal manner. However, our understanding of how compartment-specific redox dynamics might operate in retrograde signaling and stress defense responses remains limited. Here we used the genetically encoded biosensors Grx1-roGFP2 to record dynamic changes in glutathione redox potential (EGSH) in cytosol and chloroplasts of Arabidopsis leaf discs treated with flg22. ROS production was monitored using a luminol-based assay. The oxidation of both intracellular probes gradually increased over time after flg22 treatment, succeeding apoplastic ROS accumulation. In contrast to the transient apoplastic ROS burst, we detected a prolonged oxidation in both cytosol and chloroplasts upon flg22 perception which may be affected by NADPH oxidase. Our results provide new insights on the interplay between apoplastic and intracellular ROS dynamics and highlight the importance of redox balance within organelles during plant immune response.

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Enviado por: María Micaela Pérez Rodriguez

Halotolerant PGPR Pseudomonas 42P4 alleviates the negative effects of salt stress on tomato plants.

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Salinity is one of the principal abiotic stresses that limits the growth and productivity of crops. Tomato is the second most cultivable vegetable crop in the world, and Mendoza is one of the principal industrial tomato producing areas in Argentina. Tomato is classified as a salinity sensitive plant. The use of plant growth promoting rhizobacteria (PGPR) is an interesting alternative to increase production and mitigate salinity stress. Therefore, the aim of the work was to evaluate the effect of *Pseudomonas* 42P4 inoculation in salt-stressed and non-stressed tomato plants. A greenhouse experiment was conducted. Tomato seedlings were inoculated with: 1) *Pseudomonas* 42P4 and 2) control (without bacteria). The salinity treatment was applied thirty-five days after sown: 1) 150 mM NaCl solution or 2) water. Physiological parameters were evaluated one month after the imposition of salt stress. Inoculation increased root dry weight, shoot dry weight and stem diameter of salt-stressed and non-stressed plants. Relative water content values decreased from non-stressed plants to salt-stressed plants. The malondialdehyde content increased in salt-stressed control plants, however it was reduced with 42P4 inoculation. The maximum efficiency of photosystem II (Fv / Fm) was lower in the control plants under saline stress compared to the inoculated plants. Total phenolic compounds were similar between treatments in non-stress conditions; however, they were increased in stress conditions by PGPR inoculation. The results of the work suggest that *Pseudomonas* 42P4 is a PGPR capable of lowering the negative effects of salinity stress on tomato plants.

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102
QC567BJ
Area: Biochemistry and Metabolism
Tipo de presentación: Poster en formato PDF
Enviado por: Luan Luan

Influences of photoperiod on plasma membrane H+-ATPases activity and water potential in Vitis buds as one of the dormancy process control mechanisms.

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Vines have also been cultivated in tropical conditions, in which absence of season with low temperatures or temperature fluctuations favour apical dominance, promoting a continuous and vigorous vegetative development, but with irregular sprouts, thus decreasing the yield potential. Adapted to harsh winters, the vine developed a dormancy mechanism. The photoperiod has a key role in controlling the transition between the phases of growth and dormancy, with growth being sustained in long days, and growth inhibition in short days. The increase or even the maintenance of the current productivity indexes requires a better understanding of the cellular mechanisms of the dormancy process and its sensitivity to environmental signals. Our work aims to analyse possible biochemical and molecular modifications in symplastic pathways in meristem cells of axillary gems, monitoring enzymatic activities and the levels of transcripts of aquaporins and *H^+-ATPases* as a function of changes in the photoperiod, in order to characterize molecular, biochemical and electrophysiological mechanisms inherent to the processes that culminate with the entry of dormancy in vines. We seek to describe whether and how the *P-type H^+-ATPase* is influenced by the photoperiod, modifying the electrochemical gradient through plasma membrane, directly and/or indirectly impacting the water flow to the bud, with changes in the channels of MP aquaporins. Such molecular and cellular phenomena should reveal mechanisms that underlie xylemic disconnections and changes in symplastic communications via plasmodesmata, which disrupt the secondary transport of metabolites and water between meristematic cells and promote the entry of the bud dormancy.

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103
TH672DS
Area: Developmental Biology
Tipo de presentación: video presentacion
Enviado por: Letizia Cornaro

Morphological and molecular characterization of the apomictic mode of reproduction in Taraxacum officinale L.

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Plants undergo an alternation of generations that involves a diploid sporophyte and haploid gametophytes. These two generations are separated by meiosis and fertilization, distinctive processes of sexual reproduction. Plants can also reproduce asexually through apomixis. Since apomixis avoids recombination and fertilization, the progeny is genetically identical to the mother. Plants show different forms of apomixis, involving the formation of an unreduced gametophyte by apomeiosis and the development of the embryo without fertilization by parthenogenesis.

In *Taraxacum officinale* L., the common dandelion, sexual diploid and apomictic triploid cytotypes occur. The mode of asexual reproduction is a form of gametophytic apomixis – meiotic diplospory – in which the mother cell of the female spores begins meiosis but fails to segregate the chromosomes, thus it forms unreduced spores by first nuclear restitution. The surviving spore generate an unreduced gametophyte, which contains an unreduced egg cell that will develop into an embryo without fertilization. The gene controlling apomeiosis has been identified and mapped.

The purpose of our study is the morphological characterization of the process of meiotic diplospory in the apomictic dandelion, in addition to the functional and molecular characterization of the gene controlling diplospory in this species. This will deepen the knowledge on the still unclear process of asexual reproduction and will enable to unveil the genetic mechanisms that regulate apomixis. The introduction of apomixis in sexually reproducing plants could have a huge impact on plant breeding and the agriculture system, allowing the fixation of valuable traits across subsequent generations regardless the genetic complexity.

104
MN412TS
Area: Biotechnology, Research Tools, Resources
Tipo de presentación: video presentacion
Enviado por: Sandra Correia

Integrative cytological, proteomic and transcriptomic profiling of the molecular events in tamarillo (Solanum betaceum Cav.) auxin-induced embryogenic cells

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Somatic embryogenesis (SE) is a process at the frontier between plant biotechnology and plant development, based on the remarkable ability of plant somatic cells to dedifferentiate and commit to an embryogenic pathway. Based on effective protocols for SE induction in the solanaceous tree tamarillo (*Solanum betaceum*), we have generated cytological and multi-omics data to analyze the molecular networks involved in embryogenic competence acquisition, maintenance and expression in this system. Through comparative analysis between embryogenic (EC) and non-embryogenic (NEC) cells, auxin-induced callus dedifferentiation stages (CD) and embryo development (ED), we found that the balance between cell fate stability and plasticity is accomplished through temporal and spatial control of gene and protein expression, auxin distribution and chromatin organization. Proteomic profiling revealed EC increased expression of heat-shock and energy metabolism-related proteins. However, NEC invests in protein translation regulation, evidenced by the differential expression and immunolocalization of NEP-TC, a putative rRNA/tRNA methyltransferase. Endogenous IAA levels considerably increase in distinct cell niches during CD stages, reaching higher values in EC. This correlates with DNA hypomethylation during CD and EC stages, followed by a progressive increase in DNA methylation during ED, after auxin removal. More targeted approaches (*e.g.*FACS) were used to generate RNAseq and sRNAseq libraries, from cell lines with different embryogenic abilities. NEC abundantly expressed miRNAs that target genes involved in plant growth and development (miR393, miR396a), including auxin receptors (*TIR1*, *AFB3*) and responsive factors (Aux/IAA, *ARFs*), which are being further evaluated for their role in auxin-induced cell reprogramming during tamarillo SE.

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105
FS268DT
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Fernanda Corrêa

Levels of photosynthetic pigments in two arrowleaf clover genotypes subjected to waterlogging

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Winter forages of the *Trifolium* genus are very important legumes worldwide since they keep the yield quality even in the coldest periods. However, these plants are often cultivated in lowland areas that are subjected to soil waterlogging. During waterlogging, plants reduce photosynthetic pigments levels which leads to decreased photosynthetic rates. This study investigated the levels of photosynthetic pigments in two arrowleaf clover (*Trifolium vesiculosum*) genotypes (i.e., cv. BRS Piquete and LEG1109 line) exposed to waterlogging. The experiment was carried out under greenhouse conditions, where seeds were placed to germinate in pots containing vermiculite. Then, plants were irrigated with nutrient solution until the reproductive stage, when both genotypes were exposed to waterlogging. After eight days of waterlogging, leaves were harvested to access the levels of photosynthetic pigments. Chlorophyll *a* and total chlorophyll contents reduced only in cv. BRS Piquete, while the levels of chlorophyll *b* and carotenoids did not differ in any genotype. In conclusion, the LEG1109 line is more tolerant to waterlogging than BRS Piquete since the photosynthetic pigments did not decrease in LEG1109 line during waterlogging. The maintenance of pigment levels allows higher photosynthetic rates and consequently higher yield in plants subjected to waterlogging.

Financing: CAPES, CNPq, Embrapa Clima Temperado

106
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Area: Biotechnology, Research Tools, Resources
Tipo de presentación: Poster en formato PDF
Enviado por: Juan Ignacio Cortelezzi

Genetic improvement of potato tubers iron content for an increased nutritional quality.

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Iron is a mineral necessary for human health, and its deficiency causes anemia, a widely distributed disease that generates serious health problems. In Argentina, according to the National Nutrition and Health Survey, anemia is one of the most prevalent nutritional alterations, which occurs mainly in children whose homes have economic difficulties (35% of children 6-24 months and 20% of women of childbearing age). A partial solution to this problematic is the development of low-cost biofortified crops. In our laboratory we work with *Solanum tuberosum* cv. *Spunta*, designing strategies for tuber improvement through genetic engineering.

The objective of this work is to improve the nutritional quality of potato crop by increasing the iron content in tubers. We selected two genes involved in the storage of iron in plants, Nicotianamine synthase (NAS) from *Arabidopsis thaliana* and the Ferritin gene from *Phaseolus vulgaris*. NAS generates Nicotianamine (NA), a chelator of iron cations involved in its captation and transport, whereas Ferritin codes for an iron storage protein. The Pvferritin gene was placed under the regulation of the Patatin promoter to obtain tuber specific expression of Pvferritin and the HvNAS1 under the regulation of CAMV35S for a high expression throughout the plant. The vectors pPat::Fer; p35S::AtNAS and pPat::Fer-p35S::NAS were generated using the binary vector pPZP-NPTII, and are currently being used to transform potato tuber explants to obtain Fer, NAS and Fer-NAS plants. We expect to develop transgenic potato plants that combine the advantages of the expression of both genes for the biofortification of tubers.

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LR735TM
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Érica Letícia Gomes Costa

Physiological perceptions of soybean cultivated in a Crop-Livestock-Forest Integration Systen in the Cerrado

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In the intercropping between forest species and crops, the wide fluctuation of light is one of the factors that affect plant growth and development, limiting productivity. In this sense, the objective was to evaluate the physiological response of soy to this fluctuation of light when intercropped with forest species. The experimental area was arranged in the Crop-Livestock-Forest Integration System, where the soybean crop (cv. 'Brasmax Bonus') was intercropped with forest species. The evaluations were carried out at the development stage R5 (grain filling = + - 80 DAP), following two spacings according to the tree planting line, being: 1.5 meters and 5.0 meters. Plants grown on the planting lines at 1.5 meters shown in leaf area and reduced chlorophyll, but that did not compromise the performance of the photosystem and the photosynthetic rates. Plants grown at 5.0 meters, on the other hand, showed greater energy dissipation in the form of heat, avoiding damage to the photosynthetic apparatus. Water potential assessments also showed that these plants were not experiencing water stress. It is concluded that soybean grown in association with forest species presents physiological flexibility in response to changes in light radiation, indicating the absence of photosynthetic limitation and water stress.

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108
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Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Cecilia Costigliolo Rojas

BES1 controls cotyledon growth under shade or warmth.

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Under adverse conditions such as shade or elevated temperatures, cotyledon expansion is reduced and hypocotyl growth is promoted to optimise plant forage for light. The mechanisms underlying the repression of cotyledon cell expansion remain unknown. Here, we report that the *bes1* mutation abrogated these growth responses. In the wild type, the nuclear abundance of the BES1 transcription factor decreased in the cotyledons and increased in the hypocotyl under shade or warmth. Brassinosteroid levels did not mediate these effects. PIF4 and COP1 increased their nuclear abundance in both organs under shade or warmth. PIF4 directly bound the *BES1* promoter, reducing *BES1* expression. COP1 physically interacted with the BES1 protein promoting its proteasome degradation in the cotyledons. COP1 had the opposite effect in the hypocotyl, demonstrating organ-specific regulatory networks. Our work indicates that shade or warmth reduce BES1 activity by transcriptional and post-transcriptional regulation to inhibit cotyledon cell expansion.

Financing: University of Buenos Aires, Agencia Nacional de Promoción Científica y Tecnológica, European Regional Development Fund Project “Centre for Experimental Plant Biology”, National Research Foundation of Korea, Spanish Ministry of Science and Innovation, Generalitat Valenciana and Deutsche Forschungsgemeinschaft.

109
LR858NG
Area: Biochemistry and Metabolism
Tipo de presentación: video presentacion
Enviado por: Jean Coutinho Oder

METABOLIC AND PHYSIOLOGICAL RESPONSES OF THE STRAIN CCM-UFV057 (SCYTONEMATACEAE, CYANOBACTERIA) TO DIFFERENT SOURCES AND CONCENTRATIONS OF INORGANIC CARBON

Jean Coutinho Oder[1], Naira Valle de Castro[1], Allan Victor Martins Almeida[1], Pedro Augusto Marazzo de Sousa[1], Marcelo Gomes Marçal Vieira Vaz[1], Wagner L. Araújo[1]
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Cyanobacteria are photoautotrophic prokaryotes, recognized by their wide geographic distribution and large metabolic diversity. Certain species produce toxins, among which stands out microcystin (MC). However, it remains contentious which are the function of MC in cyanobacteria. The availability and source of inorganic carbon (Ci) directly affect the development of cyanobacteria. Here, we hypothesized that growth medium supplied with different concentrations and sources of Ci lead to metabolic and physiological adjustments. We therefore evaluated the effects of distinct Ci in the growth of the heterocyte-containing and MC-producer strain, *Scytonemataceae* CCM-UFV057. Growth curves were conduct under photoautotrophic conditions (irradiance of 95 µmol photons$\cdot$m$^{-2}\cdot$s^{-1}, photoperiod of 16:8 h (light:dark) and rotation of 100 rpm). The treatments were: BG-11$_0$ [medium without nitrogen, supplemented with 0,02 g$\cdot$L^{-1} of Na_2CO_3 – control (C)]; BG-11$_0$ without Ci (T1); and BG11$_0$ medium supplemented with 0,016 g.L^{-1} (T2) and 1,6 g.L^{-1} (T3) of $NaHCO_3$. The strain CCM-UFV057 showed higher growth without Ci supplementation (T1) as observed during the logarithmic (LOG) phase, where its generation time was 25% lower than in the other treatments. Under T3, CCM-UFV057 presented lower phycobiliproteins (PBP) content in both phases, LOG and stationary (STA). In contrast, the higher PBP values on LOG and STA were, respectively, found under T1 and T2. The content of total amino acids was higher on cells under T3, regardless of the analyzed phase. Different Ci supplementation modify cyanobacterial metabolism most likely by affecting also the MC production. Further analyzes are necessary to investigate the effects of Ci over MC production.

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110
HM515DM
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Patricio Cowper-Coles

Comparative responses of Plicatula group of Paspalum to cold stress under controlled and field conditions.

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Cold stress is one of the major factors limiting crop productivity. Its intensity depends on how low temperatures are (chilling vs freezing). Freezing events in northeastern Argentina affect pasture quality and limit the use of forage species in livestock productions. Different *Paspalum* species have shown diversity in their response to cold stress. The aim of the present study was to validate an experimental assay for the identification of contrasting accessions of *Paspalum* (Plicatula group) regarding cold tolerance. A group of 28 different accessions was initially subjected to 15 °C for 15 h, followed by 5 °C for 4 h and finally to -3 °C for 3 h. A visual damage rating of the canopy was conducted 24 h after removal from the chamber, with leaf damage ranging from 100 % to 8 %. These data were compared with the Normalized Difference Vegetation Index (NDVI) measurements of plants under field conditions, which ranged between 69 % and 11 % of reduction in NDVI. The two most and the two least tolerant accessions were selected to study the chilling response, in order to see the effects of low temperatures on physiological traits. ML1 and U100 accessions, corresponding to *P. plicatulum* and *P. guenoarum*, were the cold tolerant selected materials, characterized by the survival and maintenance of greener leaves. While U44 and Q4334 accessions, corresponding to *P. atratum* and *P. guenoarum*, were the nontolerant selected materials, which leaves showed wilting, browning and desiccation.

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111
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Area: Epigenetics, Chromatin, non-coding RNAs, RNA biology
Tipo de presentación: Poster en formato PDF
Enviado por: Pedro Crevillén

Conserved and distinct roles of H3K27me3 demethylases regulating flowering time in Brassica rapa

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Epigenetic regulation is necessary for optimal organism development and preservation of gene expression profiles in the cell. In plants, the trimethylation of histone H3 lysine 27 (H3K27me3) is a silencing epigenetic mark relevant for developmental transitions like flowering. The floral transition is a key agronomic trait, however the epigenetic mechanisms of flowering time regulation in crops remain poorly understood. Here we study the Jumonji H3K27me3 demethylases BraA.REF6 and BraA.ELF6 in *Brassica rapa*. Phenotypic characterization of novel mutant lines and genome-wide H3K27me3 chromatin immunoprecipitation and transcriptomic analyses indicate that BraA.REF6 plays a greater role than BraA.ELF6 in fine-tuning H3K27me3 levels. In addition, we found that *braA.elf6* mutants were early flowering due to high H3K27me3 levels at *B. rapa* homologs of the floral repressor *FLC*. Unlike mutations in *Arabidopsis thaliana*, *braA.ref6* mutants were late flowering without altering the expression of *B. rapa FLC* genes. Remarkably, we found that BraA.REF6 regulated a number of gibberellic acid (GA) biosynthetic genes including a homolog of *GA REQUIRING 1* (*GA1*), and that GA-treatment complemented the late flowering mutant phenotype. This work increases our understanding of the epigenetic regulation of flowering time in *B. rapa* highlighting conserved and distinct regulatory mechanisms between model and crop species.

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Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Neus Cubo Ribas

Polar deserts species: an opportunity to understand the basis of multiple stress cross-tolerance

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A trade-off is often assumed between productivity (e.g. photosynthesis) and resilience traits (e.g. stress tolerance), however this has been scarcely studied in plants from extreme environments. Hence, the aim of this work is to study the relationship between photosynthetic capacity and freezing and dehydration tolerance in a wide range of species, from model to polar plants. We characterized their photosynthetic capacity and performed dehydration and freezing tolerance semi-quantitative tests at leaf level. Dehydration test consisted in placing previously hydrated leaf segments into closed Falcon tubes filled with a desiccant for 48h to severely dehydrate, and subsequently rehydrate the leaves for 24h. Freezing test consisted in placing leaf segments into an isolated cryothermocycler machine, which allows different temperature cycles of freezing (-6/-9/-12/-18ºC target temperature, ramp 8ºC/h) and subsequent recovery to the initial temperature of 15ºC. Dehydration and freezing tolerances were quantified based on the percentage of recovery of the F_v/F_m between initial and recovered conditions. Our preliminary results showed differences among species in their dehydration and freezing tolerance capacities. Few species tested (<15%) showed high recovery values (>50% of recovery F_v/F_m) for both tests (*Deschampsia antarctica* and *Poa pratensis*), whereas up to 35% of the species showed high recovery for a single test. Species adapted to extreme conditions can offer new knowledge about cross-tolerance to multiple stress, which can be key for understanding the response mechanisms to successfully face these stresses.

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113
QD955CK
Area: Biotic Interactions
Tipo de presentación: Poster en formato PDF
Enviado por: Marianela Carmen Cueva Morales

Lateral organ boundaries domain 29 (LBD29) inhibits the development of lateral roots and nodules in Medicago truncatula

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Legume roots form two types of postembryonic organs, lateral roots, and symbiotic nodules. Lateral roots serve for soil anchoring as well as water and nutrient acquisition, whereas nodules are the result of a symbiotic relationship with nitrogen-fixing bacteria. MicroRNA390 (miR390) is an evolutionarily conserved microRNA that targets the *Trans-Acting Short Interference RNA3* (*TAS3*) transcript. Cleavage of *TAS3* results in the production of trans-acting small interference RNAs, which target mRNAs encoding the AUXIN RESPONSE FACTOR2 (ARF2), ARF3, and ARF4. Previous studies in our laboratory revealed that constitutive activation of the miR390/*TAS3* pathway promotes lateral root growth but impairs nodule organogenesis and bacterial infection during the nitrogen-fixing symbiosis established between *Medicago truncatula* and its partner *Sinorhizobium meliloti.* RNA-seq analysis of roots that overexpressing miR390 allowed us to identify MtrunA17_Chr1g0184271, whose induction in response to rhizobia was affected by the miR390/*TAS3* pathway. This transcript encodes a member of the LOB (lateral organs boundaries) family of transcription factors, which have been linked to the development of lateral organs in plants. Phylogenetic analysis indicated that the product of MtrunA17_Chr1g0184271 is the best homologue of the AtLBD29 gene, thus it was designated as MtLBD29. Promoter:reporter fusions revealed that expression of *MtLBD29* was associated with lateral root development but not with nodule development. In addition, overexpression of *MtLBD29* reduced nodulation. Furthermore, overexpression of *MtLBD29* has a negative impact on the initiation of lateral roots but promotes their elongation. Our results suggest that *MtLBD29* contributes to mediate root development and the formation of nitrogen-fixing nodules

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114
GD793DJ
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Facundo Curin Curin

Water use efficiency in wheat: breeding effects on Argentinean wheat cultivars released between 1971 and 2011

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Water deficit has been signaled as an important determinant of grain yield (GY) gaps between potential and actual GYs. Breeding for improved water productivity is a sustainable mean to reduce this gap. The aim of this study was to evaluate breeding effects on GY and its physiological determinants, including water use efficiencies, of two groups of five cultivars (late -LC and early -EC cycle), grown under six contrasting water environmental conditions during 2016 and 2017 seasons. Analyzed traits were GY, biomass production (B_T), harvest index (HI), crop evapotranspiration (ET_C), water use efficiency for biomass production ($WUE_{B,ETc}$) and GY production ($WUE_{GY,ETc}$). The GY increased at a rate of 0.40 and 0.11 % per year in EC and LC as a consequence of greater $WUE_{GY,ETc.}$ No breeding effects were detected on ETc in both groups. Additionally, B_T increase was only detected in EC as a product of improvement of $WUE_{B,ETc}$ in modern EC, while HI explained the GY increase in LC. The breeding efforts had no evident effect on the crop water use but had clear effects on crop biomass production in EC and its partitioning between pre and post-anthesis use in LC. The unintended positive effects of breeding on WUEs are welcome on a global scale, considering that predicted trends of increasing human demand for water will require increased water productivity rather than increased water use by crops.

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Area: Biochemistry and Metabolism
Tipo de presentación: Poster en formato PDF
Enviado por: Paz Cárcamo

Al-toxicity effect on photosynthetic parameters and antioxidant metabolism in cultivars of highbush blueberry (Vaccinium corymbosum L.).

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In the south of Chile, the Andisol soils, are characterized by excellent physic properties, but with higher Al concentration and low pH. *V. corymbosum* is an important agricultural crop, due to the antioxidant characteristics of its fruit. This species is cultivated is in soils acid, where the edaphoclimatic conditions of Chile allow the solubilization of aluminum in a toxic (Al^{3+}) ion for the plant. In this study it was evaluated the antioxidant metabolism (antioxidant activity [AA], total phenol [TP], lipid peroxidation [LP]) and physiological parameters (Pn, gs and E) in two Al-contrasting cultivars (cv.Star [Al-sensitive] and Cargo [Al-resistant]) exposed to different concentration of Al (0, 200, 400 and 800 μM Al [as $AlCl_3$]) in hydroponic solution, to pH 4.5 during 48 h. The results showed that in Star to 200 μM Al increased AA in 1.5 and 2-fold, and to 800 μM Al increases TP 2-fold, all at 24 h, while in Cargo the AA increase 1.4-fold to 800 μM Al at 24 h. The other parameters no-showed significant differences. In leaves of Star the Pn diminish in all Al-treatments 48 h, but it was significant at 400 μM Al. In addition, AA in leaves of Star showed significant differences under 200 μM Al at 24 h. In Cargo leaves, the parameter evaluated were unaltered. Finally, were observed a mayor effect in Al-sensitive cultivar under 800 μM Al treatment, while in Cargo the photosynthetic parameters, AA, LP in Al-treatments were unaltered.

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116
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Enviado por: Francesca D'Agostini

Understanding the relationship between the physiology of water transport and biosilica accumulation in selected C4 crops: an experimental approach

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Biosilica in plants (phytoliths) is being re-evaluated as an element of first importance in drought response. Phytolith formation is related to the plant's transpiration stream and therefore on water availability. For some plants of agricultural interest, the mechanisms of phytolith formation are not yet completely understood. There is an open debate on the role of genetically and environmentally controlled mechanisms. The aim of our research, conducted within the framework of the project RAINDROPS (ERC-Stg 759800), is to investigate biosilica production in selected C_4 crops to test its relation to water availability (environmental mechanism) or genetics.

We cultivated landraces of *Sorghum bicolor*, *Pennisetum glaucum* and *Eleusine coracana*, under distinct experimental water regimes. Experiments were conducted in lysimeters to keep under control the transpiration rate. Our first set of analysis concentrated on measuring phytolith accumulation in the leaves, being the site of most transpiration and consequently assumed to produce the strongest variability of silica production.

Preliminary results suggest that there are no significant differences in the biogenic silica production in relation to water treatment at the species level. Nevertheless, the variability among and within the species is high, suggesting that the three species accumulate silica differently. Within the same species, not all landraces responded equally to water treatments, indicating that silica accumulation might also be influenced by genetics. Future steps will include the analysis of chaff to obtain a complete picture of how water availability affects phytolith production and genetic analysis to explore whether the landraces are active or passive silica accumulators.

Financing: RAINDROPS (ERC-Stg 759800) https://www.raindrops-erc.infoPLANETARY WELLBEING (Universitat Pomepu Fabra, Barcelona) https://www.upf.edu/web/cases/current-projects-directed-by-cases-members/-/asset_publisher/KWjGqZWwM3ll/content/id/245334782/maximized#.YO6l3i2w1uV

117
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Area: Biochemistry and Metabolism
Tipo de presentación: Poster en formato PDF
Enviado por: Luan Baritiello Da Silva Bezerra

Premature Loss of Cellular Viability in Vitis labruscana Berries

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The loss of cell viability in grape berry mesocarp starts after the veraison and the intensity and the period of occurrence is variety-dependent. We hypothesized if this event could impair cells and result in cell death of the mesocarp. So, we evaluated the loss of viability in mesocarp throughout the developmental stages (pre-*veraison*, *veraison*, post-*veraison*) of *Vitis labruscana* (var. Niagara Rosada) berries. Bisected berries were studied from 30 to 86 days after anthesis (DAA) and evaluated in terms of the membrane integrity (cell viability) by using a vital stain (FDA), and evaluated biochemically by the reduction of MTT. We also analysed the catalase activity as well as the quantitative and qualitative characteristics of the berry, such as the diameter, weight, deformability and total soluble solids. The analyzes of the cell viability of the mesocarp indicated the loss of cell membrane integrity, initiating just after the *veraison*. The MTT analysis demonstrated a high percentage of mitochondrial activity at the end of the ripening stage. The activity of the catalase increased at the veraison, followed by a reduction at the end of the ripening. Interestingly, the size and weight of the berries were maintained, and the total soluble solids increased to values considered optimal, even when they reached a high rate of loss of cell viability. Overall, the results suggest a moderate loss of viability during the berry ripening. Moreover, the loss of cell viability in *V. labruscana* berries is premature in relation to the varieties of *Vitis sp* evaluated to date.

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118
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Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Cristiane Jovelina da Silva

Nitrate nutrition mitigates biomass loss by decreasing carbohydrate consumption in soybean plants exposed to hypoxia

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(2) Universidade Federal de Alfenas, Instituto de Ciências da Natureza, Alfenas, Brazil

Nitrate fertilization mitigates the negative effects of hypoxia in plants during soil waterlogging. Here we evaluate the effect of nitrate nutrition on fermentation and carbohydrate metabolism in soybean (*Glycine max*) plants exposed to waterlogging-induced hypoxia. Nodulated plants of soybean were grown in a greenhouse in pots containing vermiculite and daily watered with a nutrient solution without any source of nitrogen or with a nutrient solution containing KNO_3. At the reproductive stage (R1), plants were exposed to waterlogging. Ten days later, plant biomass was determined and roots were sampled to access starch and sucrose levels, and the activity of lactate dehydrogenase, pyruvate decarboxylase, alcohol dehydrogenase, and alanine aminotransferase. Hypoxia decreased plant biomass and carbohydrate levels while increased the fermentative and alanine aminotransferase activity. Nitrate nutrition partially restored the levels of carbohydrates, increased alanine aminotransferase activity, and prevented the decrease in plant biomass. Conversely, nitrate supply decreased the activity of fermentative enzymes. During hypoxia, nitrate fertilization decreases carbohydrate consumption by decreasing fermentation and enhancing the alanine biosynthesis pathway. This shift in metabolism can prevent yield loss in soybean plants subjected to soil waterlogging.

Financing: Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES), Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) and Fundação de Amparo à Pesquisa do Estado do Rio Grande do Sul (FAPERGS)

119
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Area: Abiotic Stress
Tipo de presentación: video presentacion
Enviado por: Cristiane Jovelina da Silva

Iron excess impairs mineral accumulation, antioxidant system, and biomass accumulation in soybean roots exposed to hypoxia

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Iron excess is a major challenge faced by plants in flooded soils in which soybean has been used to crop rotation with rice. The results of combined stresses, hypoxia and high iron availability, are well known for rice plants but remain to be determined for soybean (*Glycine max*). Here we evaluate the effects of hypoxia and high levels of iron in the roots of soybean. Soil-grown plants cultivated in a greenhouse until the vegetative stage V4 were transferred to a hydroponic system containing Hoagland nutrient solution and two oxygen conditions [normoxia (6.2 mg L^{-1}) and hypoxia (0.33 mg L^{-1})] and two iron levels (Fe-EDTA) (0.09 and 1.8 mM) for 72 h. During hypoxia, high levels of iron resulted in increased iron accumulation in the roots while the root concentrations of zinc, nitrogen, potassium, and calcium decreased. Additionally, the higher accumulation of iron in the roots led to an increase in the activity of the antioxidant enzymes and a decreased root biomass in plants exposed to hypoxia. Overall, during hypoxia, high iron levels in the root medium result in more severe root damage to soybean than low iron levels.

Financing: Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES), Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) and Fundação de Amparo à Pesquisa do Estado do Rio Grande do Sul (FAPERGS)

120
KD481GS
Area: Plant breeding
Tipo de presentación: Poster en formato PDF
Enviado por: Daniela Dalzotto

Secondary metabolites of Bougainvillea spinosa with antioxidant activity through callus grown in vitro under physical stress

Daniela Dalzotto[1,2], Micaela Espíndola[1], Valeria Huenelaf[1], Lucrecia Piñuel[1,2], Sandra Sharry[3], Patricia Boeri[1,2]
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Plant tissue culture is an attractive alternative source of bioactive compounds, like secondary metabolites (SM). Elicitation by abiotic factors can be an important strategy towards improved *in vitro* production of these compounds. *Bougainvillea spinosa* is a woody species native to Argentina, which has been little studied in this aspect. The objective of this work was to evaluate if different physical stresses can induce the production of SM with antioxidant activity (AO) in *B. espinosa* callus obtained *in vitro*. The callus were laid in solid MS medium at half concentration with 30% sucrose for one month in two stress conditions: 1) saline stress with 150 µM NaCl; 2) UV light stress on the fifth day of culture. A control group was maintained in ½ MS. After culture, an extraction of the SM was carried out using 65% methanol as solvent. The AO of the extracts was measured through the DPPH and ABTS methods. The results showed that the stress induced by NaCl failed to elicit the synthesis of SM with AO in respect to the control group. However, extracts obtained from callus exposed to UV light stress increased AO in both methods (91.8±8 and 150.6±7 µmol troloxEQ/100 g fresh callus for DPPH and ABTS, respectively), with respect to the control (72.1±9 and 108.3±4 µmol troloxEQ/100 g fresh callus for DPPH and ABTS, respectively). These results are relevant as they show that UV light stress could be a physical elicitor for obtaining secondary metabolites with antioxidant activity in *B. spinosa* callus.

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121
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Area: Plant breeding
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Enviado por: Daniela Dalzotto

Secondary metabolites of Bougainvillea spinosa with antioxidant activity of callus grown in vitro under physical stress

Daniela Dalzotto[1], Micaela Espíndola[1], Valeria Huenelaf[1]
(1) 1

Plant tissue culture is an attractive alternative source of bioactive compounds, like secondary metabolites (SM). Elicitation by abiotic factors can be an important strategy towards improved *in vitro* production of these compounds. *Bougainvillea spinosa* is a woody species native to Argentina, which has been little studied in this aspect. The objective of this work was to evaluate if different physical stresses can induce the production of SM with antioxidant activity (AO) in *B. espinosa* calluses obtained *in vitro*. The callus were laid in solid MS medium at half concentration with 30% sucrose for one month in two stress conditions: 1) saline stress with 150 µM NaCl; 2) UV light stress on the fifth day of culture. A control group was maintained in ½ MS. After culture an extraction of the SM was carried out using 65% methanol as solvent. The AO of the extracts was measured through the DPPH and ABTS methods. The results showed that the stress induced by NaCl failed to elicit the synthesis of SM with AO in respect to the control group. However, extracts obtained from callus exposed to UV light stress increased AO in both methods (91.8±8 and 150.6±7 µmol troloxEQ/100 g fresh callus for DPPH and ABTS, respectively), with respect to the control (72.1±9 and 108.3±4 µmol troloxEQ/100 g fresh callus for DPPH and ABTS, respectively). These results are relevant as they show that UV light stress could be a physical elicitor for obtaining secondary metabolites with antioxidant activity in *B. spinosa* callus.

Financing: PI UNRN- 40-C-864 (2021-2023). "Hacia el uso sostenible y conservación de la biodiversidad norpatagónica" Directora: Dra Patricia Boeri. Co-Directora: Dra. Sandra Sharry.

122
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Area: Plant Hormones
Tipo de presentación: Poster en formato PDF
Enviado por: Zoé Del Bel

Seed tegument: its role in the regulation of sunflower seed germination and dormancy

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Sunflower seed dormancy is imposed by embryo and/or covering layers. Our objective was to elucidate the physiological role of seed tegument (ST) in interaction with embryo and pericarp in the germination and dormancy regulation. B123 and B91 cypselas were used. Germination tests were conducted in intact cypselas, without pericarp and without pericarp or ST. Hormonal determinations were performed in dry and imbibed cypselas at 0 and 33 days of dry storage. Abscisic acid (ABA), jasmonic acid (JA) and indole-3-acetic acid (IAA) were identified and quantified by Liquid Chromatography-Tandem Mass Spectrometry. B123 cypselas (dormant) without pericarp or ST raised germination up to 50%, whereas B91 cypselas (non-dormant) was not modified. ABA and JA increased in ST and decreased in embryo of B123 dry cypselas stored for 33 days. In B91, ABA decreased in ST and embryo whereas JA decreased in embryo. IAA decreased in both lines after 33 days. During imbibition, at 0 days, ABA decreased in B123 ST and remained constant until 12h in B91. JA decreased in B123 ST. In B91, JA remained constant until 12h, and increased at 18h. IAA decreased at 3h in both lines. At 33 days, ABA decreased in B123 ST at 3h, and increased subsequently. In B91, there were no changes in ABA along imbibition. JA increased in B123 ST until 3h, contrary to registered in B91. IAA did not change in both lines. Thus, the phytohormones of ST would be involved in the regulation of germination and dormancy of sunflower seeds.

123
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Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Claudia Deluca Deluca

Characterization of the EIF5A of Physcomitrium patens and its role in the regulation of gene translation related to stress tolerance.

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Control of protein translation is a central aspect of plant growth and development, as well as adaptive responses to environmental stress. Translation initiation is a highly regulated and rate-limiting step of protein synthesis that involves more than 12 eukaryotic initiation factors (eIFs).

In this study, we have used RNA-seq data to identify heat stress responsive genes involved in translation process in *Physcomitrium patens* (*P. patens*). We identified a gene (*PpeIF5A*) induced in response to heat encoding a protein homologous to the Eukaryotic translation initiation factor 5A (eIF5A). In the present study, we cloned and functionally characterized a *PpeIF5A* from *P. patens*. We showed that *PpeIF5A* is induced by heat, drought, salicylic acid and ABA. The promoter region of *PpeIF5A* contains cis-elements that likely participate in drought, high temperature, ABA and salicylic acid stress responses. Using transient expression of PpeIF-GFP fusion proteins in *Nicotiana benthamiana* leaves, we demonstrated that PpeIF5A localizes both to the nucleus and the cytosol. To further address PpeIF5A function, constructs to overexpress and knock-out *P.patens* endogenous gene were made. Furthermore, binary vectors for constitutive and conditional overexpression were transformed in *Arabidopsis thaliana*.

There is evidence that eIF5A plays an important role in the selective translation of proteins containing stretches of polyproline. In order to identify those proteins that require the activity of this factor to be translated correctly and fulfill their cellular function under normal growth conditions and during stress, we have searched the Physcomitrium genome for genes that code for proteins with high polyproline repeats.

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124
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Area: Developmental Biology
Tipo de presentación: video presentacion
Enviado por: Mariana Demarchi

Dissecting the role of chloroplast redox state in leaf development and stress tolerance

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Plants are essential for life, and their leaves provide the basis for the growth of the entire organism. However, environmental factors can cause various types of stress, with the consequent diminution in the crop productivity. It is therefore essential to improve crops for greater productivity and resistance, and to achieve this, it is important to understand the mechanism of leaf growth and development.

The processes of cell proliferation and expansion are responsible for determining the final size of leaves. Moreover, leaf size directly influences yield by affecting photosynthates production. Also, homeostasis of reactive oxygen species (ROS) has a central role in the regulation of cell expansion during leaf growth. In leaves, most ROS come from chloroplasts, and their influence in cellular processes is regulated by a tight balance between their production and scavenging by antioxidant systems. Flavodoxin (Fld) is an electronic carrier isofunctional with ferredoxin (Fd), present in both algae and cyanobacteria, but absent in higher plants. Constitutive expression of a plastid-targeted Fld can increase tolerance to multiple stresses by acting as an antioxidant specific for chloroplasts. Therefore, Fld-expressing lines can be used as tools to probe the role played by chloroplast-generated ROS in different biological processes. However, constitutive expression of Fld also resulted in smaller leaves. Thus, the main objective of this work is to elucidate if enhanced stress tolerance and reduction of leaf size are related, by expressing plastidic Fld under the control of developmental and stress-inducible promoters in *Arabidopsis thaliana*.

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125
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Area: Evolution, Ecology, or Genetics
Tipo de presentación: Poster en formato PDF
Enviado por: Mara Depetris

Susceptibility evaluation of Lolium multiflorum (L.) biotypes to ACCase-inhibiting herbicides

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Annual ryegrass (*Lolium multiflorum*) is both a cultivated species and a weed in agricultural production systems. The present study has been conducted because there has been reports of ryegrass populations which are becoming increasingly difficult to control with ACCase inhibitor herbicides. We have evaluated the sensitivity to haloxifop-r-methyl in four ryegrass populations (EE, Victoria, HE2 and Roldán) from Entre Ríos and Santa Fe provinces. Plants from seeds were grown in pots and herbicide application was carried out on plants with three tillers. Haloxifop-r-methyl doses evaluated were 0x, 1/4x, 1/2x, 1x, 2x, 4x, 8x being x the commercial dose (93.6 g a.e./ha). Thirty days after application, the above plant tissue was harvested and dried at 60º C for 48h and dry weights were recorded. The percentage of biomass reduction was fitted to a non-linear log-logistic regression ($p > 0.05$). The herbicide doses that caused 50% growth reduction (GR_{50}) were 9.89 and 10.7 g a.e./ha for EE and Victoria populations respectively and >748 g a.e/ha for Roldán and HE2. The resistance index for Roldan and HE2 related to EE was >75. These results confirmed haloxifop-r-methyl resistance, which has explained the observed failures in ryegrass control under field conditions. All ryegrass populations were also tested at commercial doses of glyphosate, clethodim and pinoxaden. Roldan showed lower susceptibility to these active ingredients compared to other populations. According to the presented results, it can be concluded that Roldán population could become a serious problem in agricultural systems, and future research should investigate the resistance mechanisms involved.

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126
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Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Sidnei Deuner

COMPARISON BETWEEN INOCULATION AND CO-INOCULATION IN SOYBEAN PLANTS

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Soybean is the main agricultural crop in Brazil, a country that currently ranks first in production and export, accounting for approximately 50% of world trade in the crop. However, for the expression of the maximum productive potential, adequate management practices are fundamental to increase the biological nitrogen fixation process. Thus, the objective of this study was to evaluate the effect of inoculation and co-inoculation between microorganisms of the genus *Bradyrhizobium* and *Azospirillum* on the formation of nodules and productivity parameters of the soybean. The experiment was conducted in a greenhouse using pots with eight liters filled with Hydromorphic Planosol, previously fertilized and corrected according to its analysis. Cultivar FTR 3165 IPRO was used, with five treatments in six repetitions: Control (T0); Inoculation with *Bradyrhizobium elkanni* strain (T1); Inoculation with *Bradyrhizobium japonicum* strain (T2); Co-inoculation between *Bradyrhizobium elkanni* and *Azospirillum brasilense* (T3); Co-inoculation between *Bradyrhizobium japonicum* and *Azospirillum brasilense* (T4). After physiological maturation, the plants were carefully removed from the pots to count the number and diameter of nodules per plant, the weight of 10 nodules, number of pods and weight of grains per plant. As for the nodules, a greater number and weight were observed in the co-inoculation treatments (T3 and T4), in addition to the expressive increase in their diameter in the T4. On the other hand, the behavior observed for nodules in response to co-inoculation did not reflect an increase in yield parameters, where the number of pods and grain weight per plant did not differ between treatments.

127
PS616BD
Area: Biotic Interactions
Tipo de presentación: Poster en formato PDF
Enviado por: Valeria Di Paolo

Bacterial natriuretic peptide XacPNP interacts with the plant receptor AtPNPR.

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(1) Instituto de Biología Molecular y Celular de Rosario, UNR, FCByF, Ocampo y Esmeralda, Rosario, Argentina.

Peptide hormones are essential in plants and plant natriuretic peptides (PNP) are peptide hormones involved in homeostasis regulation. Hence, they are active in promotion of stomatal opening, increase in cellular cGMP levels, modulation of K^+, Na^+ and H^+ net ion fluxes, and increase in osmoticum-dependant H_2O uptake. In *Arabidopsis thaliana* the best PNP characterized is AtPNP-A, which interacts with a leucine-rich repeat (LRR) protein, denominated AtPNPR. *In silico* previous results predicted that AtPNPR is located in the plant cell membrane and is responsible for cGMP-dependent signaling when AtPNP-A is bound to its amino terminal LRR domain. This interaction triggers adaptative responses to changes in the environment. Citrus canker is triggered by the bacteria *Xanthomonas citri* subsp. *citri*. This pathogen has a PNP-like protein denominated XacPNP which shares significant sequence similarity with AtPNP-A, mainly in the active region of the latter. Our previous results showed responses similar to those triggered by AtPNP-A in the opening of stomata, and that photosynthesis is sustained during *X. citri* infection as well as the generation of assimilates. For this, our hypothesis is that bacterial XacPNP mimics AtPNP-A in eliciting physiological responses in plants, and we propose that XacPNP is able to interact whit AtPNPR to exert its function. In order to corroborate the latter, we obtained AtPNPR-Venus and XacPNP-GFP proteins fusions and determined their partial co-ocurrence in the plasma membrane. Also, we corroborated and defined the localizations of both proteins in plant cells; and obtained *in silico* protein models.

128
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Area: Plant Physiology and Ecophysiology
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Enviado por: Martín Acreche

Available water during the critical period for yield in chia (Salvia hispanica L.): effcets on yield and physiological components

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The climatic balance of the Temperate Valleys of Salta and Jujuy demonstrates the necessity of supplement rainfall with irrigation at the time when main yeild components of chia are defined. The objective was to evaluate the effect of levels of water availability during the critical period or yield in chia. The water availabilities were: control at field capacity (Tcc) and decreases of total available water of 34, 60, and 80% (T_{34}, T_{60} and T_{80}). Grain yield and its main components (number of grains, number of verticillasters and number of grains per verticillaster) decreased *ca.* 40% in T_{60} and T_{80}, whereas the reduction in grain yield and number of grains was 20% in T_{34}. The treatments T_{60} and T_{80} presented lower LAI (at 7-pairs of unfoldd leaves and flowering) and percentage of intercepted radiation (lower maximum PAR and lower rate of increase in interception) than Tcc, which resulted in lower intercepted accumulated radiation, total dry matter and radiation use efficiency. Crop evapotranspiration decreased 30-40% in T_{60} and T_{80} and 10% in T_{34}. This reduction was associated with higher proportions of evaporation than transpiration during the critical period compared with Tcc, which resulted in lower water use efficiencies in T_{60} and T_{80}. Summaryzing, water restriction during the critical period of chia affects grain yield and its main numerical and physiological components. Management strategies tending to reduce the high proportion of evaporation compared to transpiration should be designed.

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Enviado por: Julian Diez Ochoa

Allopathic effect of Secale cereale (L.) M. Bieb. on Lolium sp.

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Rye is widely acknowledged as an allelopathic crop, however its effect on major weeds has not been studied in depth. To optimize management strategies, it is necessary to generate information on the possible allelopathic effects on weeds. The objective of this study was to evaluate the allelopathic effect of rye (*Secale cereale* var. Fausto-INTA) over annual ryegrass (*Lolium* sp.). For this purpose, two experiments were performed. A field experiment which consisted on the evaluation of emergence of ryegrass in a barley crop with contrasting predecessors, corn (CS) and rye (RS). A laboratory experiment, in which ryegrass seeds were incubated on Petri dishes containing CS soil with the addition of (i) distilled water (control); (ii) extracts obtained from leaves (H_a and H_b) or roots (Z_a and Z_b) of rye, at the tillering or milky grain stage, respectively; (iii) in the presence of rye stubble (R). The allelopathic effect of soil extracted from the rye root zone at tillering (C_a) and bedding (C_b) and from RS soil was also evaluated. In the field, ryegrass emergence was higher in RS than in CS, reaching 40 pl/m^2. After two weeks, the final germination percentage was stimulated by H_b, Z_b, R, C_b and RS soil treatment (p<0.05). The results suggest that the rye variety evaluated has a residual positive allelopathic potential on *ryegrass.* These allelochemicals are produced at advanced stages of development and remain for at least 8 months in the stubble and soil. Further studies are required to confirm or reject the above hypothesis.

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Enviado por: Pablo Dileo

Net photosynthetic rate evaluated in Argentinian cotton accessions (Gossypium hirsutum L.)

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Measuring and understanding physiological parameters of crops is important to find genotypes with high performance and target future directions for crop breeding. The aims of this study were to estimate the net photosynthetic rate (P_N) in accessions from the INTA cotton germplasm bank (BGSP), and to compare the P_N in leaves from different positions in the plant and phenological stages. Eight accessions were sown in pots in a randomized complete blocks design, with four replications, under greenhouse conditions. P_N was measured at 56, 71 and 84 days after sowing (DAS) under light intensity ranging from 900 to 1500 µmol photons.m^{-2}.s^{-1}. Statistical analysis was performed using a linear mixed-effect model with the accessions, DAS and leaf positions as fixed effects and blocks and individuals as random effects. The highest average P_N was obtained at 56 DAS (26.5), whereas the lowest average P_N were obtained at 71 and 84 DAS (20.7 and 14.9, respectively). P_N showed similar decreasing patterns in all the accessions studied. Also, the P_N decreased from the top to the lower leaves in the three DAS evaluated. Additionally, we found significant interaction between DAS and accessions. BGSP-00269 showed the highest P_N at 56 DAS, but one of the lowest P_N at 84 DAS. In contrast, BGSP-00159 obtained the lowest value at 56 DAS and the highest value at 84 DAS. The differential behavior on P_N among the accessions and phenological stages evaluated could allow us to establish physiological to genotypic associations as a tool for selection in breeding programs.

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Area: Cell Biology
Tipo de presentación: Poster en formato PDF
Enviado por: Ayelen Mariana Distéfano

Glutathione peroxidase inhibition and heat stress induced autophagy during ferroptosis-like cell death

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Ferroptosis is an oxidative iron-dependent mechanism of cell death characterized by particular morphological, biochemical and genetic features described in eukaryotes and bacteria. In 2017, our laboratory reported the first evidence of ferroptosis in plants. We showed that canonical ferroptosis inhibitors (Fer-1, CPX or D-PUFA) were able to suppress cell death in 6 days-old Arabidopsis seedlings exposed to a heat shock. Analyses of HS-treated Arabidopsis roots showed ferroptosis specific hallmarks: iron-dependent accumulation of reactive oxygen species (ROS) and lipid ROS and depletion of glutathione (GSH) and ascorbic acid. As an emergent role for autophagy has been recently described in animal cells undergoing ferroptosis, we studied if autophagy is also triggered during ferroptosis in plants. By using 35S::GFP-ATG8a transgenic lines we showed that autophagy is induced upon HS. Fer-1 and CPX did not modified the autophagy flux triggered, which suggested that autophagy might be induced early in the cell death pathway. The same results were obtained when molecules like calcium, ROS or GSH were tested, indicating a role downstream or independent of the autophagic route. Since in human cells ferroptosis is induced after the accumulation of lipid peroxides upon the depletion/or inhibition of glutathione peroxidase 4 (GPX4), which could also trigger autophagy, we will analyse the role of plant GPXs during ferroptosis and HS-triggered autophagy. As Arabidopsis plants impaired in autophagy related genes showed reduced HS-induced cell death, our next goal is to study analyse ferroptosis features in those lines.

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132
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Enviado por: Natalia Raquel Dolce

Cohniella jonesiana (Orchidaceae) seed storage behaviour

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Cohniella jonesiana is a wild orchid with great ornamental value that inhabits in northern Argentina. This species is threatened because of the extensive disturbance of their natural habitat and indiscriminate harvesting of naturally growing plants. Consequently, it is imperative to develop effective preservation strategies for this orchid species. Seed storage has particular application for germplasm conservation of wild endangered and rare species since it allows conservation of diverse genotypes, besides the small storage space requirements due to minute size. In this study, it was examined the storage behaviour of *C. jonesiana* seeds at different temperatures. Green capsules containing mature seeds were collected 140, 145 and 150 days after hand pollination. Capsules were surface sterilized, opened in a laminar flow hood and then seed samples were removed and stored at 27, 4, -20, and -196ºC up to 36 months. Moisture content (MC) and *in vitro* germination were determined for fresh seeds from each capsule. Seeds from 140 to 150 days-old capsules (6-7% MC) stored at -196 ºC showed high germinability (85-90 %) even 36 months after collection, revealing no significant differences with fresh seeds. On the other hand, germinability decreased rapidly in seeds stored at 27º or 4ºC (3 months) and more slowly in seeds kept at -20ºC (18 months). Thus, long-term storage of *C. jonesiana* seeds is feasible by cryopreservation through direct immersion in liquid nitrogen without any previous treatment. This is a key knowledge when facing the genetic diversity preservation of this wild orchid.

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Area: Biochemistry and Metabolism
Tipo de presentación: video presentacion
Enviado por: Douglas Domingues

Metabolic alterations in roots of two contrasting Coffea arabica cultivars after hexanoic acid priming revealed by transcriptomic and GC-MS metabolomic analysis

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Coffee (*Coffea* spp.) is one of the most important agricultural commodities in the world. *Coffea* plants are sensitive to a diverse range of biotic and abiotic stress; however, despite its economic importance, there is little information about physiological changes taking account molecular responses. In this sense, hexanoic acid (Hx) is a natural priming agent with proven efficiency in induce plant defense responses to stress. In order to investigate how Hx could modulate root metabolism, we applied this elicitor in roots of two *C. arabica* cultivars (Catuai Vermelho and Obatã) grown in nutrient solution. Transcriptome and metabolome analysis of roots were performed, reveling diverse molecular responses. Based on FPKM ratio and statistical analyses, we identified 1545 differentially expressed genes (DEGs). Functional annotation of DEGs using Blast2GO showed that organic substances, nitrogen compounds and primary metabolic processes were the most altered biological process by Hx. We identified 108 metabolites were identified in this organ by gas chromatography-mass spectrometry (GC-MS). Combining partial least squares discriminant analysis (PLS-DA) and ANOVA, we found 37 differentially abundant metabolites among cultivars and conditions, including amino acids, carbohydrates, lipids and organic acids. Carbohydrates are particularly reduced in response to priming. These results represent the first overview of key molecules modulated by Hx in this tropical crop.

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Area: Developmental Biology

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Enviado por: Deolindo Luis E. Dominguez

Evaluation of pollen viability, germinability and longevity in Leptochloa crinita accessions

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Leptochloa crinita is an important native forage grass of arid regions. This strictly-autogamous species reproduces by self-fertilization. For reasons yet unknown, attempting artificial sexual crosses among different *L. crinita* genotypes has been, so far, unsuccessful. In this work, pollen viability and longevity in 21 *L. crinita* accessions was evaluated. Pollen was collected from 2-year-old plants, from November to March, during the 2019/2020 season. To this end, inflorescences with most of their flowers in anthesis were collected between 7 and 8 am, and pollen viability was evaluated by staining the pollen grains with acetocarmine glycerol, whereas *in-vitro* germination was used to examine the germinability of pollen grains. Pollen longevity was determined by evaluating its viability and germinability in increasing time periods from the opening of the anthers (0, 1, 2 and 3 hours). Results revealed high pollen viability (80-90%), which did not decline over time (i.e., polen longevity exceeded 3 hs), for all of the accessions. Pollen germinability was 90% at opening of anthers (time 0), 40-60% after 1 hour, 20-30% after 2 hours, and 0-10% after 3 hours. Altogether, our results suggest that pollen fertility -but not pollen viability or longevity- may be a critical factor when attempting directed sexual crosses in *L. crinita* breeding programs.

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Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Deolindo Luis E. Dominguez

Morphological and physiological traits associated with forage biomass productivity in Leptochloa crinita accessions

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Leptochloa crinita is an important C4 perennial native grass widespread in the arid and semi-arid rangelands of the American continent. Previous studies have revealed broad genetic variability in forage biomass production among *L. crinita* accessions. The aim of this work was to evaluate morphological and physiological traits associated with biomass productivity in *L. crinita* accessions. A two-year replicated trial was carried out with 21 accessions of *L. crinita* from the IADIZA (CONICET) Germplasm Bank. The plants were field-cultivated, ensuring standard irrigation and fertilization conditions for all the accessions. During two vegetative cycles (seasons 2016/17 and 2017/18), total leaf area, and foliage and roots biomass, were monitored independently, at four sampling times during cultivation. In addition, the following variables were measured weekly in all the accessions: stomatal conductance, chlorophyll index, and maximum efficiency of photosystem II (Fv/Fm). Consistently for both years, significant differences ($p<0.05$) were found among the accessions for all the variables analyzed, indicating genetic variation for forage biomass productivity and related traits in the *L. crinita* germplasm. Higher forage biomass productivity was associated with higher photoassimilates partitioning to the foliage ($r=0.70$), stomatal conductance ($r=0.91$) and total leaf area ($r=0.77$). Additionally, accessions with high forage productivity exhibited a faster development of leaf area than accessions with low forage production. These results provide insights regarding possible physiological mechanisms conditioning forage yield in *L. crinita.*

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Area: Abiotic Stress
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Enviado por: Deolindo Luis E. Dominguez

Genetic variability for drought tolerance in Leptochloa crinita

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Leptochloa crinita is a C4 perennial forage grass native to the American continent, and represents an important component of the arid and semi-arid rangelands. A two-year partially replicated trial was carried out using 21 accessions of *L. crinita* from the IADIZA (CONICET) Germplasm Bank, with two treatments: i) irrigation, and ii) drought stress. Plots of both the irrigated and drought treatments were watered weekly during the first 40 days after the transplant. After this period, irrigation was suspended in the ‘drought’ plots. The following variables were measured weekly in all the accessions in both treatments: number of panicles/plant, stomatal conductance, chlorophyll index, and maximum efficiency of photosystem II (Fv/Fm). Also, foliage and roots biomass, and total leaf area per plant was measured, independently, at four sampling times during cultivation. Significant differences ($p<0.05$) among the accessions were found for all the variables analyzed, suggesting genetic variability in *L. crinita* germplasm for drought tolerance. Consequently, it was possible to identify accessions that maintained a good biomass yield under drought conditions. The different responses to water deficit observed in the drought-tolerant accessions were associated with a rapid stomatal closure (lower stomatal conductance) at the onset of the drought stress, smaller leaf area, larger root system, and lower aerial/root biomass ratio. In contrast to previous studies reporting negative correlations between drought tolerance and forage productivity in other species, we found no such relationship in *L. crinita*. The identified drought-tolerant accessions are valuable resources for forage production and livestock raising in arid regions.

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Area: Abiotic Stress
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Enviado por: Marcela Dotto

Characterization of two F-BOX proteins involved in maize drought tolerance

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One of the major threats to agricultural production is water limitation, which often leads to drought stress and results in compromised growth, development and yield of crop species. In this context, drought tolerance has been intensively studied in search for potential targets for molecular approaches to crop improvement. However, drought adaptive traits are complex and our understanding of the physiological and genetic basis of drought tolerance is still incomplete. It has been shown that Arabidopsis plants overexpressing miR394, a 20-nt-long regulatory microRNA and *lcr* plants harboring mutations in its regulated gene, *LEAF CURLING RESPONSIVENESS*, are highly tolerant to severe drought conditions. Therefore, we explored this aspect of the miR394-LCR regulatory module in maize, a species of significant agronomical interest in our country and high value to world-wide crop production. We characterized the miR394 pathway in maize and identified two genetic *loci* producing an evolutionarily conserved mature zma-miR394, which targets two transcripts coding for F-BOX proteins, named hereby ZmLCR1 and ZmLCR2. Analysis of growth and development of single and double *zmlcr* mutant plants indicate these mutations do not affect plant fitness negatively when they grow in normal watering conditions, but mutants showed better survival than WT under drought stress conditions. This increased drought tolerance is based on a higher photosynthetic activity in the mutants, resulting in a more efficient water use under limiting conditions. Our results indicate that the miR394-ZmLCR module is involved in drought stress tolerance in maize and the ZmLCR genes are remarkable candidates for maize crop improvement.

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138
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Enviado por: María José Duarte

Assessment of miR156 and miR172 expression level in Ilex paraguariensis leaves.

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Currently, the genetic improvement of yerba mate based on the selection of elite genotypes is limited due to the impossibility to propagate adult plants. In general, woody species lose the competence to form adventitious roots as they progress from the juvenile to the adult vegetative phase. Recent studies suggest that miR156 and miR172 participate in the regulation of the ageing process. Therefore, to compare the miRNA expression levels between genotypes at different vegetative phases, it is necessary to verify that their expression is stable among plants in the same phase. To determine whether miRNAs quantitative expression is affected by leaf position, total RNA was isolated from the 3rd, 7th, 12th, and last leaf (counting from the shoot apical meristem) from plants of similar ages obtained by macropropagation. Three different protocols using stem-loop primers were evaluated to reverse transcribe mature miRNAs 156 and 172 into cDNA. Then, real-time PCR with the SYBR green method was employed to quantify their expression level. The results obtained suggest that the method described by Varkonyi-Gasic et al. in 2007 (Plant Methods 3:12), is the most effective for yerba mate leaves, getting the older leaf on the stem the most stable expression of miR156 and miR172.

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Enviado por: Jose Antonio Duarte Conde

Looking for specialized ribosomes in plants. Characterization of the riboprotein families L10 and L24.

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Translation and its regulation play an important role in plant adaptation but ribosomes have been considered passive molecular machines regarding which mRNA they translate. This view is changing as studies showing evidence for their active role in translational regulation in mammals and bacteria are appearing [1]. The likelihood of ribosomal specialization is higher in plants, with up to seven paralogs per family of ribosomal proteins in Arabidopsis, and there are some hints pointing towards differential paralog roles. However, whether this heterogeneity for selective translation of specific mRNAs under particular cell conditions has yet to be demonstrated.

Our research tries to answer this question characterizing two families of ribosomal proteins, RPL10 and 24. Both share characteristics that make them good candidates to look for paralog specialization, as the two of them are composed of multiple genes (A, B, and C) that are ubiquitously expressed. In addition, specific functions have been described for at least one paralog of each family [2,3].

We have been able to show that there is phenotypic variance within paralog mutants in each family, in both control and abiotic stress conditions. We are now expanding our phenotypic and molecular characterizations of these paralogs using transgenic lines and polisome profiles with the aim to shed some light on the regulatory roles of the ribosomes.

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Enviado por: ABDELHALIM KHALED ELAZAB

Photosynthetic organs contributions to grain yield genetic gains in Chilean winter wheat

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Investigating the key traits associated with genetic gains in grain yield (GY) is essential for developing winter wheat (*Triticum aestivum* L.) breeding strategies. The study objectives were analyzing if the flag leaf and ear photosynthetic contributions are associated with the genetic gains in GY, and their relationship with other agronomical and physiological traits. Thus, six winter wheat genotypes of different release years were grown under optimal conditions in a greenhouse trial during 2019. Grain yield increased by 126 kg h^{-1} yr^{-1}, with the harvest index's change being the key factor affecting these gains. Compared to the control treatment, ear shading decreased ear contribution to grain filling by 16.35%, while both flag leaf and awn removal increased contribution to grain filling by 4.46 and 5.90%, respectively. Ear photosynthetic contribution estimated by source manipulation treatments showed a significant increase with the release year (0.54% yr^{-1}). Whole ear gas exchange measures correlated positively with GY, and both dark respiration and gross photosynthesis showed positive correlations with the release year. The main findings of the study were: (a) GY gains in Chile were mainly due to the increased harvest index (HI), while the aerial biomass (AB) did not play a significant role in these gains; (b) the increased ear size besides the terminal heat stress during the study highlighted the ear role as the primary photosynthetic contributor to grain filling; and (c) using source manipulation techniques as an indirect selection trait for high ear photosynthesis appeared to be promising.

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Enviado por: Alejandro Enet

Contribution of autophagy to the control of subcellular redox states

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Autophagy is a highly conserved degradation pathway, being essential for cellular homeostasis. In this sense, reactive oxygen species has traditionally been associated with increases in the formation of autophagosomes and the degradation of cytoplasmic components. However, previous results of the lab group showed that modifications in the redox state of the glutathione pool given by the generation of H_2O_2 and / or $^{*}O_2$, evaluated through GRX-roGFP2 and ORP1-roGFP2 type biosensors, had a inhibitory effect on the flow of autophagosomes to the vacuole. In this work, we show that transitory oxidative treatments promote the formation of autophagic bodies once the redox sensors return to values close to the basal reduction. In order to evaluate the role of autophagy in this type of stress, mutant *atg7* expressing the GRX-roGFP2 construct targeting to the cytoplasm, chloroplast and peroxisome were generated. The degree of oxidation between wildtype and *atg7* lines was compared during foliar development, observing a significant increase in the degree of oxidation in both organelles during foliar senescence in *atg* mutant. Also, it was observed that *atg7* plants presented a higher level of oxidation in chloroplasts and peroxisomes after 10mM H_2O_2 and transferred to the control condition for 24 hours. The increase in the formation of autophagosomes and their flow to the vacuole after oxidative stress, added to the fact that *atg* mutants showed greater oxidation during senescence and after oxidative stress would provide more evidence that link the autophagy process to the control and degradation of oxidized organelles post oxidative stress.

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Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Verónica Vanesa Ergo

Increasing nitrogen availability during the seed-filling period improves grain weight and grain industrial quality in soybean under drought

Increasing nitrogen availability during the seed-filling period improves grain weight and grain industrial quality in soybean under drought

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Increasing o maintaining crop productivity and quality under drought conditions is one of the main challenges for agriculture in a climatic change scenario. The objective of this study was to evaluate the increase in nitrogen (N) availability in the seed-filling period in soybean on grain weight (G_{weight}), protein and oil concentrations ($G_{protein}$ and G_{oil}, respectively) in irrigated-plots and drought conditions in genotypes contrasting in Gprotein. We conducted field experiments testing two non-transgenic genotypes: high (HP) and low (LP) $G_{protein}$. Treatments included two water levels: irrigated- and drought-plots (with a soil water content≤ 25% of field capacity from R5, beginning grain filling), and two N levels: unfertilized-plots and fertilized-plots (600 kg.N.ha-1 equally split at vegetative, beginning bloom, and beginning pod). Regardless of water and N levels, the HP genotype, exhibited greater G_{weight} (18%) and $G_{protein}$ (5%), and lower G_{oil} (4%) than the LP genotype. In irrigated-plots, N fertilization decreased G_{weigh}t (17%) compared to non-fertilized treatment, decreasing protein and oil contents at similar rates (~20%), without significant impact on Gprotein and Goil. Drought-treatments, independently of the genotype, reduced 38% the G_{weight},41% the protein content and 52% the oil content, increasing $G_{protein}$ by 7%. Interestingly, in these plots reductions of Gweight, protein and oil contents were slightly higher without N fertilization compared to fertilized treatments in both genotypes, but more pronounced in HP. Based on these results we hypothesized that under drought conditions fertilization addition mitigated the decrease N supply from other sources (i.e. soil, biological fixation and/or remobilization), and thus increasing $G_{protein}$.

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Area: Abiotic Stress
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Enviado por: Verónica Vanesa Ergo

Does an increase in available nitrogen fertilization during the seed-filling period improve maximum photosynthesis and crop production in field-drought soybean?

Does an increase in available nitrogen fertilization during the seed-filling period improve maximum photosynthesis and crop production in field-drought soybean?

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The objective of this study was to evaluate the increase in nitrogen (N) availability on maximum photosynthesis rate (A_{max}), total biomass (TB), and grain yield (GY), in irrigated-plots and droughtplots in soybean genotypes contrasting in grain protein (GP) concentration. We conducted field experiments testing high(42%) and low(38%) GP genotypes. Treatments included two water levels: irrigated-plots and drought-plots (with a soil water content ≤ 25% of field capacity from R5, beginning grain filling), and two N levels: unfertilized-plots and fertilized-plots (600 kg.N.ha-1 equally split at vegetative, beginning bloom, and beginning pod). The A_{max} was measured during the grain filling period (GF), and TB and GY at beginning of seed-filling period and full maturity, respectively. Drought-plots reduced the A_{max} 14%, 48%, and 41% at 6, 16, and 33 days after R5 (DAR5) compared to irrigated-plots, regardless genotype and nitrogen level. The highest A_{max} reduction in irrigatedplots was observed from 33 DAR5, whereas in drought-plots occurred 17 days earlier (16 DAR5) and then, GF duration was 13 days shorter than in irrigated-plots. The low GP genotype showed 15% higher A_{max} at 6 DAR5 than the high GP genotype, among water and N level. Independently of genotype and N treatments, drought-plots reduced 44% and 68% TB and GY, respectively, compared to irrigated-plots. In summary, an increase in N availability did not improve A_{max}, TB, and GY. Thus, we reject our hypothesis stating "nitrogen fertilization improves these variables under irrigation, and even more in drought in low GP genotype compared to a high GP one".

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Area: Biotechnology, Research Tools, Resources
Tipo de presentación: Poster en formato PDF
Enviado por: Fabiana Daniela Espasandin

Genetic transformation of Lotus tenuis with NHX1 antiporter gene.

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Salt stress negatively affects plants due to osmotic effects, ion toxicity and nutritional disorders. One of the strategies to protect from this stress is to avoid ion toxicity by compartmentalization of Na^+ in vacuoles mediating by Na^+/H^+ antiporters of the NHX type located in the tonoplast. To study the importance of NHX1 antiporter of *L. tenuis (LtNHX1)* in plant salt tolerance, by mean of *Agrobacterium tumefaciens*-mediated transformation, we obtained *L. tenuis* plants overexpressing or silencing *LtNHX1*. The first binary vector contained the *LtNHX1* coding region under the control of CaMV35S constitutive promoter (35S:NHX1), while the other vector contained an inverted repeat of a 272-bp fragment of *LtNHX1*, to trigger post-transcriptional gene silencing under the control of the CaMV35S promoter (35S:PTGS). Both vectors carry the bialaphos acetyltransferase gene (*bar*), which confers resistance to glufosinate-ammonium. After 90 days of culture on selection medium, 36% of the leaf explants inoculated with *Agrobacterium* harbouring 35s:NHX1 regenerated, forming 3 or 4 adventitious buds/explants, without callus formation. Thus, we obtained three transgenic lines. Moreover, 54% of the explants inoculated with *Agrobacterium* harbouring 35S:PTGS produced 1.5±0.5 adventitious buds per responsive explant resulting in two transgenic lines. Consequently, we consigned a transformation efficiency of 3.75% and 2.75%, respectively. In all cases, the transformation was confirmed by PCR. Finally, the transgenic shoots were transferred to a fresh MS medium without growth regulators for elongation and rooting to evaluate the biochemical and physiological responses of the plantlets to salt stress.

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KF311BD
Area: Biotic Interactions
Tipo de presentación: video presentacion
Enviado por: Andrés Eylenstein

Phylogenetic and expression analysis of FIP2 and the BTB/POZ domain-containing protein family in Medicago truncatula

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Small monomeric GTPases play essential roles during nitrogen-fixing symbiosis between legumes and rhizobia. ARFA1 is a member of the ARF family of small GTPases, which are known to mediate vesicle budding and transport in a wide range of biological processes. A yeast two-hybrid screening using Medicago truncatula ARFA1 as bait reveled that this GTPase interacts with MtFIP2, which exhibits high identity to a protein identified in Arabidopsis thaliana as a possible interactor of the formin-like protein AFH1 implicated in actin microfilaments organization. FIP2 possesses a BTB/POZ domain, suggesting it may act as a substrate-specific adaptor of the E3 ubiquitin ligase CUL3. To expand the current knowledge about FIP2 and the BTB/POZ protein family, we performed a phylogenetic analysis of the BTB/POZ proteins in M. truncatula. Fifty-eight proteins were identified in the reference genome and used to construct a phylogenetic tree that showed a high degree of divergence between the members of this family. We then investigated the expression profiles of BTB/POZ genes in several organs and nodule zones. The expression patterns of the BTB/POZ family members were found to be diverse and there was a low correlation between FIP2 expression pattern and other members of the family, suggesting that FIP2 function might not be redundant with other members of this family. Finally, a co-regulation analysis indicated that a large proportion of the genes co-expressed with FIP2 participates in processes related to the putative function of this protein, including vesicle trafficking, cytoskeleton dynamics and protein degradation.

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Enviado por: ERNESTA ANDREA FABIO

Evaluation of competitive skills of corn plants in late planting that emerged under conditions of space and temporary variability. An innovative physiological approach to site-specific management in precision agriculture.

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Non-uniform plantings generate intraspecific competition, establishing hierarchies between dominant and submissive plants within the furrow. The objective was to evaluate the impact of the hierarchies between plants in the furrow (dominant and subdued) on the growth and the components of the yield in late maize that emerged under conditions of spatial and temporal variability. The test was carried out in the FCA-UNC School Field, with mechanical seeding of the hybrid AX 7761, on 12/15/2019. After emergence, 6 treatments were configured: T1: control with equidistant plants; T2: Temporal variability in 20% of the plant stand; T3: Temporal variability in 50% of the plant stand, T4: equidistant plants at half density T5: great spatial variability 3 emerged plants and two continuous faults on the row. T6: Combined spatial and temporal variability. From the analysis of results, it is concluded that the differences were significant between dominant plants among themselves and the one submitted in T3, T5 and T6. All T4 plants produced two spikes and their performance was superior throughout the trial. The main contribution of this research is the quantification of yield losses due to competition between plants: 3.5% reduction in T2 and T3; 13% increase in T4; T5 decreased by 32%; while T6 -15.4%. It is important to achieve precise plantings to eliminate spatial variability in late maize

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LC873HT
Area: Biotechnology, Research Tools, Resources
Tipo de presentación: Poster en formato PDF
Enviado por: PAULA DEL CARMEN FERNANDEZ

Characterization of Sunflower Leaf Senescence Process at Different Nitrogen Supplies in Two Contrasting Inbred Genotypes

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Leaf senescence is the last stage of leaf development in plants, which is characterized by a decline in photosynthetic activity, an active degeneration of cellular structures and the recycling of accumulated nutrients to areas of active growth such as buds, young leaves, flowers, fruits and seeds. It is a process with economic impact since it can affect the yield due to the greater or lesser opportunity of the plants to maintain the active photosynthetic system during prolonged periods, especially during the stage of filling of grains affecting the weight and oil content of the plant. Leaf senescence is a complex mechanism controlled by multiple genetic and environmental variables. The visual symptoms of the leaves are detectable long after the activation of the signaling cascade of the process. The objective of this work aims to deepen the study of the leaf senescence process in sunflower in response to different nitrogen supplies using a broad overview approach of integration with physiological and phenotypical variable profiles. The field assay of two differential inbred lines previously selected from sunflower INTA Breeding Program bank were analyzed through different leaf developmental stages, in plants grown under different nitrogen supply at INTA Castelar. The results from this project will contribute to elucidate the metabolic pathways involved in the differential triggering and progression of the senescence process in sunflower, enabling the design of future comprehensive studies, allowing the detection of key nutritional biomarkers useful for genetic improvement of this oil crop of great importance for Argentine production.

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Area: Cell Biology
Tipo de presentación: video presentacion
Enviado por: Vitor Favaretto Pinoti

SCI1 (Stigma/style Cell-cycle Inhibitor 1) interacts with RNA Helicase 35, a novel DEAD-box RNA Helicase associated with splicing and transcription machinery.

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In previous studies, we characterized the SCI1 (Stigma/style Cell-cycle Inhibitor 1) gene, which controls cell proliferation in the gynoecium of *Nicotiana tabacum* and is regulated by the transcription factor (TF) AGAMOUS. However, the molecular mechanism through which SCI1 controls cell proliferation remains elusive. Therefore, a yeast two-hybrid (Y2H) screening of a tobacco stigma/style cDNA library using SCI1 as bait was performed. The RNA helicase 35 (NtRH35), a previously uncharacterized DEAD-box RNA Helicase, was identified in the screening. The interaction between SCI1 and NtRH35 was confirmed by bimolecular fluorescence complementation (BiFC) and *in vitro* pulldown. Further (co)localization and BiFC experiments showed that SCI1 and NtRH35 localize and interact in splicing speckles. Moreover, BiFC assays showed NtRH35 and SCI1 interaction with the splicing-related proteins U2a`, RS2Z33 and SR45. Furthermore, the NtRH35 Y2H screening identified the homolog of the arabidopsis RNA processing-related proteins CPSF30, CACTIN, and NKAP. Similarly, homologs of members of the TCP (TCP1; TCP4; TCP7), Trihelix (AT3G58630; At2g44730), Zf-HD (AT4G24660-HB22) families of TFs, and the homolog of the chromatin modifier HUB1 were also identified in NtRH35 Y2H screening. Interestingly, NtRH35 overexpression and silencing plants presented an increase and decrease in leaf area, respectively. Additionally, NtH35 silencing plants also exhibited reduced petal and stamen length and increased stigma diameter similar to the TCP4 gain-of-function phenotype. Altogether, we describe SCI1 association with NtRH35, a DEAD-box RNA helicase associated with the splicing and transcription machinery, demonstrate NtRH35 function in plant development, and suggests a link between SCI1 and TCP4 pathway in cell proliferation control.

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149
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Area: Evolution, Ecology, or Genetics
Tipo de presentación: Poster en formato PDF
Enviado por: María Belén Fernández

A comprehensive phylogenetic study reveals the existence of bifunctional photolyases in photosynthetic bacteria

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Photolyases are flavoenzymes from the cryptochrome/ photolyase family (CPF). They repair DNA damage induced by ultraviolet- B radiation in a blue and UV-A light driven mechanism. Photolyases are specific for the repair of cyclobutane pyrimidine dimers (CPD), the major UV-B damage, and pyrimidine-pyrimidone (6–4) photoproducts (6–4PP). The first bifunctional photolyase, that repair both types of damages, was recently reported in the antartic bacteria *Sphingomonas* sp SV9. We performed BlastP analysis to determine if this enzyme would be present in other species. All the retrieved sequences corresponded to bacteria proteins and matched the criteria of E- values lower than 0.001 (being lower to $1x10^{-63}$) and percentage identities higher than 30%. Subsequently, both partial sequences and those with percentage identities below 85% were identified and discarded. Then, we performed multiple sequence alignment (MSA), alignment curation and phylogenetic tree inference. These analysis revealed that over a total of 149 sequences, 55 were predicted as bifunctional photolyases. MSA analysis showed conservation of tryptophan´s important for electron transfer required for lesion repair in the predicted bifunctional photolyases. It was also observed that aminoacids involved in FAD and DNA lesion binding were conserved. A widespread distribution of bifunctional photolyases was observed among bacteria, including different genus from proteobacteria, planctomycete, bacteroidetes, acidobacteria and cyanobacteria. The latter are the only photosynthetic organisms encoding this enzyme. Finally, phylogenetic analysis including 6-4PP, CPD and bifunctional photolyases and other members from the CPF demonstrated that bifunctional enzymes may represent a transition from 6-4PP to CPD specific photolyases.

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RM224DH
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Ivana Fernández Moroni

SALINITY AND OSMOTIC POTENTIAL IN SEED GERMINATION OF Habranthus tubispathus. PRELIMINARY STUDY.

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H. tubispathus is a summer flowering geophyte native to sub-humid and semi-arid zones of central Argentina. Even though its high ornamental value in xero-gardening is well known, physiological studies about their performance under stress conditions are scarce. The objective of this study was to determine the influence of water deficit and salinity on seed germination. Seeds were collected 55 days before the trial in a spontaneous population in the suburban area of Bahía Blanca, Buenos Aires. Germination tests were carried out for 18 days at 25 / 20ºC, with PEG6000 and sodium chloride to simulate water deficiency (0 to -1 MPa) and salinity (0 to 6 dSm^{-1}), respectively. Maximum germination average was 75% under non stress conditions. Salinity and water deficit reduced the percentage and germination rate until they were completely inhibited at -0,75 MPa and 6 dSm^{-1}. The beginning of germination was delayed at least 1 day at 4 dSm^{-1} and accumulated germination was reduced more than a half with respect to the control (no stress). These results suggest that germination of *H. tubispathus* is affected by moderate salinity and water deficit. The information gained from this study identifies for the first time physiological thresholds for seed germination under salinity and water deficit that will allow to predict its potential to colonize new environments or define management practices.

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SQ476TH
Area: Epigenetics, Chromatin, non-coding RNAs, RNA biology
Tipo de presentación: Poster en formato PDF
Enviado por: Milagros Ferrari

DNA methylation and histone modification: Roles in the reprogramming of the gene expression during symbiosis

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Legume plants have the capacity to associate with soil bacteria collectively known as rhizobia when the nitrogen availability in the soil is low. Rhizobia incorporate atmospheric nitrogen into reduced forms assimilable by plants in a process known as a biological nitrogen-fixation (BNF). In this process the plant forms a new organ, the nodule, where the bacteria reside and BNF takes place. The formation of nitrogen fixing is accompanied by dramatic changes in gene expression in the root cells engaged in symbiosis. We have previously showed that translational changes of pre-existing mRNAs contribute to this reprogramming of gene expression. Among translationally regulated mRNAs, were those encoding proteins involved in DNA methylation as well as in histone methylation and acetylation, suggesting that these epigenetic marks might affect the transcription of specific *loci* during symbiosis. Recently, we have focused our studies on a histone lysine demethylase (LSD1), which catalyzes oxidative demethylation of di or tri-methylated lysines. *LSD1* is subjected to alternative splicing generating two transcript isoforms, a long isoform that encode the functional protein, and a shorter one that encode a truncated protein. The long isoform increases its association to the translational machinery in presence of rhizobia. Currently, we are characterizing the function of this protein during symbiosis as well as the changes in histone methylation in plants with reduced levels of LSD1. These results would provide a better understanding of the epigenetic marks in the reprogramming of gene expression during an agronomically important process such as the BNF.

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Enviado por: María A. Ferrer

Sound vibrations alter phenolic metabolism in Solanum lycopersicum cv. Micro-Tom leaves

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Audible sound waves have been demonstrated to trigger substantial metabolic changes in plants. Some of these changes are associated to enhanced development and productivity under both stressing and non-stressing conditions and hence sound treatments have a great potential in the regulation of plant performance. Treatment of tomato plants with different audible frequencies (0, 100, 500, and 1000 Hz; 90 dB SPL) for three days, two hours per day, altered phenolics patterns in leaves at the two sampling times chosen in this work (three, T1, and seven, T2, days after the beginning of sound treatments). Total soluble phenol levels slightly increased with respect to control in leaves of 100 Hz-treated plants at T1, but significantly decreased in 500- and 1000-Hz-treated samples at T2. Hydroxycinnamic acids contents decreased with respect to control at both sampling times in 500- and 1000 Hz-treated plants, accounting in part for the above mentioned decrease in soluble phenols. Anthocyanin levels did not significantly vary between treatments at T1, but a strong decrease was observed for all the sonic treatments, especially for the 1000 Hz one, at T2. A very similar trend was observed for leucocyanidins. However, concentrations of non-extractable, oligomeric proanthocyanidins tended to increase with respect to control at T2, with 500- and 1000 Hz-treated plants showing the highest values at this sampling time. Some of these changes were related to variations in enzymatic activities involved in phenolic metabolism (peroxidase, PAL, PPO), confirming that sound has the power to evoke notable alterations in phenolic profiles.

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153
RP374FH
Area: Plant breeding
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Enviado por: Maria Laura Fiasconaro

Application of different doses of compost for partial or total substitution of the commercial substrate in nursery. Case study on pepper and tomato seedlings

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Purpose. The search for new cultivation substrates arises as a necessity in response to the decrease of peatlands. Our purpose was to evaluate the use of different composts as growing media in the production of vegetable seedlings (pepper and tomato).

Method The composts were produced from: discarding carrots (ZC), fats (FC), and biosolids (BC) from the dairy industry. They were applied as total substitutes for peat in different doses according to the species to germinate: control (CS-commercial substrate) and three growing media prepared with perlite: 25, 35, and 45% of ZC, FC, and BC for pepper seedlings and 40, 55 and 70% of ZC, FC, and BC for tomato seedlings. When the plants were ready for transplantation they were harvested and different data were collected to assess the development of the seedlings in the different growth media.

Results The results obtained suggest the possibility of total substitution of the CS by compost ZC, FC, and BC to produce pepper and tomato plants in commercial nurseries. The plants cultivated with compost presented a higher concentration of total dry matter compared to the controls. The photosynthetic pigments were affected by the presence of FC and BC, whereas the concentration of TSP was favored by BC.

Conclusion Ours results suggest that it is feasible to perform a total substitution of the commercial substrate for the production of pepper and tomato plants in commercial nurseries with composts of different origins and compositions.

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FB889NQ
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Nicolás Raúl Figueroa

Morphological and functional photosynthetic analysis of tobacco plants expressing a cyanobacterial flavodoxin under normal growth conditions

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Overexpression of a chloroplast-targeted cyanobacterial flavodoxin (Fld) has been proven to protect the function of the photosynthetic machinery under adverse environmental conditions that normally lead to a ferredoxin (Fd) decline. It was suggested that, under these conditions, Fld is able to productively replace Fd as an active electron carrier with the advantage of displaying a higher stability when plants experience oxidative stress. Interestingly, when both carriers are present, a series of phenotypic effects are observed which are unrelated to Fd replacement. Here, we performed a thorough functional analysis of the photosynthetic machinery of Fld-expressing tobacco plants grown under control conditions. We show that, when compared to their WT counterparts, Fld plants have increased contents of chlorophyll a, carotenoids and higher chlorophyll a/b ratio, all of which is often associated with antenna size alterations. Indeed, using chlorophyll *a* fluorescence and P700 spectroscopy we showed that Fld plants harbor smaller antennae in both photosystems. Accordingly, resolution of thylakoid membrane proteins showed that Fld plants have lower relative contents of light harvesting complex proteins. Further functional analyses indicated that transgenic plants display increased photosystem I and II quantum efficiency and higher CO_2 assimilation rates. Taken together, the results indicate that Fld plants exhibit many characteristics that parallel high light-acclimated plants and suggest that they would be primed to tolerate conditions of high irradiation.

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Enviado por: Thalita Mendes

Phytoremediation potential of Cajanus cajan in Mn contaminated soil: effect on N fixation

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Cajanus cajan is commonly used in human and animal food, as a green manure and also for the recovery of degraded areas, due to the germination capacity of this species in compacted soils. In this work, we investigated the decontamination potential of this species in soils with high concentrations of Mn^{2+}, the response to nodulation, in addition to the quantification of the concentration of ureides and amino acids. The contamination was made from an aqueous solution of MnCl2 at the following concentrations; 0, 80, 100, 120, 140 and 160 mg/dm-*3*. After 60 days, the experiment was collected. The manganese content in tissues (leaves and roots) was quantified also nodulation status, amino acids and ureides concentration. There was no influence on nodulation between treatments, but data on mass and number of nodules showed significant differences between treatments. We observed an increase in the content of amino acids in the nodules from the dose of 140 mg dm-3, which may be related to the legume response mechanism to the stress caused by excess manganese, and this response is directly associated with the maintenance of nodulation and fixation. The variation in the number of nodules is likely due to their compromised half-life, where new nodules appear for compensation. Due to the considerable accumulation of manganese in roots and shoots and the metabolic response data obtained, *C. cajan* proved to be highly tolerant to manganese doses and could be a potential phytoremediation agent of this metal in contaminated soils.

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156
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Enviado por: Andrea Luciana Fleitas

Vesicular degradation mediated by CV (Chloroplast Vesiculation) proteins is differentially regulated in drought-tolerant and sensitive soybean genotypes

Vesicular degradation mediated by CV (Chloroplast Vesiculation) proteins is differentially regulated in drought-tolerant and sensitive soybean genotypes

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Soybean is the main rainfed crop in Uruguay. Being grown during summer, it inevitably goes through periods of water deficit, which cause yield losses. In this work, we have identified two soybean genes that encode chloroplastic vesiculation proteins (GmCV1 / GmCV2) which are induced under stress conditions. GmCV transcripts accumulate in the shoot and in root under water deficit conditions and they accumulate more intensely in sensitive genotypes (TJS2049) than in tolerant genotypes (N7001). CV proteins were previously described in Arabidopsis and rice as proteins that participate in the degradation of chloroplastic proteins during stress-induced senescence. We have observed that the vesicular degradation pathway mediated by CV genes was the most strongly induced pathway during stress-induced senescence in soybeans. On the other hand, autophagy markers and ATI1 / 2-mediated degradation were more induced in the N7001 genotype, while the degradation mediated by SAVs (Senescence Associated Vacuoles) did not show considerable differences between genotypes. Analysis of the activity of the GmCV1 and GmCV2 promoters in treatments with salt, methylviologen, light or nitrogen deprivation and natural senescence showed that these genes are induced in response to stress treatments and senescence. Response to homone treatments were also addressed. Differential induction of the GmCV1 and GmCV2 promoters suggests a functional specialization between the soybean CV genes.

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157
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Enviado por: Andrea Flemmer

Safflower (Carthamus tinctorius L.) grain and oil yield in response to different effective soil depths

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Safflower, a winter oil crop adapted to dry climatic conditions, is an alternative for the diversification of production in arid and semi-arid areas, such as the southwest of the Buenos Aires province. In this region, the effective soil depth is limited by the presence of a petrocalcic horizon at variable depth, which can limit crop root development and therefore crop yield. The aim of this study was to quantify grain oil and oleic acid content and grain and oil yield per unit area of two high oleic spring-type safflower genotypes in response to different effective soil depths (31-36 and 74-75 cm). Plants of Montola 2000 and CW99 OL were fall sown and grew under field conditions (38°25’49’’S; 62°17’10.30’’W) for two years (2017 and 2018). Grain oil content was mainly affected by the genotype (41% in CW99 OL higher ($p<0.05$) than 38% in Montola 2000). Oleic acid content was mainly affected by the year, reaching 79% and 81% in 2017 and 2018, respectively. Instead, grain and oil yield per unit area were mainly affected by the genotype and the effective soil depth being 20-26% higher ($p<0.05$) in CW99 OL than in Montola 2000 and 30-31% higher ($p<0.05$) at the higher effective soil depth. The highest values of grain (2439 $kg.ha^{-1}$) and oil (967 $kg.ha^{-1}$) yield observed at the higher effective soil depth were mainly explained by filled grain number ($r=0.70$ and 0.62, respectively; $p<0.01$).

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158
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Enviado por: Rodrigo Richard Rabello Fonseca Lucas

Reserve substances and budburst in Vitis labruscana as affected by short and long photoperiod cycles

Reserve substances and budburst in Vitis labruscana as affected by short and long photoperiod cycles

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Endodormancy is a strategy used by grapevine buds to cope with natural conditions such as low temperatures and photoperiod, thereby causing metabolic reduction and loss of vascular connection with the mother plant. Budbreak gives rise to a new growth cycle for a grapevine; in temperate regions, this phenological event takes place naturally. In tropical regions instead, temperature and photoperiod are inconsistent with natural budbreak, causing inconsistent pattern and sprouting. In this work, we aimed to determine grapevine bud reserves during budbreak in different natural photoperiod throughout a year. In addition, we aimed to determine whether buds are induced to endodormancy in such photoperiod conditions, associating the reserve presence to the axillary bud development. Vitis labruscana cv. Niagara Rosada cultivated in greenhouse were pruned twice: over short photoperiod (SDP) and over long photoperiod (LDP). To determine the presence of bud reserve, we carried out histochemical experiments and optical microscopy, and biochemical assays to quantify reserves such as soluble proteins, soluble sugars, and starch hydrolysis based on enzymatic activity to predict starch consumption. We observed that buds exhibited high concentrations of reserves initially, followed by a slight consumption under LDP. In the SDP, we observed an elevated concentration of reserves throughout the entire development of budbreak. In this study, the pruning period influenced the bud development, leading to an endodormancy-like behavior at SDP. The presence of a possible grapevine endodormancy in low latitude regions, is the highlight of this work.

Keywords: Grape, Light, Phenology, Bud, Carbohydrate, Protein
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159
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Area: Epigenetics, Chromatin, non-coding RNAs, RNA biology
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Enviado por: María Clara Fontana

Role of the RdDM pathway in the expression of transgenerational vernalization effects in Arabidopsis thaliana

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Plants can respond to environmental changes experienced throughout their life cycles and even those experienced by previous generations, developing strategies to adjust developmental transitions to conditions that ensure progeny's survival. In *Arabidopsis thaliana*, progeny responses to environments of previous generations have been associated with the function of small RNA synthesis genes and with DNA methylation frequency changes, suggesting a role for the RNA-directed DNA methylation pathway (RdDM). Vernalization (a period of cold that signals winter) impacts developmental transitions transgenerationally and has the potential to influence ecological and evolutionary processes. To understand the process by which seasonal environmental changes influence the development of plants across generations, we characterized responses to maternal vernalization on key progeny traits, and evaluated their correlation with the phenotypes of RdDM pathway mutants. Our results show that environmental cues experienced by plants even early in their life cycles (vernalization) have a strong influence on developmental traits of at least one subsequent generation. This effect on progeny germination, flowering time and reproductive biomass production is at least partially regulated by the RdDM pathway as RdDM mutants show significantly different responses when compared with the wild type genotype and between maternal treatments. Altogether, our results show a complex interaction between environments experienced by different generations and the mechanisms regulating epigenetic memory.

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Enviado por: Agustina Paula Fortuny

Transcriptome analysis of two tomato genotypes and their hybrids

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RNA sequencing (RNA-Seq) is an accurate tool used to analyse gene expression across transcriptomes and enables detection of novel genes related to interesting features. Previously, 20 hybrids obtained by crossing five tomato (*Solanum lycopersicum* L.) cultivars following a full diallel mating design were evaluated to estimate heterosis and reciprocal effect on agronomic traits and metabolites. In this work, the transcriptome profiles of red ripe fruits of four genotypes selected from those previous results were analysed by RNA-Seq. The aim was to detect differentially expressed genes (DEGs) among the genotypes. Three biological replicates of the cultivars Querubín FCA (Q) and Gema FCA (G) used as parental lines, as well as their hybrids Q x G and G x Q were evaluated. Illumina Novaseq 6000 platform was used to conduct paired-end-sequencing (2 x 150 bp) for each sample. Next-generation sequencing generated ~560 million reads. After removing low-quality reads and trimming adapter sequences, only high-quality reads (99.43%) were retained. Read alignment against *S. lycopersicum* reference genome ITAG 4.0 achieved an average-mapping rate of 93.01%. For each sample, 17,887 genes were used for differential expression analysis. Six comparisons were made between the four genotypes. Using a FDR < 0.001 and $\log_2$FC |2|, 200 DEGs were detected when all comparisons were considered. Enriched GO terms were: stimulus-response, either endogenous or exogenous, biotic or abiotic (biological processes), transcription factors (molecular function), and nucleus (cellular component). Transcriptome profile analysis enabled to find DEGs among the genotypes with the highest number when hybrids were compared.

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161
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Enviado por: romina frare

Characterization of NOD26-type aquaporins in nodules of Medicago truncatula and Medicago sativa.

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Legumes are important cultivated species in part due to symbiotic nitrogen fixation by rhizobia. Medicago truncatula is the closest plant model of alfalfa. In this work, we present the genomic and functional characterization of the NOD26a and NOD26b genes of the Medicago truncatula and Alfalfa. These genes code for aquaporin proteins of the NOD26-like sub-family. With the hypothesis that these NOD26 channels are located in
the symbiont nodule fulfilling functions related to nodulation, N2 fixation and / or the establishment of symbiosis, we explored the expression profile of each NOD26 in the whole plant through real-time PCR tests and it confirmed that MtNOD26a and MtNOD26b are highly expressed in nodules. In addition, the generation and evaluation of transgenic events pMtNOD26a::GUS and pMtNOD26b::GUS showed a strong GUS activity in nodules being the most intense expression in the nitrogen fixation zone. We apply different strategies to characterize the physiological role of these aquaporins. On the one hand, single mutant T-DNA insertion plants of Medicago truncatula were obtained for each aquaporin and these plants showed affected nodulation patterns, delay in nodulation, and deficiency in nitrogen fixation. In addition, we generated alfalfa mutants via CRISPR/Cas9 gene editing. Through the analysis of the HRFA profiles and sequencing of these mutants of alfalfa, we found the Knock-out for both NOD26 and we evaluated the nodulation patterns and nitrogen fixation of these mutants under conditions of limited nitrogen.

162
TK641QM
Area: Biochemistry and Metabolism
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Enviado por: Daniele Parma Dani

Harnessing genetic variation in metabolic traits to understand evolutionary pressures on Cleomaceae photosynthesis

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In Cleomaceae distinct photosynthetic mechanisms are found. Thus, this group is of key importance to understand the evolution of carbon concentrating mechanisms. To gain more insight into the evolution of C_4 photosynthesis in this family, we examined fifteen species that have different forms of growth, collected from different Brazilian biomes. We performed a detailed characterization of photosynthetic, anatomical and biochemical parameters in all collected species. In this regard, in addition to the A_N/C_i and A_N/PPFD curves, which have been performed so far for a limited number of Cleomaceae species, we have also collected leaf samples throughout the day for biochemical analyzes. Based on these analyzes, we could separate the species into four groups: one formed by the C_4 species *Gynandropsis gynandra* and three with C_3 photosynthesis, harboring members of the genera *Cleoserrata* and *Tarenaya*. The groups comprising C_3 species exhibit clear variation in anatomical, physiological and biochemical parameters, suggesting a great natural variation between these species. Furthermore, the unrecognized variation in leaf structure and physiology within the studied species indicates varying degrees of development to the C_3-C_4 photosynthetic mechanism. In addition, the studied access of *G. gynandra*, despite exhibiting physiological, biochemical and anatomical characters coherent with C_4 species, clearly differ from African and Asian accessions already described. Considering the great diversity of biochemical, physiological and anatomical traits found between species, we conclude that a group of species, especially herbaceous ones, have a tendency towards a physiological, metabolic and anatomical response pattern similar to the C_4 species.

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163
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Area: Developmental Biology
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Enviado por: Jesica Frik

Interaction between the DC1 domain containing protein BINUCLEATE POLLEN and the NAC transcription factor VOZ1 is required for pollen development in Arabidopsis

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Development of the male gametophyte is a tightly regulated process that requires precise control of cell division and gene expression. A relevant aspect to understand the events underlying pollen development regulation constitutes the identification and characterization of the genes required for this process. In this work we showed BINUCLEATE POLLEN (BNP) is essential for pollen development and germination. BNP is an uncharacterized protein that harbors DC1 domains with putative diacylglycerol binding activity. Pollen grains carrying the defective *BNP* allele failed to complete mitosis II and are impaired in pollen germination. By yeast two hybrid screening and bimolecular fluorescence complementation assays, we identified and confirmed the interaction with Vascular plant One-Zinc finger 1 (VOZ1) and VOZ2, members of the NAC family of transcriptional regulators. BNP and VOZ1/2 proteins were mainly detected co-localized in prevacuolar compartments. We also observed that during pollen development VOZ1 changes its distribution from exclusively cytoplasmic, at early stages, to be localized also in the nucleus in mature pollen. VOZ1 nuclear localization resulted impaired in mature pollen grains from *bnp* insertional lines, evidencing a role of BNP in VOZ1 nuclear translocation. We propose that BNP could function as a scaffold protein recruiting VOZ1 and likely VOZ2 to prevacuolar compartments into assemblies that facilitate VOZ1/2 translocation to the nucleus and therefore modulate their activity as transcriptional regulators.

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164
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Area: Biotic Interactions
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Enviado por: Pablo GONZALEZ

Effects of SOD overexpression in Sinorhizobium meliloti and Mesorhizobium japonicum over Medicago sativa and Lotus japonicus grown in salt stress condition.

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Drought and salinity conditions are the major factors affecting nitrogen fixation by legume-rhizobium symbiosis. The increase of intracellular reactive oxygen species (ROS), as a consequence, leads to activation of antioxidant system both in plant and bacteria as physiological response to prevent the toxic effects of oxidative stress.

The *mlr7636* superoxide dismutase gene was constitutively overexpressed in *Sinorhizobium meliloti* and *Mesorhizobium japonicum* MAFF303099 to test if the enhanced sod activity in bacteria contributes to mitigate the effects of salt stress on legumes. Salt stress treatments were 200 mM for Medicago sativa PROINTA Súper Monarca and NaCl 150 mM for *Lotus japonicus* MG20 in seed germinating pouches. Salt stress affected nodulation in both, *M. sativa* and *L. japonicus* when inoculated with non sod overexpressing strains. However, in stress, the inoculation of *S. meliloti* sod+ to *M. sativa* has restored the effects of salinity on nodulation, whereas inoculation of *M. japonicum* sod+ has inhibited nodulation on *L. japonicus*. In spite of inhibition of nodulation, the *M. japonicum* sod+ inoculation has mitigated the effects of salinity on *L. japonicus* promoting growth of aerial biomass and roots when compared to non-inoculated treatment. The effects seen in *M. japonicum* sod+ on *L. japonicus* in salinity might be due to plant growth promoting mechanisms.

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165
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Enviado por: Delfina Gagliardi

HWS and its role as a co-factor involved in miRNA biogenesis

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MiRNAs are 21-24 nt molecules that regulate most developmental and stress response pathways in plants. Since HASTY (HST) was first identified, it was proposed to export plant miRNAs from the nucleus to the cytoplasm, a premise based on its homology with human EXPORTIN 5. Recently, it has been shown that HST interacts with MED37 subunits and acts as a scaffold to recruit DCL1 to MIRNA *loci*, promoting the transcription and processing of pri-miRNAs, and later the non-cell-autonomous function of miRNAs, rather than the direct export of processed miRNAs from the nucleus. Complementary to these studies, and aiming to elucidate the role of HST, we performed a suppressor screening on *hst-15* mutants. Among the plants with a reversion of the typical hst-15 phenotype we identified a new mutant allele of the F-box HAWAIIAN SKIRT encoding gene. HWS has been previously linked to miRNA biogenesis, but its role remains uncertain. Additionally, plants constitutively expressing full-length HWS—but not a truncated version lacking the F-box domain—show morphological and molecular phenotypes resembling those of mutants defective in miRNA biogenesis and activity. Here, we explore the molecular crosstalk between HWS and HST to regulate the miRNA pathway. We found that HWS is capable of interacting with different components of mediator complex *in vivo* possibly promoting its degradation. Our data suggest that HWS does not directly affect HST stability but rather the pathway downstream of this protein.

166
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Enviado por: Xurxo Gago

‘Home but not Alone’: the allotetraploid Allosorus tinaei, an intermediate solution for xerophytic environments compared with their diploid parentals

‘Home but not Alone’: the allotetraploid Allosorus tinaei, an intermediate solution for xerophytic environments compared with their diploid parentals

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The allotetraploid rocky fern Allosorus tinaei (Tod.) Christenh. (AT) and its diploid parents, A. hispanicus (Mett.) Christenh. (AH) and A. pteridioides (Reichard) Christenh. (AP),frequently live in small rock cracks south-oriented exposed to high radiation and temperature and with restricted water availability. A. hispanicus develop “resurrection” leaves meanwhile A. pteridioides show deciduous leaves, and they form contact zones occupying different microhabitats. Specifically, AH is more xerophytic than AP, and the allotetraploid has intermediate water requirements (Garmendia, 1986; Pangua et al., 2019). Thus, this complex is an excellent model system to understand photosynthetic capacity and drought tolerance responses in semi-arid environments. Plants were grown in a growth chamber at 25/22.C 12/12h photoperiod under 500 µmol photon m-2 s-1 PAR radiation in 0.5 l pots with 3:1 soil:perlite sustrate. We performed a moderate drought stress (monitored by the reduction of photosynthesis (**An**), stomatal conductance (**gs**) and soil humidity) and recovery experiment. Leaf gas-exchange and chlorophyll fluorescence of 6-8 individuals per species were characterized by a Li-COR 6800 (Li-COR, USA) (flow 400 µmol air s-1, 25.C, 1200 µmol m-2 s-1 PAR radiation). Photosynthesis modelling was performed following previous methodologies (Bellasio et al., 2016; Sharkey et al., 2016). Chlorophyll, flavonol and anthocyanin content was measured by a fluorometer DUALEX (Force-A, France). We employed the TEROS-10 soil moisture sensor (Meter, USA) to measure soil humidity.

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167
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Enviado por: Jimena Gaido

Effects of inoculation with new Bacillus strains over wheat (Triticum aestivum) growth and yield under a field condition assay

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Wheat (*Triticum aestivum*), one of the major crops in the world, is affected by different stresses that are partially overcome by the use of agrochemicals. New strategies with low environmental impact are rising, such as the utilization of plant growth promoting rhizobacteria (PGPR). The aim of the present work was to determine PGPR ability of six new *Bacillus* strains over wheat crop grown under field conditions. Mercurio Klein seeds were inoculated with a *Bacillus* suspension (potato-dextrose medium, ON, adjusted at DO=1) or a dilution of the culture media as control, and then sown in a plot, using one sowing line of 2m per treatment separated by 17cm from each other. Growth and yield related parameters were determined on different days after sowing (DAS). The plants developed from seeds inoculated with *Bacillus sp*. and *B. megaterium* showed a higher number of tillers at 70 DAS than control (6,2±2,7 5,5±1,9 5,3±2,2 vs 3,4±1,1 respectively, media±SE, $p<0,05$, $n=10$) and one of the *Bacillus sp*. strains gave rise to a higher number of spikes (5,7±0,9) at 100 DAS than control (4,4±2,2). After harvest, at 135 DAS, it was found that seeds inoculated with a *B. megaterium* strain showed augments regarding the control ($p<0,05$, $n=15$) in the number of spikes (4,1±1,6 vs 2,7±0,7) and tillers (3,1±1,6 vs 1,7±0,7) per plant, number of grains per plant (106,8±39,7 vs 73,1±13,3) and grain weight (mg) per plant (3,4±1,6 vs 2,2±0,6). These results allow us to select the *B. megaterium* strain to be furtherly studied as a potential bioinoculant.

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Area: Plant breeding
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Enviado por: Luciana Ayelen Galizia

Root system architecture phenotyping under field conditions in a maize diallel mating design

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Even if during the last decades root system architecture has been highlighted as a promising trait for achieving a Second Green Revolution little is known about its genetic control and variability, specially under realistic field conditions. The objectives of this work were to characterise root length in two contrasting genotypic groups (GG; inbreds and hybrids) at the beginning and ending of the critical period for grain yield determination and to quantify the heterosis level. A diallel mating design comprising 6 inbreds and the 15 derived hybrids was evaluated in a field experiment carried out at Pergamino during the 2013-14 season, under irrigated and N fertilized conditions. A soil core of 5 cm diameter to 2 m depth was obtained for each plot at each sampling date (V_{14} and R_2). The samples were divided into 20 cm layers, washed and scanned to determine root length. When comparing total root length of the GG significant differences were found only at the R_2 sampling, mainly due to the greater deepening of the hybrids. At R_2, the mean % heterosis was 42% for the whole root system and of 79% for the 120-200 cm layer. Root length at R_2 at the 120-200 cm layer was positively correlated with grain yield (r=0,43, p<0,001). Genetic variability within GG was detected for total root length and for the reached length in each soil layer. These results demonstrate how promising root system traits can be. Further research is needed to establish which traits could be useful for breeding.

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FJ777BN
Area: Biotechnology, Research Tools, Resources
Tipo de presentación: Poster en formato PDF
Enviado por: Jimena Gallardo

Reproductive mode assessing of Eragrostis curvula using specific sequences

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Eragrostis curvula is a South African forage grass that reproduces both sexually and asexually through the production of maternal clonal seeds (apomixis). The most precise characterization of the reproductive mode is by cytoembryological analyses, which is very laborious and time consuming. The objective of this work was to develop a sensitive technique to assess the reproductive mode of *E.* curvula plants to replace or complement the cytoembryological analysis. To do this specific sequences obtained by GBS (Genotyping by sequencing) from individuals of a mapping population obtained from the cross between a sexual (OTA-S) and a facultative apomictic (Don Walter) cultivar were used. Reads were mapped against a previously sequenced floral transcriptome of the apomictic Don Walter cv., mapping approximately 32% of the GBS reads of each individual. Then, transcripts that did not mapped on reads of the sexual hybrids and mapped on reads of all the apomictic hybrids were chosen and, based on these sequences, specific primers were designed for seven candidate transcripts. Validation was carried out with the parental genotypes of the mapping population and also with other *E. curvula* genotypes that were previously characterized by cytoembryology. As a result, only one set of primers could be selected that allowed to precisely differentiate plants according to its reproductive mode (closely linked to the trait), being this gene now a new candidate involved in apomictic pathways.

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KL146BP
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Yutcelia Carolina Galviz Fajardo

ROS production in rice subjected to recurrent drought depends on the availability of nutrients and light

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Plants subjected to recurrent stimuli often exhibit responses influenced by memory-based mechanisms that, eventually, optimize plant performance. Since such mechanisms can demand an extra-energy cost, it is reasonable to infer some dependence on the availability of nutrients and light. Stresses, such as those caused by drought, can affect ROS production, altering the redox homeostasis of plants. This work aimed to evaluate the effects of recurrent drought on ROS production in rice plants (*Oryza sativa* L.) growing under controlled conditions, without nutrient supply, and under shade. In each condition, plants were subjected to 1, 2, or up to 3 drought stimuli. Contents of superoxide radical ($O_2^{\bullet-}$), hydrogen peroxide (H_2O_2) and, lipid peroxidation (MDA) in leaves and roots were quantified. Leaf relative water content dropped in response to all drought treatments. Under the three conditions evaluated, $O_2^{\bullet-}$ contents in leaves and roots tended to increase as the plants suffered more drought events, but the highest contents were observed in leaves of plants under shade. H_2O_2 content was similar in leaves of plants without nutrient supply, regardless of drought stimuli. However, H_2O_2 content increased due to recurrent drought for the other two conditions, as well as observed in the content of MDA. In roots, H_2O_2 and MDA contents were higher in plants experiencing the first drought when compared to those subjected to 2 or 3 drought stimuli. In general, positive or negative memory effects on ROS production were observable in rice plants subjected to recurrent water stress according to the growing condition.

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171
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Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: María Dina García

Aerenchymal-tissue and cell-wall thickening in roots of subtropical Poaceae under waterlogging may explain no differences in plant growth between treatments.

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Plants of three species, *Chloris gayana* Kunth 'Finecut' (CgF), *Panicum coloratum* 'Klein Verde' (PcKV) and *Panicum virgatum* 'Shawnee' (PvS), were grown six weeks in pots with alkaline-sodic soil (pH=8.3; CE_s=0.93 dSm^{-1} and ESP=26.2 %) kept at field capacity. Then plants were subjected 26 days to two water conditions: waterlogging (pots were submerged in water, 5.8 % O_2) and field capacity (control). Plants showed no differences in dry matter accumulation between water-condition treatments (DGC, $p \leq 0.05$). CgF stood out for its highest total dry mass per plant, regardless the water condition ($p<0.0004$). Histological evaluation was performed on samples of the middle portion of 2 mm-diameter roots. Aerenchyma was observed in the roots of all three species when subjected to waterlogging. Another morphophysiological change that helps to maintain an adequate level of oxygen within roots under waterlogging is suberin and lignin deposition in endodermis and exodermis cell-walls. CgF, PcKV and PvS differed ($p<0.0001$) (mean±MSE in mm) in endodermis (18.49±0.29; 23.10±0.37; 21.09±0.47; respectively) and exodermis thickness (37.80±1.31; 66.8±1.57; 58.96±1.73; respectively) and waterlogging increased this thickness ($p<0.0001$) 11 % in endodermis and 26 % in exodermis. The number of exodermal cells (NEC) and the thickness of the internal tangential cell-walls (TITCW) of the endodermis showed significant interaction between species and water condition ($p <0.0001$). Waterlogging increased NEC and TITCW (%) in CgF (21 and 31, respectively) and PvS (51 and 65, respectively) but not in PcKV.

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172
DK311MD
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Leonela Analía García

Irradiance affects sugar distribution and storage in the sunflower plant

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In sunflower, photoassimilates accumulated at flowering contribute up to 15% of grain final weight. It is assumed that these reserves are located in the stem and promoted by increase radiation, but little information about their distribution in plants under different light levels is available. To analyze this, sunflower plants (Advanta 5304) were field grown in Balcarce, Argentina in 2018/9 and 2019/20, under three irradiances: 50% shading, control (both at density = 5.5 plants m^{-2}) and thinned (to 25%). Treatments were set at apex induction into reproductive stage (approximately 10 leaves > 4 cm in length). We measured the concentration and amount of soluble carbohydrates in leaf, stem (upper, middle, basal), receptacle, and roots at flowering.

In both years, the increase in irradiance between shaded and controls led to higher sugar concentration in all plant organs. However, irradiance rise between controls and thinned plants did not significantly promote sugar concentration in middle and upper stem parts, in which most of these reserves were stored, while carbohydrate concentration increased about 100% in roots. Intermediate promotion values were found for receptacle and basal internodes. On the other hand, higher radiation determined large increases in the weight of all plant organs, and this was particularly remarkable between control and thinned plants, leading to a strong increase in sugar total amount per plant.

Our results suggest that sunflower has a high morphological plasticity to changes in radiation, which may strongly affect plant capacity to deliver reserves to grains, while maintaining relatively constant stem sugar concentrations.

173
LJ798JC
Area: Signal Transduction
Tipo de presentación: Poster en formato PDF
Enviado por: Julián García Bossi

“CHARACTERIZATION OF CALCIUM TRANSPORTERS DURING POLLEN TUBE GROWTH IN Arabidopsis thaliana”

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In plants, calcium signals are involved in multiple physiological processes such as stomatal opening, stress responses, and polarized growth of root hairs and pollen tubes. These signals are given as repetitive oscillations of cytosolic free Ca2+ where the intensity and amplitude correlate according to the stimulus. Pollen tube growth occurs through the concerted action of different factors such as pH, ROS, actin and a calcium gradient. Any imbalance between these factors causes aborted pollen tubes and therefore, defects in fertility.

In this work, we propose to perform a functional study of the P2B type calcium pumps (Autoinhibited Ca2+-ATPases, ACAs), in pollen tubes of Arabidopsis thaliana. These pumps are mainly located in vacuole, endoplasmic reticulum and/or plasma membrane and are involved in removing calcium from the cytoplasm. Studies conducted with ACA insertional mutants have shown that these pumps have a physiological role beyond the maintenance of Ca2+ homeostasis.

From a total of 14 ACAs reported in the Arabidopsis genome, we study single and multiple mutants of those genes specifically expressed in mature pollen. So far, we report that double mutants show a significant deviation in the expected segregation ratio, a decrease in siliques length and a smaller number of seeds compared to the wild type genotype.

174
GH372RL
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Selene García Hernández

Role of DGK1 and DGK2 in Membrane Contact Sites.

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Eukaryotic cells have regions of interaction between two organelles where some proteins, which act as tether, bring both membranes closer (10-30 nm) without fusion, named membrane contact sites (MCS). Two organelles that can form MCS are endoplasmic reticulum (ER) and plasma membrane (PM). ER-PM CS play important metabolic functions such as communication between both membranes, lipid homeostasis and $Ca2+$influx. Our group has identified that AtDGK1 and AtDGK2 (Diacylglycerol kinase 1, AT5G07920 and Diacylglycerol kinase 2, At5g63770) form a complex with a well-known protein located at ER-PM CS, Synaptotagmin1 (SYT1, At2g20990).Upon perception of stress, phospholipase C is activated at PM to hydrolyse PIP(4,5)P2 or PI4P in order to generate diacylglycerol (DAG)and inositol phosphates. DAG is phosphorylated by diacylglycerol kinases (DGKs) to produce phosphatidic acid (PA). DAG and PA are important signalling molecules. There are seven DGKs encoded in Arabidopsis thaliana genome, but only DGK1 and DGK2 have a transmembrane domain that anchors them to the endoplasmic reticulum, the rest are cytoplasmic. DGK1 and DGK2 appear to play a role in stress response as both are induced by exposure to low temperatures.Also,our group has foundthat dgk2knockout mutant produces lowerresistance to freezing. Using confocal microscopy, we have analysed the subcellular localization of these two proteins and their interaction with SYT1 and between them using FRET and co-immunoprecipitation studies. Our studies suggest that DGK1 and DGK2 act in concert with SYT1 to regulate the production of PA at ER-PM CS and highlight the importance of these proteins for the correct response to stress tolerance.

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175
SM931QF
Area: Abiotic Stress
Tipo de presentación: video presentacion
Enviado por: Georgina Paula García Inza

Mechanisms of regulation of oleic and linoleic acid content in olive oil due to the effect of high temperature. Integrating molecular and ecophysiological scales.

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Ambient temperature during olive fruit growth modulates the proportion of the main fatty acids in the oil. Experiments in which temperature was manipulated showed that the oleic acid concentration decreased 0.7%°C^{-1} with the increase in temperature. Fatty acid unsaturation is mediated by fatty acid desaturases, such as the *FAD2* gene family that is involved in the conversion of oleic to linoleic acid, the main fatty acids that determine olive oil quality. The aim of this work was to elucidate the mechanisms behind olive oil fatty acid composition in response to high temperature, integrating responses at the gene expression and ecophysiological scale. Trees of cultivars Arbequina and Coratina were placed in field open top chambers during the period of active oil accumulation. Two treatments were applied: control and heated (+3 ° C, compared to control) for 36 days. Gene expression and fatty acid analysis revealed that oleic acid in mesocarp oil significantly decreased 2.6 and 6.6 percentage points in 'Arbequina' and 'Coratina' after 36 days of exposure to high temperature. This response was consistent with the upregulation of the relative transcript abundance of *FAD2-5* in 'Arbequina' and 'Coratina' and *FAD2-2* in 'Coratina'. Linoleic acid content was linearly related to *FAD2-5* transcript abundance (R^2=0.6 and R^2=0.4, for 'Arbequina' and 'Coratina', respectively). This work points out how temperature modulates the proportion of the main fatty acids through the transcriptional regulation of the *FAD2* genes, affecting oil quality.

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176
FQ156RC
Area: Biotechnology, Research Tools, Resources
Tipo de presentación: Poster en formato PDF
Enviado por: Gabriela Gerhardt da Rosa

The use of putrescine in the regeneration of Butia exilata e Butia lallemantii (ARECACEAE) flower bud explants in vitro

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The genus Butia (Becc.) (Arecaceae) comprises fruit palms, with medicinal potential, found in countries such as Brazil, Paraguay, Argentina and Uruguay. With exclusively sexual propagation, seeds with slow, low and uneven germination, its use is difficult, so alternatives are sought, such as the regeneration of these plants in vitro, through the use of different parts such as inflorescences. The experiment was carried out at Embrapa, using floral buds separated from the rachiles, subjected to disinfestation in a laminar flow chamber, sectioned with a scalpel and immersed in ascorbic acid solution, until inoculated in medium modified MS and in the following treatments: T1 - control (no putrescine added); T2 - with 250 μM-1 of putrescine; T3 - with 500 μM-1 of putrescine; T4 - with 750 μM-1 of putrescine and T5 with 1000 μM-1 of putrescine. The inoculated material was kept in a growth room, in the dark, for 30 days, after which it was evaluated whether there had been regeneration of flower buds or not. Plant regeneration of explants of both species was not observed, however, there was a significant difference for swelling, tissue growth and greenish color promoted at different concentrations of putrescine. A higher percentage of swollen explants, with greenish yellow coloration is observed in the T3 treatment for both species, as well as a decline in swelling when the putrescine concentration increases in the T4 and T5 treatments. It is concluded that a higher percentage of swollen explants was obtained when 500 μM-L1 of putrescine was applied.

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177
LK115LR
Area: Developmental Biology
Tipo de presentación: Poster en formato PDF
Enviado por: Virginia Gigena

Evolution, expression patterns, and functional characterization of MADS32 in grasses

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Grass family differs from other angiosperms because of their modified flowers. Grass flowers lack of the conventional sepals and petals, having instead two bract-like organs called lemma and palea. The homology of the lemma and palea is yet a theme of discussion. To understand the identity of these novel organs we study the molecular evolution, expression patterns, and perform the functional characterization of MADS32, a MIKC-type MADS-box transcription factor with a known function in the marginal zone of the rice palea. The phylogenetic reconstruction showed that MADS32 is present in basal angiosperms and monocots. Based on RT-PCR assays we found that MADS32 is expressed in several plant organs, in particular in young inflorescences. To understand the role of MADS32 during development we study the overexpression of the MADS32 homolog from *Setaria viridis* on the model species *Arabidopsis thaliana*. The phenotypes of the overexpressing lines showed variations in several stages of vegetative and reproductive development. Interestingly, the flowers of the transgenic lines presented fused sepals indicating genetic evidence on the homology of the palea with the sepals of dicotyledons.

178
FM655QM
Area: Biotechnology, Research Tools, Resources
Tipo de presentación: Poster en formato PDF
Enviado por: Iván Gitman

Protease inhibitors as stress-responsive effectors in potato. Biotechnological applications

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A bioinformatic analysis allowed us to identify 142 protease inhibitors (PIs) in the potato genome. This multigene family regulates protein *turn-over* preventing catabolism of essential proteins during metabolic processes and plays a role in the defense against heterologous proteases from pathogens and pests. PIs have been proposed as an alternative to chemical pesticides for the control of herbivorous insects, and as abiotic stress-protective factors. However, an unbalanced expression of PIs may compromise plant’s endogenous proteolytic processes. Thus, it is very important to explore which endogenous processes they regulate, which are their specific targets, and how their activity is regulated. According to RNAseq data available at the SPUD DB, five PIs are among the 49 genes induced upon different abiotic, biotic and hormone treatments. Three of them, Soltu.DM.03G018520, Soltu.DM.03G018580 and Soltu.DM.03G018600, are Kunitz-type PIs (KTIs) located in a QTL for *Phytophthora infestans* resistance in chromosome 3 at 43 Mbp. Soltu.DM.03G018520 and Soltu.DM.03G018580 are among the most expressed genes in the genome under control conditions. RT-qPCR assays performed using RNA from *in-vitro* plants cultured under control conditions or exposed to 150 mM NaCl during 24 h, confirmed the induction of these two KTIs under salt stress. Currently we are conducting expression analysis in plant tissues and in plants exposed to long-term (3 weeks) salt stress. In the future we aim to characterize these genes in overexpressing or knockdown plants to elucidate their potential as biotechnological tools.

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179
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Area: Epigenetics, Chromatin, non-coding RNAs, RNA biology
Tipo de presentación: Poster en formato PDF
Enviado por: Axel Giudicatti

HYL1-dependent recruitment of HOS15 to MIRNA loci regulates micro RNA transcription in plants

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Post-transcriptional gene silencing mediated by microRNAs (miRNAs) modulates numerous developmental and stress-response pathways. In a previous work, we used a Luciferase-based forward genetic screening to identify genes required for miRNA biogenesis and activity. Among the isolated mutants with impaired miRNA activity, we identified a new allele of the gene encoding HIGH- EEXPRESSION-OF-OSMOTICALLY-RESPONSIVE-GENES-15 (HOS15). HOS15 was previously described as a partner of HDAC and E3-Ubiquitin-ligase complexes and was typically associated with cold, drought and ABA responses by controlling gene expression.

Here, we characterize HOS15 in the context of the miRNA pathway. Using Y2H and microscopy assays we found that HOS15 directly interacts with HYL1 but not with other proteins of the pathway. Also, we found that an over-accumulation of HOS15 lead to HYL1 degradation. Interestingly, we found that HOS15 associate with MIRNA loci to regulate some miRNAs transcription. But most importantly, HOS15 recruitment to miRNA encoding genes is lost in *HYL1* mutants or plants expressing a HYL1 phosphorylated-mimic. Moreover, HYL1 dimerization is also required for this recruitment. This suggests that HOS15 specificity for miRNA genes is caused by its interaction with HYL1, which is likely to recognize such loci by the hairpin structures of nascent pri-miRNAs. In turn, such recruitment of HOS15 will modulate pri-miRNA transcription creating a regulatory feedback loop. We propose a dual role of HOS15 in miRNA biogenesis. First, HOS15 can promote the transcription of miRNA genes based on the HYL1 recruitment to *MIRNA* locus. Second, HOS15 can modulate HYL1 protein levels through degradation to indirectly affect miRNA processing.

180
SQ828DG
Area: Abiotic Stress
Tipo de presentación: video presentacion
Enviado por: Marisol Giustozzi

MBD proteins in Arabidopsis: involvement in plant responses after irradiation with UV-B radiation

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In eukaryotes, DNA methylation is one of the most important epigenetic regulations. In particular, the modification of cytosines is related to gene silencing. In animals and plants, there are specialized methyl CPG binding domain protein (MBD) proteins that have the ability to interpret these modifications. MBD proteins act together with chromatin modifying complexes by repressing transcription, and play a biological role regulating genomic stability. In maize, MBD101 acts facilitating methyltransferase activity under stress conditions. In Arabidopsis, there are 4 proteins MBD domain proteins, which show homology to maize MBD101: MBD1, MBD2, MBD3 and MBD4.

In recent years, an increase in the levels of ultraviolet B radiation reaching the earth's surface has been measured. Plants, being sessile organisms, are exposed to ultraviolet B radiation, causing lesions in macromolecules such as proteins, DNA, RNA and lipids. Thus, the aim of this work is to investigate the function of MBD1, MBD2, MBD3 and MBD4 proteins in Arabidopsis thaliana in UV-B exposed plants. For this purpose, we analyzed *mbd1*, *mbd2*, *mbd3*, *mbd4* mutant plants grown under UV-B conditions. Our results show that *mbd1*, *mbd2*, *mbd3*, *mbd4* mutants show increased DNA damage after UV-B exposure. Moreover, plants with decreased levels of each of these MBD proteins showed lower programmed cell death than wild-type plants. These plants also present alterations in cell proliferation both in control and after UV-B conditions. Together, our results suggest that MBD1, MBD2, MBD3, MBD4 participate in DNA damage responses after UV-B in Arabidopsis.

181
MC725MR
Area: Other
Tipo de presentación: Poster en formato PDF
Enviado por: Rodrigo Gomez

Loss of a single chlorophyll binding site in the CP29 antenna subunit affects the supramolecular organization and function of photosystem II.

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Land plants' life depends on the energy captured from sunlight by complex protein-pigment systems present in the thylakoid membranes of chloroplasts called photosystems (PSs). These complexes efficiently transform light into chemical energy providing ATP and reducing power for CO_2 conversion into biomass. In plants two kind of PSs exist, PSI and PSII, sharing a similar organization with a core complex, were charge recombination takes place, surrounded by a peripheral antenna system composed of light-harvesting complexes (LHCs), involved in light absorption. Also, the LHCs play a crucial role in photoprotection under situations of excess illumination through non-photochemical quenching (NPQ) mechanisms. The PSII antenna is composed by trimeric complexes linked to the reaction center by monomeric subunits, forming supercomplexes. The relative size of these supercomplexes is dynamically adjusted in response to illumination conditions and determines the whole macro-organization of the grana fractions into the thylakoid membrane. CP29 is one monomeric subunits of PSII antenna critical for the fast activation of NPQ and the assembly of the largest forms of PSII supercomplexes. In this work, an Arabidopsis CP29 know-out deletion mutant was complemented with a CP29-H242L sequence carrying a single residue substitution that abolish the chlorophyll b614/b3-binding site implicated in the efficient energy transference from the antenna system to PSII core. Plants carrying the CP29-H242L version show an extensive reorganization of the photosynthetic complexes in the grana, affecting the plastoquinone diffusion and thus the whole photosynthetic process and photoprotection properties, with strong modification of NPQ capacity.

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Area: Biochemistry and Metabolism
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Enviado por: Diego Gomez Casati

Functional and structural characterization of the mitochondrial Iron-Sulfur Cluster Complex of Arabidopsis thaliana

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Several proteins including a cysteine desulfurase (AtNFS1) and frataxin (AtFH) are involved in the formation of Fe-S groups in *Arabidopsis* mitochondria, specifically, in Fe and sulfur loading onto scaffold proteins, and the subsequent formation of the mature Fe-S cluster. We recently found that the small mitochondrial chaperone, AtISD11, and AtFH are positive regulators for AtNFS1 activity. Moreover, when the three proteins were incubated together, a stronger attenuation of the Fenton reaction was observed compared to that observed with AtFH alone. Moreover, we found that these three proteins physically interact, and sequence alignment and docking studies showed that several amino acid residues reported as critical for the interaction of their human homologous are conserved. Our results suggest that AtFH, AtNFS1 and AtISD11 form a multiprotein complex that could be involved in different stages of the iron–sulfur cluster (ISC) pathway in plant mitochondria.

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183
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Enviado por: Matias Gonzalez

Physiological responses and phytoextraction potential of Canna indica L. under Zn(II) and Cu(II) stress.

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In the last years, soil heavy metal contamination has become one of the most serious environmental problems due to being not biodegradable and having high persistence in the environment. Phytoremediation is a low-cost technique for the treatment of large areas with medium or low concentrations of heavy metals but its success depends, among other variables, on proper species selection. A pot experiment was carried out to determine the usefulness of *Canna indica* (a South America native species) as a Zn(II) and Cu(II) phytoremediator species. The plants were grown until reaching adequate biomass for the application of three increasing Zn(II) (1000, 2000 and 3000 mg.kg^{-1}) and Cu(II) (500, 1000 and 1500 mg.kg^{-1}) solutions. Seven days later, dry weight, relative membrane conductivity, chlorophyll, carotene, malondialdehyde, soluble proteins and shoot Zn(II) and Cu(II) contents were measured. Zn(II) treatment caused a decline in the dry weight, chlorophyll and carotene contents, whereas the relative conductivity, malondialdehyde and soluble proteins content, all in the aerial part, showed the opposite pattern. Cu(II) applications caused a decrease in the dry weight, chlorophyll, carotene and soluble protein content, while the opposite pattern was observed for relative conductivity and malondialdehyde content. Shoot heavy metal content reached values approximately 70 (1580 mg.kg^{-1}) and 12 times higher (145 mg.kg^{-1}) for Zn(II) and Cu(II) than the control respectively. Although some physiological functions were altered, the plants could grow without major alterations. Our results suggest that *Canna indica* can be used for the phytoremediation of polluted soils with moderate concentrations of Zn(II) and Cu(II).

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Oxidative stress reduction and quality increase in apples by the application of phospholipid and polysaccharide biofilm

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Apple crops in north Patagonia grow under high temperature and solar radiation conditions that promote oxidative stress and induce quality decrease in fruit. Biofilm treatments that cover fruit skin, reduce oxidative processes and could decrease apple physiopathy disorders. The aim of this work was to evaluate the effect of a biofilm made of phospholipids and polysaccharides (Parka®), in apple fruit (*Malus domestica* Borkh) cultivar 'Granny Smith' on its oxidative metabolism and quality. Trees were sprayed with Parka® (9.5 l/ha) water solution, in October, November and December. Non-treated trees were used as Control. Oxidative disorders, quality factors and physiopathies (solar damage and blush) were evaluated at harvest. Parka treatment reduced lipid peroxidation by 15% and it attenuated chlorophyll degradation by 22%. Antioxidant capacity and total polyphenols were not modified. Parka treated fruit showed lower soluble solids concentration compared to Control (10.5 vs. 11.6 ºBrix), and significantly higher firmness (76.4 vs. 72.8 N). Differences in fruit weight and size between treatments were not detected. Parka treatment significantly decreased the amount of fruit with sun damage, consequently increased the amount of healthy fruit compared to Control. The biofilm Parka attenuates oxidative stress caused by high solar radiation and temperature, reduces ripeness advance and improves the quality of apple fruit.

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185
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Area: Epigenetics, Chromatin, non-coding RNAs, RNA biology
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Enviado por: Lucía Gonzalo

Co-transcriptional miRNA processing promotes non-cell-autonomous silencing.

Co-transcriptional miRNA processing promotes non-cell-autonomous silencing.

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The biogenesis of plant micro RNAs (miRNAs) is a dynamic and highly regulated process. In the last few years, several miRNA biogenesis factors were found associated with the MIRNA-encoding loci. Thus, it was suggested the possibility that the miRNA biogenesis complex initiates its assembly early during transcription. It is also possible that such early assembly lead to the co-transcriptional processing of nascent pri-miRNAs. We analyzed plaNET-seq data searching for processing intermediates still bound to the RNA Polymerase II to test this hypothesis. This experiment allows us to confirm the co-transcriptional processing of miRNAs and that such a process is different depending on the pri-miRNA processing mechanic. In this sense, we found that the loop-to-base processed mechanism is entirely conducted co-transcriptionally. In contrast, base-to-loop processing requires a second post-transcriptional step to release the mature miRNA. Interestingly, we found that co-transcriptional processing and a more canonical post-transcriptional processing co-exist for most miRNAs and that the balance between both mechanisms is variable and dynamic. Furthermore, we found that the formation of DNA:RNA hybrid between 5'-end ssRNA arm of pri-miRNA nascent and MIR loci promotes its own co-transcriptional processing.

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Area: Plant Hormones
Tipo de presentación: Poster en formato PDF
Enviado por: Jorge González-Villagra

Preharvest salicylic acid application effects on fruit quality and yield in Aristotelia chilensis plants subjected to irrigation deficit.

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Drought stress decrease fruit quality and crop yield. Salicylic acid application (SA) has shown to be a promising tool to cope with drought stress in plants. *Aristotelia chilensis* (Mol.) is an endemic fruit species of Chile. However, there are not information in *A. chilensis* in response to SA application. Therefore, we aimed to evaluate the preharvest SA application on fruit quality and yield in *A. chilensis* subjected to irrigation deficit. Three-year-old plants growing under field conditions were subjected to: 1) well-watered plants (WWP: 100% crop evapotranspiration (ETc), and Irrigation deficit plants (IDP: 60% ETc) based on ETc. A single application of 0.5 mM SA was performed at fruit colour change by spraying fruits and leaves of both irrigation treatments. IDP showed 20% higher total soluble solids compared to control plants; however, not differences were observed with SA. Meanwhile, titratable acidity (TA) was significantly reduced in IDP without SA compared to WWP with SA. IDP with SA showed higher equatorial (15%) and polar (10%) diameter compared to IDP without SA. Meanwhile, no changes were observed between WWP and IDP with SA. Same tendency was observed in fruit fresh and dry weight, where IDP with SA exhibited higher (about 15% and 10%, respectively) levels compared to IDP without SA. Water deficit also reduced fruit yield (about 15%) compared to WWP, meanwhile, SA recovers fruit yield in IDP, showing no changes between control and IDP with SA. Thus, SA improve fruit quality and fruit yield in *A. chilensis* plants subjected to drought stress

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Enviado por: Sergio Andrés Granados Ortiz

EFFECTS OF SELENIUM FOLIAR APPLICATION ON PHYSIOLOGICAL PARAMETERS IN FOUR SUNFLOWER GENOTYPES UNDER SALINITY

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In this contribution, the effects of Selenium (Se) foliar application, under the form of sodium Selenite (Na_2SeO_3), on the physiology of four sunflower hybrids (NEON, DK 4045, DF 816, and SUNGRO 70 CP) subjected to saline stress were evaluated. Plants were grown in a "walk-in" culture chamber at 16 h photoperiod and 28°C/18°C daytime/night temperatures. The Se was sprayed with an atomizer, and four doses of 0.25 mg Se pl^{-1} were applied up to complete 1 mg Se pl^{-1}. The physiological parameters: membrane damage, relative water content (WRC), osmotic potential (PO), osmotic adjustment capacity (AO), oxidation damage (DAB staining), total antioxidant capacity (ABTS method), and catalytic enzyme activity (CAT), were examined. SUNGRO 70 CP showed the highest increase in membrane damage (13.77%) compared to control plants. In control plants, membrane damage was reduced by Se. Salinity decreased WRC in all genotypes; NEON was the most affected (-9.21%). Salinity decreased osmotic potential (PO) for DK 4045 and SUNGRO 70 genotypes and increased DAB-stained tissue in SUNGRO 70 CP (327%). Only DK 4045 did not show a significant increase in H_2O_2 accumulation under saline conditions. SUNGRO 70 CP and DK 4045 genotypes showed a decrease in ABTS activity under salinity. Finally, the saline-stressed DF 816 hybrid highlighted a significant increase in CAT activity, which was attributed to the Se foliar treatment. In conclusion, the Se foliar application reduced the oxidative damage under saline conditions and contributed to improve physiological parameters.

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Enviado por: Cecilia Grossi

Methylobacterium sp. 2A influences root development through auxin signalling

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The plant root system determines the capacity to acquire nutrients and water and plays a critical role in adaptation. Auxins are the “root forming hormones of plants” and some root-associated beneficial bacteria can stimulate root growth secreting indole acetic acid (IAA). *Methylobacterium* sp. 2A is a pink-pigmented rhizobacterium that can enhance Arabidopsis growth and lateral root density. Two proposed IAA biosynthesis pathways were predicted in its genome: the indole-3-acetamide (IAM) and the indole-3-acetonitrile (IAN) pathways. Moreover, it can produce high levels of IAA *in vitro*. In this work, we aim to shed light on the influence of this isolate on root behavior. For this, *DR5:GUS* tomato plants were grown *in vitro* on MS medium and roots were inoculated with 10 µl of a bacterial suspension (OD_{600} 0.05 in 0.85% NaCl). Histochemical and fluorometric analyses were conducted at 10 dpi. Also, roots of Arabidopsis *DR5:GUS* plants were inoculated at stage 1.0 with 2 µl of the above-mentioned suspension and pictures were taken at 7 dpi. Furthermore, an Arabidopsis auxin mutant, *iaa19*, which is defective in lateral root formation, was inoculated and the number of lateral roots was quantified at 4 and 7 dpi. Upon inoculation, the expression of the auxin-responsive promoter *DR5* was induced in the roots of tomato and Arabidopsis plants, and lateral root formation was improved in *iaa19* plants (37 and 44% at 4 and 7 dpi, respectively). Our results suggest that *Methylobacterium* sp. 2A promotes lateral root formation through modulating auxin signaling.

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189
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Enviado por: Florencia Viviana Guastaferri

Strawberry PIP regulation by membrane tension increments may have a cooperative mechanism ruled by homo- or heterotetramerization

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FaPIP1;1 and FaPIP2;1 are aquaporins from *Fragaria x ananassa* that modulate plasma membrane (PM) water permeability (P_f) during strawberry ripening. FaPIP2;1 promotes high membrane P_f when expressed in *Xenopus laevis* oocytes and reduces its water transport capacity under cytosolic acidification. When FaPIP2;1 is coexpressed with FaPIP1;1, both PIPs form heterotetramers and exhibit an enhanced pH gating sensitivity. This shows that interactions between different subunits modify the cooperativity among monomers, so we propose that FaPIP2;1-FaPIP1;1 heterotetramers are a suitable model to study the cooperativity in mechanical regulation of aquaporins. In the current work we studied the osmotic behavior of *Xenopus* oocytes expressing FaPIP2;1 alone or together with FaPIP1;1. Our aim was to evaluate FaPIP2 homotetramers and FaPIP2-FaPIP1 heterotetramers response to membrane tension changes, holding the hypothesis that they have different sensitivity to mechanical regulation. By means of osmotic experiments we found that FaPIP2;1 homotetramers responds just like mechanosensitive aquaporins do, showing low P_f at high Δosm, whereas FaPIP2;1-FaPIP1;1 heterotetramers show the same P_f at all tested gradients. Simulations performed with a model that states that P_f depends on initial permeability and the cell pressure-volume curve, show that the difference between homo- and heterotetramers osmotic responses is due to the regulation mediated by membrane tension increments rather than their initial intrinsic permeability. Hence, FaPIP2;1-FaPIP1;1 heterotetramers appear to be at least less sensitive to membrane tension changes than FaPIP2;1 homotetramers. This suggests that the interaction between different types of monomers affect the mechanosensitivity of aquaporins evidencing a cooperative effect in the gating mechanism.

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190
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Enviado por: Gustavo Gudesblat

Expression of SARS-CoV-2 Spike RBD protein in Arabidopsis thaliana seeds

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Arabidopsis thaliana seeds have been previously used to express antibodies with high yields. Here, we expressed the Receptor Binding Domain (RBD) of the Spike protein of SARS-CoV-2 virus, responsible for the binding of the virus to the ACE2 receptor, in *A. thaliana* seeds. The RBD was fused to the C-terminus of a murine immunoglubulin G2a (IgG2a), also called Fc-tag, which was shown to increase the stability and yield of several proteins expressed in plants. The Fc-RBD fusion was cloned downstream of the promoter of a seed storage protein gene in a binary vector, and transformed in *A. thaliana* by floral dip. The expression of Fc-RBD was tested by ELISA using HRP coupled anti-IgG antibodies in protein extracts obtained from seeds of T1 segregant plants. A western blot using the same antibody revealed the presence of a predominant band of the expected size (108 kDa), as well as some bands of lower MW, most likely corresponding to degradation products. An initial attempt of Fc-RBD purification using a Protein A-Sepharose column was successful, however more protein degradation was observed, and the overall yield was low, around 200 ug per gram of seeds. Currently we are in the process of selecting lines with higher expression and attempting to optimize the purification process. If yield can be increased, Fc-RBD expression in seeds could be a cost effective system to produce kits for the clinical detection of SARS-CoV-2 antibodies in serum.

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Enviado por: Antonio Guglielmini

Thermo-photoperiodic responses in buckwheat (Fagopyrum esculentum Moench) cultivar Mancan for modelling crop phenology

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Interest in buckwheat is increasing due to the hight quality protein content and the absence of gluten in its grains (achenes), both attributes being more valued in a food for human consumption. To expand de agricultural frontier of buckwheat it is necessary to know the thermo-photoperiod response. Although it is considered a quantitative short-day plant, there is not a clear characterization of this response throughout all phenological phases of crop cycle. Five field experiments were carried out between 2005-2019 growing seasons. Treatments consisted of a combination of different sowing dates of cultivar Mancan in two locations (CABA and Chacabuco, Buenos Aires) in a randomized complete 3 block design. The photoperiod explored throughout sites and sowing dates ranged from 11.2 to 15.4 hours. Main phenological events: emergence (Em), first flowers open (FFlO), first brown fruits (FBrF) and end of fruit ripening (EFrR) were determined and the duration of phases measured in thermal time units (°Cd, base temperature 5 °C). Crop cycle increased with increases in mean photoperiod explored during Em–EFrR phase (271.0 ± 30.7 °Cd/hour; r^2= 0.70) and should be mainly ascribed to variations in FFlO–FBrF phase (183.3 ± 27.7 °Cd/hour; r^2= 0.56). While Em–FFlO and FBrF–EFrR phases showed much lower photoperiod sensitivity responses (72.6 ± 12,2 °Cd/hour; r^2= 0.51 and 82.4 ± 15.2 °Cd/hour; r^2= 0.45, respectively. The linear relationships found in all cases suggest that optimum photoperiod is shorter than 11.2 hours for this species. Awareness of the photoperiodic sensitivity response of each ontogenic stage will allow calibration to construct simple phenological model.

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192
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Area: Abiotic Stress
Tipo de presentación: video presentacion
Enviado por: Anthony Guihur

Quantitative proteomic analysis to capture the role of heat-accumulated proteins in moss plant acquired thermotolerance

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The growing impact of global warming and its adverse effects on crop yields is urging for more research on molecular mechanisms by which plants may cope with increasingly frequent extreme heat waves. At dawn of a scorching summer day, land plants must anticipate upcoming extreme midday temperatures by timely establishing molecular defences that can keep heat-labile membranes and proteins functional. A gradual morning pre-exposure to increasing sub-damaging temperatures induces heat-shock proteins (HSPs) that are central to the onset of plant acquired thermotolerance (AT). To gain knowledge on the mechanisms of AT in the model land plant *Physcomitrium patens*, we used label-free LC–MS/MS proteomics to quantify the accumulated and depleted proteins before and following a mild heat-priming treatment.

High protein crowding is thought to promote protein aggregation, whereas molecular chaperones prevent and actively revert aggregation. Yet, we found that heat priming (HP) did not accumulate HSP chaperones in chloroplasts despite an altered photosynthesis machinery, although protein crowding was six times higher than in the cytosol. In contrast, several HSP20s strongly accumulated in the cytosol, yet contributing merely 4% of the net mass increase of heat-accumulated proteins. This is in poor concordance with their presumed role at preventing the aggregation of heat-labile proteins. The data suggests that under mild HP unlikely to affect protein stability. Accumulating HSP20s leading to AT, regulate the activity of rare and specific signalling proteins, thereby preventing cell death under noxious heat stress.

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Enviado por: Mariela Monteoliva

Biochemical traits to classify genotypes by drought tolerance in legumes

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Drought is one of the main limitations for agriculture in Argentina, especially for legumes such as soybean and peanut. However, the direct selection of tolerant genotypes on the fields required long periods of time due to the unpredictability of the environmental conditions. Our group uses an alternative approach to classify the genotypes in controlled conditions at early stages, which are then validated on the fields. Additionally, we use different traits to evaluate and monitor the genotypes under a controlled drought, such as proline (compatible osmolyte which accumulated under dehydration), and chlorophylls (photosynthetic pigments which have been correlated to higher yields under stress for several crops). We aim to develop strategies to reduce breeding times for legumes. Seeds were provided by the EEA Marcos Juarez and Criadero El Carmen germplasm banks, for soybean and peanut, respectively. We grew the plants in a greenhouse and exposed the plant to a controlled drought (30% for soybean and 15% for peanut) at early developmental stages (3rd or 6th leaves respectively). Here we report how proline, chlorophyll, and antioxidant ability, as well as some morphological traits, are useful to classify soybean and peanut genotypes according to their drought tolerance.

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Enviado por: José Gándara

EFFECT OF DROUGHT ON WATER STATUS, HYDRAULIC PROPERTIES AND GROWTH IN Eucalyptus grandis AND CLONAL HYBRIDS WITH RED GUM SPECIES

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In Uruguay, afforestation with clonal hybrids between *E. grandis* and Red Gum is evaluated. This study was designed to analyze the effect of drought on water status and growth in clones of *Eucalyptus grandis* (G1, G2, G3) and hybrids with Red Gum species (*E. grandis x camaldulensis*, GC; *E. grandis x tereticornis*, GT). At the age of six months, two cycles of water stress were imposed as a function of transpirational loss under greenhouse conditions. Predawn leaf water potential (ψ_{pd}), midday leaf water potential (ψ_{md}), leaf relative water content (RWC), stomatal conductance (gs), and plant growth were measured across each cycle. Daily fluctuation of ψ was calculated as $\Delta\psi = \psi_{pb} - \psi_{md}$. Pressure-volume curves were elaborated to calculate functional parameters, Leaf-specific hydraulic conductivity (k_L), the percentage loss of hydraulic conductivity (PLC), and vessel diameter were measured. Drought reduced height (20%) and diameter (17%) with no genotypic effects. Under such conditions, Red Gum hybrids showed the highest gs, $\Delta\psi$, and RWC, with GC having higher stomatal conductance than G3 (22%), G1 (25%), and G2 (48%). Embolism removal increased k_L by twofold (1.85 higher) with GC reaching the highest value($3,51 \pm 0,28$ kg m^{-1} MPa^{-1} s^{-1} and $7,63 \pm 0,53 \times 10^{-4}$ kg m^{-1} MPa^{-1} s^{-1}, with and without embolism respectively). This clone had the highest vessel diameter (18%) and was more vulnerable to cavitation since its PLC was on average 47% higher than others'. GC had higher cell-wall flexibility (lower ε), which implies a better adaptation to cell-water loss.

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Area: Abiotic Stress
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Enviado por: Gabriel Gómez Ocampo

BBX21 increases photosynthesis and water use efficient in potato plants under moderated drought through reducing non-stomatal limitations.

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The B-box (BBX) proteins are zinc-finger transcription factors with a key role in growth and developmental regulatory networks mediated by light. AtBBX21 overexpressing (BBX21-OE) potato (*Solanum tuberosum*) plants, cultivated in optimal water conditions, have higher photosynthesis rates and stomatal conductances without penalty in water use efficiency (WUE), with a higher tuber yield. In this work, we cultivated potato plants in two water regimes: 100% and moderated drought (35% of field capacity) that imposed leaf water potentials between -0.3 and -1.2 MPa for vegetative and tuber growth in a window time of 14 d or 28 d, respectively. We found that 42-d-old plants of BBX21-OE showed higher photosynthesis rates and WUE than wild-type Spunta (WT) plants during the morning in moderated drought. The same pattern of response was also observed for tuber yield. Mechanistically, we found that the advantage of BBX21-OE lines under moderated drought was mainly supported by non-stomatal limitations. BBX21-OE lines have a higher mesophyll conductance (g_m) than WT and, consequently, a higher CO_2 concentration ratio between the chloroplast and the stomatal cavity (Cc/Ci). We also found a higher photosynthesis rate in BBX21-OE lines at the same Cc (Phot/Cc ratio) under moderated drought, determined by higher maximum capacity of electron transport (J_{max}) values than those observed for WT plants, without differences in the maximum rate of Rubisco carboxylase activity (Vc_{max}). Our work suggests that BBX21 protein enhances potato yield under moderate drought by increasing photosynthesis through a reduction of non-stomatal limitations.

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LL669MN
Area: Plant Physiology and Ecophysiology
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Enviado por: Leila Hamze

Olive reproductive phenology along a latitudinal-altitudinal gradient in Argentinian growing regions

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Olive reproductive phenology is influenced by environmental factors including air temperature. Nevertheless, detailed information about olive phenology is scarce outside of the Mediterranean Basin. The aim of this study was to evaluate the effects of location, cultivar and year on two olive phenophases: reproductive budburst (BBCH53) and full flowering (BBCH65) at north and central western Argentinian growing regions. Phenological observations were taken weekly in seven olive cultivars at six locations along a latitudinal (29°-33°S) and altitudinal (450-1246 masl.) gradient during two growing seasons. The gradient had differences of up to 5.5°C for the mean temperature during winter and early spring (i.e. pre-flowering period). The dates for BBCH53 occurred over an extended time period of 70 days (August 6 to October 15) depending on the location x cultivar x year combination, while BBCH65 occurred over 38 days, starting on October 1. Significant differences between locations and cultivars were found for both phenophases. BBCH53 showed a delay at the lowest, more northerly latitude location relatively to the others, probably because of lower chilling accumulation. BBCH65 occurred earliest at the lowest latitude/altitude and the latest at the highest latitude. Location explained most of the variability in the dates for both phenophases, while cultivar accounted for about 6%. The duration of the period between BBCH53 and 65 was negatively related with the average air temperature during the same period. These results from an ample temperature range will be useful for modeling efforts.

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197
RQ347BS
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Eduardo José Haverroth

The dgt mutation modifies the biochemical responses to drought and recovery in tomato plants

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The low-auxin-sensitivity tomato mutant, *dgt*, when compared with its wild-type, has shown some hydraulic differences and modified leaf gas exchange capacity. As such alterations might impact its drought response, we investigated to what extent some biochemical compounds would change in response to drought and recovery in tomato mutant *dgt* and its wild-type (WT, cv. Ailsa Craig). Biochemical analyses were performed on leaf material collected from: i) irrigated plants; ii) plants at critical drought, and iii) plants rehydrated after reaching critical drought. The genotypes present marked differences in the time to reach critical drought: whereas the WT achieved the critical drought at 6 days, it took 18 days of water withholding to *dgt* plants experience the same condition. The water deficit strongly reduced the starch content for both genotypes when compared with irrigated plants; however, after the rehydration, only the WT could recover its starch levels. WT showed increases in non-structural carbohydrates (NSC) content under drought conditions, but the NSC returned to control levels after rehydration; on the other hand, the *dgt* showed an 80% reduction in NSC under drought and such reduction was persistent after rehydration. After the stress condition and rehydration, remarkable increases in the content of amino acid, proline, protein, and chlorophyll were observed in *dgt* plants. Conversely, these same parameters did not change in WT plant. These results imply that *dgt* plants have a modified biochemical response to drought and it remains to be seen how such modifications impact growth and reproduction after drought relief.

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RD325MM
Area: Plant breeding
Tipo de presentación: Poster en formato PDF
Enviado por: Fernando Hernández

Genome-wide association mapping of post-harvest dormancy in cultivated sunflower

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In sunflower, fruits often display post-harvest dormancy (PHD), which negatively affect the quality of hybrid seed. Marker-assisted selection (MAS) is a useful tool to increase selection efficiency, especially for traits which need extensive phenotyping efforts, as PHD. However, the lack of markers associated with target traits is a major bottleneck in MAS. To find marker-trait associations (MTA), we performed genome-wide association mapping of PHD. PHD was evaluated in 76 sunflower lines (37 maintainer and 39 restorer lines), genotyped at ~14 K SNP markers. Fruits were produced in two environments (field and greenhouse), and germination evaluated under three conditions: two weeks after harvest at 20 / 10 °C (T1) or constant 25 °C (T2), and six weeks after harvest at constant 10 °C (T3), totaling five treatments (2 environments x 3 conditions except seeds from the greenhouse in T2). Two traits, the proportion of germinated fruits at five (G5) and 16 (G16) days were measured. We found 13 MTA (-log10 > 4), eight for G5 and five for G16. No SNPs were associated with more than one trait/treatment, evidencing the complex genetic architecture of PHD in sunflower. In the associated loci, dormant alleles were found at high frequency (mean = 0.36; 0.07 - 0.9). In lines, the cumulative number dormant alleles varied from 1 to 8 (of 13) and it significantly explained PHD variation in 5 / 10 trait-treatment combinations (r^2 = 0.08 - 0.32). Validating these markers in biparental populations and/or unrelated genotypic collections is necessary for their application in MAS.

CH529RD

Area: Developmental Biology

Tipo de presentación: Poster en formato PDF

Enviado por: Tamara Hernández-Verdeja

GENOMES UNCOUPLED1 role during plastid and seedling development in Arabidopsis

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One of the most dramatic challenges in the life of a plant occurs when the seedling emerges from the soil and exposure to light triggers expression of genes required for establishment of photosynthesis. This process needs to be tightly regulated as premature accumulation of light harvesting proteins and photoreactive chlorophyll precursors cause oxidative damage when the seedling is first exposed to light. Photosynthesis genes are encoded by both nuclear and plastid genomes and to establish the required level of control, plastid-to-nucleus (retrograde) signalling is necessary to ensure correct gene expression. Here we show that the GENOMES UNCOUPLED1 (GUN1) is already present in the dark non-photosynthetic plastids, and that GUN1 levels decrease when the seedlings are exposed to light and the plastids develop into functional chloroplasts. In the dark, the GUN1-mediated retrograde signal controls the expression of nuclear encoded genes. Particularly, GUN1 represses the transcription factors *GOLDEN2-LIKE1* and *2* (*GLK1* and *GLK2*) that regulate the expression of components of the light harvesting complex, and chlorophyll biosynthetic enzymes. This mechanism restricts excessive accumulation of the phototoxic chlorophyll intermediates in the dark and thus ascribes GUN1 as a safeguard during the critical step of seedling emergence from darkness. Thus, we propose that GUN1 main function is to assist in the coordination of plastid and seedling development during the transition from skoto- to photomorphogenesis, in order to protect the seedling upon the emergence from the soil.

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200
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Area: Abiotic Stress
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Enviado por: Carolina Huercano Rubens

NTMC2T5: newly identified ER-Chloroplast contact sites proteins involved in abiotic stress.

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Membrane contact sites (MCS) are microdomains where two membranes of two different organelles are closely apposed. MCS are essential for non-vesicular transport of lipids. Some proteins mediating lipid transport in MCS contain specific domains, as the synaptotagmin-like mitochondrial lipid-binding (SMP) domain. This domain is present in SYT proteins which are localized in ER-PM MCS. In the case of ER-Chloroplast MCS, this non-vesicular transport should be very important as vesicular transport do not occur. To our knowledge, no protein is known to be involved in direct transfer of lipids between ER and Chloroplast outer membrane.

We have studied the occurrence of other SMP proteins in *A. thaliana* and *S. lycopersicum* by searching remote orthologs of human E-syt1 (SMP protein). By using transient expression in *N. benthamiana* leaves followed by confocal microscopy we have identified one family (NTMC2T5) of proteins with two homologs in *A. thaliana* and only one member in *S. lycopersicum* that are anchored to the outer membrane chloroplast and interacting with the ER. In addition, to determine whether these proteins are involved in abiotic stress tolerance, we have analysed seed germination rates of Arabidopsis mutants for these genes under different conditions. Mutants have shown lower germination rates in media supplemented with NaCl and lower rates of expanded cotyledons in media supplemented with ABA. These results are revealing the first identified proteins localized in ER- Chloroplast MCS which might have a role in lipid transfer. Our results suggest they might be involved in abiotic stress signalling through an ABA-dependent pathway.

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201
QQ388FR
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: MARIA IGLESIAS

Responses of plant water status to deficit irrigation and warming in young olive trees (Olea europaea)

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Changes in rainfall patterns and increases in average temperature are expected with climate change. Yet, little information is available as to how plant water status will respond to the combination of water deficit and increased air temperature in fruit trees species. The aim of this study was to evaluate the individual responses of deficit irrigation and warming and their combination on plant water status during the Spring in young olive trees. Two temperature and two irrigation levels were applied in open top chambers between August and December of 2018 and 2019 to 2-3 years-old trees grown in pots (cv. 'Arbequina' in 2018; 'Coratina' in 2019). The temperature levels were a near-ambient control and an elevated treatment that was 4 °C above the control, while the two irrigation levels were 100% and 50% of irrigation needs. Midday stem water potential (SWP), stomatal conductance and leaf temperature were measured periodically, and the difference between leaf and air temperature (ΔT) was calculated. The SWP generally decreased due to irrigation deficit and warming when applied individually. When both treatments were combined, an additive response was observed. In contrast, stomatal conductance was consistently decreased by deficit irrigation, but was often not affected by warming. Irrigation deficit did not affect ΔT, but it was significantly decreased by warming early in the season, which is indicative of greater evaporative leaf cooling at higher air temperature. The results emphasize the need for manipulative field experiments in studying the physiological responses to water availability and warming with global change.

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202
BK325LK
Area: Biotic Interactions
Tipo de presentación: Poster en formato PDF
Enviado por: Fernando Ibañez

Evolution of LysM-RLK gene family in wild and cultivated peanut species

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LysM-RLKs are transmembrane proteins containing three extracellular LysM domains, one transmembrane region, and one intracellular kinase domain. These proteins are ample in plants and are crucial for differentiation among structurally similar microbial molecular signals or patterns. In legumes, LysM-RLK perception of rhizobial lipo-chitooligosaccharides known as Nod factors (NFs), triggers a signaling pathway related to the onset of symbiosis development. On the other hand, activation of LysM-RLKs upon recognition of chitin-derived short-chitooligosaccharides initiates defense responses. In this work, we identified the members of LysM-RLK family in cultivated (*Arachis hypogaea* L.) and wild (*A. duranensis* and *A. ipaensis*) peanut genomes and reconstructed the evolutionary history of the family. Within this phylogenetic framework, we reinterpreted the functional data reported for peanut LysM-RLKs. In addition, potential roles of two identified proteins during NFs and chitosan inoculation were assessed by gene expression analyses and protein modeling. Results indicated that peanut LysM-RLK is a highly diverse family. Digital expression analyses indicated that specific *A. hypogaea* LysM-RLK receptors were up-regulated during the early and late stages of symbiosis. Also, expression profiles and 3D protein folding predictions of selected receptors revealed particularities possibly related to their capacity to participate in NF or chitosan recognition. The analyses of LysM-RLK in the non-model legume peanut can contribute to gain insight into the molecular basis of legume-microbe interactions and to the understanding of the evolutionary history of this gene family within the Fabaceae.

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203
QM587GH
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Julia Iparraguirre

Macrocystis pyrifera algae extracts combined with Azospirillum brasilense ameliorate the Zea mays plants growth submitted to different water conditions

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To improve crop yields the application of fertilizers to provide nutrients to soils is recommended. An alternative option to substitute nutritional supplements of chemical origin is the use of biofertilizers. This study characterized and analyzed the composition of mineral nutrients, phytohormone-type compounds and metabolomics profile of the extract of the brown alga Macrocystis pyrifera. This extract was also combined with the plant growth promoting bacterium Azospirillum brasilense (Az39) and the effectiveness as a biofertilizer of natural origin was evaluated on Zea mays plants under two different water irrigation treatments. Algae extract combined with Az39, possess a high content of nitrogen, magnesium, phosphorus, gibberellins, cytokinins, auxins and carbohydrates. Consequently, the application of algae and bacteria combination exerted a positive effect on corn growth, both in plants exposed to field capacity conditions and those under water deficit conditions. Thus, this suitable biofertilizing formula may to be used in the corn cultivation under different climatic conditions and water regimes, reducing the dependence of chemical fertilizers and providing an improvement towards sustainable and environmentally friendly agriculture.

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204
DH258HT
Area: Plant Hormones
Tipo de presentación: Poster en formato PDF
Enviado por: Alon Israeli

Multiple Auxin-Response Regulators Enable Stability and Variability in Leaf Development

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Auxin-signal transduction is mediated by the antagonistic activity of transcriptional activators and repressors. Both activators and repressors belong to gene families, but the biological importance of this complexity is not clear. Here, we addressed this question using leaf development as a model by analyzing mutants in multiple auxin-response components. In developing compound leaves, auxin promotes leaflet formation and blade growth, and in the regions between leaflets, auxin response is inhibited by the Aux/IAA protein ENTIRE (E). e mutants form simple leaves due to ectopic blade growth in the intercalary domain. Using this unique loss-of-function phenotype and genome editing of auxin-response factor (ARF) genes, encoding auxin-response activators, we identified the contribution of specific ARFs to the e phenotype. Mutations in the related ARFs SlMP, SlARF19A, and SlARF19B, but not SlARF7, reduced the leaf blade and suppressed the e phenotype in a dosage-dependent manner that correlated with their relative expression, leading to a continuum of shapes. While single e and slmp mutants affected blade growth in an opposite manner, leaves of e slmp double mutants were similar to those of the wild type. However, the leaf shape of e slmp was more variable than that of the wild type, and it showed increased sensitivity to auxin. Our findings demonstrate that the existence of multiple auxin-response repressors and activators stabilizes the develop- mental output of auxin and that tuning their activity enables shape variability. The increased complexity of the auxin response therefore balances stability and flexibility in leaf patterning.

205
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Area: Developmental Biology
Tipo de presentación: video presentacion
Enviado por: Alon Israeli

Auxin-GA interaction in tomato leaf development

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Cell proliferation and expansion are crucial to determining organ shape and function. The plant hormone auxin controls these two phases in many developmental processes throughout the plant's life. However, how a single molecule executes such two different outcomes is still unknown. Here, we used the compound leaves of tomato to investigate the basic principles underlying auxin-mediated leaflet initiation (proliferation) and blade growth (expansion). We found that auxin affect the gibberellin (GA) pathway in opposite manner. Long auxin treatment promotes the expression of GA biosynthesis genes, suggesting that GA mediates auxin in leaf development, as was shown in many other processes. Genetic analysis of GA biosynthesis deficient mutants in backgrounds of increased auxin signaling suggested that auxin and E-mediated ectopic growth is partially regulated by GA biosynthesis. Interestingly, the expression of many GA degradation genes, *GA2ox* is rapidly induced by auxin and when mutated, leaflet initiation is impaired, suggesting that auxin-mediated leaflet initiation requires low GA levels. In addition, we found that GA acts non-autonomously during leaf development. GA is produced in leaflets and moves to the intercalary domain to inhibit further initiation. We propose a model by which organ development is coordinated by the interaction of two hormonal ques: Auxin, a local growth regulator that activates GA, which has a broader effect on organ-wide differentiation.

206
FC387SR
Area: Biotic Interactions
Tipo de presentación: Poster en formato PDF
Enviado por: Vanesa G. Jacobi

Volatiles released by mutant corn seedlings with morphological features for shade avoidance are preferred by the stinkbug Dichelops furcatus.

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The Neotropical stink bug *Dichelops furcatus* F. (Hemiptera: Pentatomidae) has recently become a new pest of corn (*Zea mays* L.) in Argentina and Brazil. This stink bug species feeds on corn seedlings reducing the number of plants per hectare and crop yield. Volatile organic compounds (VOCs) released by corn seedlings are used by *D. furcatus* adults as host-associated cues. Since plant-plant competition affects both plant growth and defenses, it is possible that VOCs emission can be adjusted to the physiological changes. Corn plants perceive neighbor competition by phytochromes B1 and B2, and phytochrome B corn mutants show shade avoidance features in absence of plant-plant competition signals. In this study, we assessed *D. furcatus'* olfactometer orientation to VOCs emitted by seedlings of the wild type corn inbred line France 2 (WT) and its isogenic mutants lacking either phytochrome B1 (Phy B1) or B2 (Phy B2). Besides, VOCs released by the corn lines were collected and analyzed by using a coupled gas chromatography – mass spectrometry (GC-MS). We observed that *D. furcatus* orientated towards VOCs released by Phy B1 mutant seedlings rather than to VOCs of either WT or Phy B2 seedlings ($p<0,05$; Chi square goodness of fit test). Analysis of collected volatiles showed that Phy B2 seedlings emitted higher amounts of methyl salicilate and indole ($p<0,05$; ANOVA). The results suggest that crop conditions with high intra-specific competition increase attraction of *D. furcatus* to corn seedlings.

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BP462FN
Area: Biotic Interactions
Tipo de presentación: Poster en formato PDF
Enviado por: Francisco Ignacio Jasso Robles

Arabidopsis thaliana polyamine oxidase 1 overexpression affects plant response to Pseudomonas syringae pv. tomato DC3000

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Polyamines are low molecular weight aliphatic amines that play an essential role in different cellular processes and in response to abiotic and biotic stimuli. The main polyamines are the diamine putrescine, the triamine spermidine and the tetraamine spermine. It has been shown that polyamine catabolism is important in the plant defense response against pathogens, like hemibiotrophic bacteria of the genus *Pseudomonas*. Spermidine and spermine are oxidative deaminated by flavin-dependent polyamine oxidases (PAOs) producing hydrogen peroxide. Being the later an important signalling molecule that depending on the site where it is produced differentially modulates the plant response after pathogen recognition. In this work we studied the role of polyamine oxidase-mediated polyamine catabolism in *Arabidopsis thaliana* in response to *Pseudomonas syringae* pv. *tomato* DC3000 (*Pst*). In particular, we focused on the role of spermine catabolism mediated by AtPAO1. Therefore, a *35S::AtPAO1* overexpression line was generated and its phenotype was analyzed during plant-*Pst* interaction. In order to evaluate this phenotype, reactive oxygen species content, PAO and respiratory burst oxidase homologue (RBOH) activities were measured in presence or absence of *Pst* and spermine supplementation. Colony forming units were also estimated. The *35S::AtPAO1* overexpression line was more susceptible to *Pst* infection than wild type (WT) plants and this phenotype was alleviated with spermine supplementation. Differences among this *35S::AtPAO1* overexpression line, a previously characterized loss-of-function *Atpao1* mutant line and WT plants are discussed to elucidated the role of AtPAO1 in plant defense.

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208
SL395PG
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Enviado por: Felipe Jesus

Central clock genes and starch metabolism in Sugarcane

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LATE ELONGATED HYPOCOTYL (LHY) and TIMING OF CAB 1 (TOC1) comprise the central loop of the plant circadian clock, a transcriptional machinery that controls many physiological processes, including the dynamic of starch degradation. We harvested the leaf +1 of nine genotypes of field-grown sugarcanes to quantify the relative expression of *ScLHY* and *ScTOC1* and measure starch content in four different time points (ZT03, ZT07, ZT12 and ZT27) by enzymatic assay. Genotypes with a lower amplitude of *ScLHY* (< 6 dCt) have more starch in ZT3 than plants with a high amplitude of this morning gene. Varieties with lower amplitude of the *ScTOC1* gene (< 2 dCt) have more starch in ZT 7, mid-day, than plants with high amplitude. Four varieties showed high variation in starch content among the four time points, ANOVA $p<0.05$, and three also differ between time points. In fact, the starch content in IN84-105 does not show significant differences only between morning ZTs. This genotype has a high amplitude of *ScLHY* (7.5 Ct) but a low amplitude of *ScTOC1* (1.6 Ct). Our results suggest that the amplitude of the core circadian clock genes is essential to regulate the fine-tune of starch metabolism in sugarcane.

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209
MD354CB
Area: Systems, Synthetic, and Computational Biology
Tipo de presentación: video presentacion
Enviado por: Nathan Johnson

Leveraging public datasets to explore transcriptional connections between abiotic stresses

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Plants sense and respond to their environment through intricate transcriptional pathways. Responses relating to abiotic stresses for nitrogen and water availability have been well-studied in model and crop plants. While these pathways yield unique outcomes, there is also frequently overlap in the transcriptional responses between these treatments. By utilizing the wealth of publicly available sequencing data, we have a powerful tool to compare and find important connections for these stresses. Searching online repositories, we found over 500 sequencing libraries relating to drought, nitrogen, and ABA-hormone treatments. We completed and normalized their metadata profiles, allowing for universal comparisons of treatment details and regimes. Differentially expressed genes were derived for each experiment and further filtered to find genes which are consistently regulated for a given treatment. Utilizing this high-confidence set of genes dependent on these stresses, we are able to look for connections between their regulatory networks. We find significant overlap for genes involved in nitrate and drought treatments, in addition to ABA and drought gene which serve as a positive control. Examining expression of these high-confidence DEGs shows very strong correlation of between ABA and drought treatments. Nitrate and drought treatments instead show a less-strong but clear negative correlation. This protocol is a powerful approach to interrogate the relationships between highly-studied pathways with lots of sequencing data. With this strategy, we are able to capture relevant genes which may be tissue, treatment, or cryptically responsive on a transcriptional level, improving the precision and sensitivity of gene regulation studies.

Financing: Millennium Institute for Integrative Biology (iBio); Millennium Science Initiative, Chile

210
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Area: Biotic Interactions
Tipo de presentación: Poster en formato PDF
Enviado por: Marcelo Juarez

Isolation, characterization and transcriptomic analysis of an argentinean Phytophthora infestans isolate during early infection of Solanum tuberosum var. Spunta

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Potato (*Solanum tuberosum*) is among the most important food crops worldwide. One of the most devastating pathogens affecting potato crops is the oomycete *Phytophthora infestans*, the causal agent of potato late blight (LB). In Argentina, potato crops are dominated by Spunta, a variety that is susceptible to local strains of *P. infestans*. A sustainable and effective strategy to manage LB is to breed disease resistance into potato following a knowledge-based approach. This requires the characterization of local *P. infestans* population structure and dynamics, as well as building a catalogue of effector proteins secreted by relevant isolates. The repertoire of pathogen´s secreted effectors will determine not only the outcome of infection but also the robustness of LB resistance strategies deployed in the field. Nonetheless, this information is very limited for local *P. infestans* population. The aim of this project is to build key knowledge on argentinean *P. infestans* population. In order to fulfil this goal, we obtained a local *P. infestans* isolate (PiNSL-19) from field infected material, and genotypified it using a previously validated panel of 12 SSRs. We used this isolate to infect Spunta leaves to collect total RNA at several time points after inoculation. RNAseq was performed on this samples by Illumina sequencing. We could identify infection stage specific upregulated effectors, including those recognized by previously described potato immune receptors, and some uncharacterized RxLR effectors. Together with DNA sequencing (in progress) and qPCR validation, we will be able to determine the effector repertoire and peculiarities of PiNSL-19.

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211
GQ731NN
Area: Biochemistry and Metabolism
Tipo de presentación: Poster en formato PDF
Enviado por: Karoline Geralda Mendes Karoline

Anthocyanin overexpression severely compromises plant fitness under low light in tomato plants

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Anthocyanins are flavonoids with functions that range from pigmentation to UV protection in plants. As cyanic plants present the shade avoidance syndrome, we asked whether an excessive accumulation of anthocyanins could incur a high metabolic cost, thus increasing the minimal light requirements for plant growth. To addres this question, we used plants of *Solanum lycopersicum* grown under 25 (LL), 50 (ML), and 100 (HL) µmol photons m^{-2} s^{-1}. Two genotypes were used: the cultivar Micro-Tom (MT) and the heterozygote for 35S::*ANT1*$^{TAL-2}$ (ANT1): MT has a low anthocyanin content; in contrast, ANT1 plants overexpress a transcription factor for the accumulation of anthocyanins. ANT1 plants had their height and leaf area severely reduced at all light intensities. At 90 days after germination, the genotypes presented contrasting differences regarding developmental stage and survival: 100, 30, and 0% of MT individuals reached anthesis at HL, ML, and LL, respectively; in contrast, ANT1 plants at ML and LL did not reach anthesis and the event was observed at only 50% of ANT1 individuals at HL. Noteworthy, whereas MT plants presented a 100% of survival rate regardless of treatment, all ANT1 plants at the LL treatment had died by the end of the experiment (the survival rate was 90% for HL and ML). Therefore, we conclude that anthocyanins increase the plant light compensation point, and overexpressing the pigment in plants grown under low light might be detrimental to plant growth.

Keywords: *Solanum lycopersicum*, shade avoidance, metabolic cost, light compensation point.
Financing: CNPq.

212
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Area: Plant Hormones
Tipo de presentación: Poster en formato PDF
Enviado por: Santiago Julian Kelly

Changes in leaf hormone concentrations in soybeans growing under non-inductive photoperiods after flowering.

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In soybeans (*Glicine max* L. Merr) short days induce or accelerate flowering. In plants exposed to non-inductive photoperiods (*i.e.* long days) after flowering the duration of post-flowering developmental stages is lengthened, with a concomitant delay of leaf senescence and pod development. Since changes in hormone concentrations could underlie these responses, the aim of this work was to determinate if non-inductive photoperiodic after flowering altered leaf hormonal concentrations. Plants of soybean growing under field conditions were exposed to inductive (natural day length) or non-inductive (natural day length + 4 hs artificial light) photoperiods starting at flowering. At 17, 24, 36 and 58 Thermal days (Td) after flowering, leaf concentration of salicylic acid (SA), indole acetic acid (IAA), jasmonic acid (JA), abscisic acid (ABA), zeatin (Z), dihydrozeatin (DHZ), isopentenyladenine (iP) and gibberellic acid (GA1 and GA3) were measured. At 17, 24 and 36 Td there were no significant differences between photoperiods in the concentration of none of these hormones. At 58 Td the plants under non-inductive photoperiod had significantly higher leaf concentrations of GA1, Z and iP compared to inductive photoperiods. The increased concentrations of Z and iP may be partly responsible for delayed leaf senescence, whereas changes of GA1 could be associated to delayed development of pods.

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LS672DJ
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Belen Kettler

High night temperature during post-flowering in field-grown maize increases night respiration and reduces kernel number and photosynthesis

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This study aimed to evaluate the effect of high night temperature (HNT) during maize post-flowering (R1+2d to R1+16d) on kernel number (KN), crop growth rate expressed in thermal units (CGR_{TU}), night respiration (Rn), photosynthesis (Amax), and cell membrane stability (CMS). An experiment was conducted at Corrientes (27°28’45’’S; 58°47’06’’W) in a split-plot design with three replications during the 2019 spring season without water-nutrient restrictions. Two thermal conditions were assayed using polyethylene shelters (main plots): (i) HNT from 1900-0700h, and (ii) ambient night temperature (ANT). Two hybrids (Te, temperate; and St, subtropical) were randomly assigned to subplots within each main plot. At R1+2d and R1+16d, CGR_{TU} was estimated through aboveground biomass sampling. The KN was estimated at harvest. Leaf gas exchange was measured in ear leaves during the night (Rn) and midday (Amax). The CMS was estimated by the electrical conductivity of ear leaf discs. Night mean temperature during post-flowering period was 27.7°C and 23.3°C for HNT and ANT, respectively. The KN was reduced by 9% ($p<0.05$) in both hybrids by HNT with non-significant changes in kernel weight and grain yield. Reductions in KN were explained by declines in CGR_{TU} ($r=0.75$; $p<0.01$). The HNT caused a larger effect in Rn on Te (+40%) compared to St hybrid. The HNT reduced Amax significantly ($p<0.05$; 18%, among hybrids) but CMS remained unchanged at the end of the heating period. In summary, HNT decreased KN by reduce growth and hastened development (CGR_{TU}), and by reduced Amax, increased Rn and thus altered carbon balance.

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214
JQ434QJ
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Federico Nalli

Leaf photosynthesis and NDVI during maize reproductive stages: relationships with grain yield under two contrasting growing seasons

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This study aimed to identify the association among leaf photosynthesis (Amax), normalized difference vegetation index (NDVI) and grain yield (GY) in four maize hybrids growing in two contrasting seasons. Experiment was conducted at Corrientes (27°28'45''S; 58°47'06''W) with adequate water and nutrient conditions in a split-plot design with three replications during 2019-2020. Main plots consisted in two growing seasons (GS): early or late (E_{GS} and L_{GS}, respectively). Four hybrids with different genetic background formed the subplots. GY was estimated by manual harvest (4 m^{-2}). Amax was measured in ear leaves *ca.* once a week from R1 to R4. NDVI was obtained from a multispectral camera mounted on an unmanned aerial vehicle. Amax and NDVI data were averaged across moments. Photo-thermal conditions (*i.e.*, Q) during reproductive stages were modified between GS (0.46 and 0.34 MJ °Cd^{-1} for E_{GS} and L_{GS}, respectively). Delayed sowing date significantly ($p<0.0001$) decreased GY (7781 and 5206 kg ha^{-1} for E_{GS} and L_{GS}, respectively; averaged across genotypes), which was also influenced by genotype ($p=0.03$). Delaying GS, reduced Amax more than NDVI (15% and 4% averaged across hybrids, respectively). GY and Amax were positively correlated in E_{GS} ($r=0.9$; $p<0.0001$) and L_{GS} ($r=0.83$; $p<0.001$). NDVI was associated with Amax only for L_{GS} ($r=0.7$; $p<0.01$) and it was not associated with GY. Amax explained GY ($p<0.05$) in all hybrids in both GS, whereas NDVI was correlated with GY only for one hybrid ($r=0.86$; $p<0.05$). NDVI values were close to saturation may explain the poor association with GY in comparison with Amax.

Financing: - PI 18A011: Secretaría General de Ciencia y Técnica, Universidad Nacional del Nordeste (UNNE).-PD I-060: Programa Nacional de Eco-fisiología y Agroecosistemas – Instituto Nacional de Tecnología Agropecuaria (INTA).

215
BS832QS
Area: Biotic Interactions
Tipo de presentación: Poster en formato PDF
Enviado por: Cristina Kirolinko

Auxin Response Factor 2 (ARF2), ARF3, and ARF4 Mediate Both Lateral Root and Nitrogen-Fixing Nodule Development in Medicago truncatula

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AUXIN RESPONSE FACTORS (ARFs) constitute a large family of transcription factors that mediate auxin-regulated developmental programs in plants. *ARF2, ARF3,* and *ARF4* are post-transcriptionally regulated by the microRNA390 (miR390)/*Trans-Acting Small interference RNA 3* (*TAS3*) pathway through the action of *TAS3* derived trans-acting small interfering RNAs (ta-siRNA). Constitutive activation of the miR390/*TAS3* pathway promotes elongation of lateral roots but impairs nodule organogenesis and infection by rhizobia during the nitrogen-fixing symbiosis established between *Medicago truncatula* and its partner *Sinorhizobium meliloti*. However, the involvement of the targets of the miR390/*TAS3* pathway, i.e., *MtARF2*, *MtARF3*, and *MtARF4a/b,* in root development and establishment of the nitrogen-fixing symbiosis remained unexplored. Here, promoter:reporter fusions showed that expression of *MtARF3* and *MtARF4a* was associated with lateral root development; however, only the MtARF4a promoter was active in developing nodules. In addition, up-regulation of *MtARF2*, *MtARF3*, and *MtARF4a/b* in response to rhizobia depends on Nod Factor perception. We provide evidence that simultaneous knockdown of *MtARF2*, *MtARF3*, *MtARF4/b* or mutation in *MtARF4a* impaired nodule formation, and reduced initiation and progression of infection events. Silencing of *MtARF2*, *MtARF3*, and *MtARF4a/b* altered mRNA levels of the early nodulation gene nodulation signaling pathway 2 (*MtNSP2*). In addition, roots with reduced levels of *MtARF2*, *MtARF3*, and *MtARF4a/b* as well as *arf4a* mutant plants exhibited altered root architecture, causing a reduction in primary and lateral root length, but increasing lateral root density. Our results suggest that these ARF members are common key players of the morphogenetic programs that control root development and the formation of nitrogen-fixing nodules.

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216
BG926FM
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Douglas Antônio Posso

Superoxide accumulation in leaves of guava and poivre-rose trees in response to daily environmental fluctuations

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Superoxide is one of the reactive oxygen species produced in plants due to daily environmental fluctuations and exposure to stressful conditions. This study aims to show the fluctuation in the superoxide levels in the leaves of two tree species in natural conditions. The superoxide accumulation was quantified in the leaves of guava (*Psidium guajava*) and poivre-rose (*Schinus terebinthifolia*) trees at 10, 12, and 14 h grown in natural conditions of light and temperature. Fully expanded leaves in the north direction of the shoot at 2.5 m height were collected and analyzed. While the guava leaves increased superoxide accumulation at noon and decreased at 14 h poivre-rose leaves slowly increased the superoxide during the day. These two trees respond differently to the daily environmental fluctuations. While the guava tree seems to be more resilient to the natural condition' fluctuations, the poivre-rose tree is more acclimated to the natural daily fluctuations.

Financing: Capes and CNPq

217
KP441MJ
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Jesica Kobashigawa

Effect of Silver Nanoparticles Synthesized by Fungi on the Growth of Phaseolus radiatus Seedlings

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In recent years the use of nanomaterials has been increasing in different branches of technological and biotechnological applications due to their physicochemical qualities. In the last years the increasing use of silver nanoparticles are causing major exposure to the environment, being toxic against plants, animals and microorganisms and changing the microbial community of soil and water. In the recent years, a number of studies have been performed to understand the toxicological impacts and possible hazards of different nanoparticle exposures to human and the environment, but there is still a major gap in knowledge about the toxicity effects of nanoparticle exposures. *Phaseolus radiatus* L. is an important commercial crop belonging to the legume family and it is recommended as a testing species by the Organization for Economic Co-operation and Development (OECD) and the American Society for Testing Materials (ASTM). In this work, biologically synthesized silver nanoparticles using the fungi *Tulasnella albida*, *Cerinosterus* sp. and *Penicillium* sp. were employed to test the effect of these nanoparticles in *P. radiatus* seedling growth, based on the following indicators: stem length, root length, fresh weight, and dry weight. Water, the filtrate of each fungus and a solution of $AgNO_3$ were used as controls. The results would indicate that the nanoparticles affect more negatively root and stem length rather than weight of the seedlings, having the major impact those nanoparticles produced by *Penicillium sp*. This work contributes to increase the knowledge about the possible impacts of nanoparticles that enter the environment on plant organisms.

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MB692LF
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Iryna Kovalyshyn

Membranes permeability as drought resistance indicator for winter wheat (Triticum aestivum L.)

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Global trend of climate change leads to increasing of air temperature and precipitation redistribution on the earth's surface. In Ukraine it reflects in increasing of area with insufficient precipitation and appearing of new droughts territories. It leads to lower crops yield, among which winter wheat occupies leading position in Ukraine.

As natural cell barriers, membranes are first affected stress. It influences membrane by increasing their permeability and biochemical processes disruption. Therefore, aim of study was to establish the cell membranes stability of winter wheat varieties, which differ in origin.

Membranes permeability of leaf cells was determined for 4 varieties of the Institute of Plant Physiology and Genetics of the National Academy of Sciences of Ukraine (IPPG) selection (Bohdana, Podolianka, Natalka, Khurtovyna), 3 – Southern Ukrainian selection (Mudrist odeska, Yednist, Albatros odeskyi), and 3 – Western European selection (Dromos, Koreli, Tonacia), which are grown in IPPG collection. By level of drought resistance, they distributed in following order: South Ukrainian varieties > varieties of IFRG > Western European varieties.

According to the degree of cell membranes permeability, studied groups of varieties were distributed in following order: IPPG varieties (18.7±0.94%) > Western European varieties (18.2±1.14%) > Southern Ukrainian varieties (15.6±0.48%). Varieties of IPPG and Western European selection showed inverse correlation between electrolyte leakage and drought resistance ($r=-0.736$ and $r=-0.917$), while in varieties of Southern Ukrainian selection there was a direct relationship between these indicators ($r=0.850$). Thus, winter wheat genotypes of different origin varies in direction of the relationship between drought resistance and permeability of membranes.

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219
NR275BT
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Valdelice Oliveira Lacerda

Oxidative damage in Zeyheria tuberculosa leaves caused by excess iron and manganese

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The antioxidant system in plants plays an important role, preventing reactive oxygen species (ROS) from causing damage to structures fundamental to plant metabolism. Thus, the main of this work was to evaluate if excess of iron (Fe) and manganese (Mn) can cause oxidative damage in *Zeyheria tuberculosa* (Vell.) Bureau ex Verl leaves. For this, seedlings were exposed for 20 days to the following treatments: Bolle-Jones complete nutrient solution - CNS (T1), CNS + Fe 9 ppm (T2), CNS + Mn 18 ppm (T3) and CNS + Fe 9 ppm + Mn 18 ppm (T4). Oxidative damage was assessed by quantifying hydrogen peroxide (H_2O_2) and lipid peroxidation by quantifying thiobarbituric acid reactive species. The experimental design was entirely randomized, composed of 4 treatments and 6 replicates. The data were submitted to variance analysis (ANOVA) and the Tukey test at 5% significance using the R® software. With this study, it was observed that T2 and T4 presented a higher concentration of H_2O_2 in *Z. tuberculosa* leaves, with an average of 1170.792 ηmol H_2O_2 g^{-1} MF and 1050.396 ηmol H_2O_2 g^{-1} MF, respectively. However, only T4 showed a significantly elevated lipid peroxidation rate in *Z. tuberculosa* leaves. Thus, it can be concluded that excess iron triggers processes that increase the production of ROS generating oxidative damage in *Z. tuberculosa* seedlings and manganese presents synergistic potential on this damage, mainly in relation to lipid peroxidation.

Keywords: Ipê-felpudo; Abiotic stress; Trace elements.
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KP513SQ
Area: Other
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Enviado por: Valdelice Oliveira Lacerda

Postharvest conservation of Alstroemeria hybrida L. cv. Angelina flowers submitted to commercial preservatives and different potting solutions

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The market of ornamental flowers has shown to be a promising economic activity in Brazil. However, the quality and durability of the flowers depend on a series of factors that start from the cultivation to the postharvest treatment, which when neglected, generate great financial losses to the producer. Thus, this work aimed to evaluate the efficiency of commercial preservatives (Flower® and Florissant®) and pot solutions containing sucrose, silver thiosulfate (STS), sodium hypochlorite and silver nitrate in the postharvest longevity of *Alstroemeria hybrida* L. cv. Angelina (Alstroemeria). For this, flowers were subjected to the following treatments: T1 - distilled water (control); T2 - Flower® (15mL/L); T3 - Florissant® (5g/L); T4 - STS (0.2mM) + Sucrose (20g/L) + Sodium Hypochlorite (800mg.L) and T5 - Silver Nitrate (0.2mM) + Sucrose (20g/L) + Sodium Hypochlorite (800mg/L). The experiment was conducted in an entirely randomized design with 5 repetitions and an experimental unit composed of 2 floral stems. The data were submitted to variance analysis and the means were compared using the Scott-Knott test at 5% probability. The commercial preservatives Flower® and Florissant® promoted the best post-harvest conservation, prolonging in 3.6 days the vase life of *A. hybrida* in relation to the control and in 6.6 days in comparison to the other treatments. Thus, commercial preservatives proved to be efficient in the conservation of Alstroemeria cut flowers.

Keywords: Alstroemeria, Shelf life, Flower®, Florissant®.
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SN937FM
Area: Plant Physiology and Ecophysiology
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Enviado por: Federico Ladux

Light quality environment and photomorphological responses of young olive trees

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Plant proximity in super high density (SHD) olive orchards leads to high levels of leaf area index (LAI). Horizontal light reflection by leaves of neighboring plants often reduces R/FR and B/G ratios and can trigger different photomorphological plant responses even before direct shading occurs in many annual crop plants. The objectives were to characterize whether LAI modifies R/FR and B/G ratios in olive trees; and to assess the morphological responses of three olive cultivars to light quality. For the light characterization, different spatial arrangements of olive trees growing in pots were used to obtain different LAI. Plants of Arbequina, Arauco and Coratina cvs were subject to different light quality treatments including a laterally positioned FR-mirror that reduced horizontal R/FR and a green vegetation fence that reduced both horizontal R/FR and B/G. Both treatments had their own control. Increasing LAI led to decreases in R/FR from 0.84 to 0.56 and B/G from 0.81 to 0.76. The individual leaf area was reduced 26% by the FR-mirrors in Arbequina, and increased 18% in Arauco. The above/below ground biomass ratio were lower with the FR-mirrors in Arbequina and Coratina. The green-fence treatment and its control did not show any statistically significant morphological differences for the cultivars evaluated, but a cluster analysis grouped together the overall morphological responses to FR mirrors and green fences. These first results in olive trees suggest that cultivar differences in response to light quality may be relevant for understanding adaptation to dense orchards and identifying cultivars for them.

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222
HC345NC
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: María Paula Laserna

Dynamic of zein deposition and kernel hardness in maize as affected by grain filling environment

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Maize kernel hardness defines the aptitude for dry milling industry. Zein proteins play an important role in kernel hardness determination. They classify into two groups (Z1 and Z2) and their depositions are largely determined by the genotype, despite the grain filling environment might modify them. The aim of this work was to study how the reduction of incident radiation (which cause a reduction in photosynthesis) at different moments of the grain filling period affects the dynamics of zein deposition and their effect on kernel hardness. Two experiments were performed at two locations (Balcarce and Pergamino, Argentina). On three maize hybrids with contrasting endosperm hardness (flint, semident and dent) we evaluated: (i) control (not shaded); (ii) early shaded (ES, reduction of 50% of radiation during the first half of the grain filling period); and (iii) late shaded (LS, reduction of 50% of radiation during the second half of that period). Kernel samples were taken weekly from 15 days after silking up to maturity to quantify zein content by RP-HPLC. At harvest total protein percentage (P%; by Kjeldahl) and zein abundance (by RP-HPLC) were quantified, and kernel hardness was estimated by coarse-to-fine ratio. Shading treatments slightly affected the dynamics of Z1 and Z2 deposition, and when this effect was detected, did not modify the Z1/Z2 ratio, P% and hardness of kernels at harvest. Finally, the hybrid that showed a reduction in kernel hardness with the ES treatment, did not showed differences in Z1 or Z2 deposition.

223
DJ912TR
Area: Epigenetics, Chromatin, non-coding RNAs, RNA biology
Tipo de presentación: Poster en formato PDF
Enviado por: Gabriel Lasmar dos Reis

Analyzes of novel microRNAs associated with the anthocyanin biosynthesis pathway in tomato

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Anthocyanins are flavonoid compounds performing critical biological processes in plants. In addition, due to antioxidant properties, their dietetic intake is associated with the prevention of a range of chronic diseases in humans. However, these health benefits are only achieved when considerable amounts of anthocyanins are incorporated into the diet. Considering that produce is daily present in our meals, incrementing the anthocyanin content of horticultural crops is desirable, especially in tomato, the most consumed vegetable worldwide. To achieve this goal, identifying the factors that directly regulate genes controlling the anthocyanin biosynthesis pathway is critical, including microRNAs (miRNAs). In our study, we aimed to identify and validate miRNAs that regulate anthocyanin-related genes in tomato. Through miRNA target prediction, we identified miR5368, miR6024-3p, and miR9471b-3p as putative regulators of *ANTHOCYANIDIN SYNTHASE* (*ANS*), *SlAN1* (*bHLH150*), and *CHALCONE SYNTHASE* (*CHS*), respectively. Preliminary validation of the effect of these miRNAs on the expression of their target genes was carried out by RT-qPCR on the cultivar Micro-Tom. Our results revealed high expression levels of these miRNAs in all tissues analyzed. Furthermore, we observed an inverse expression pattern between these miRNAs and their predicted target genes. Therefore, our results suggest that the miR5368, miR6024-3p, and miR9471b-3p act on the anthocyanin biosynthesis pathway by negatively regulating the expression of the genes *ANS*, *SlAN1*, and *CHS*, respectively. We are currently generating transgenic plants to demonstrate the functional links between these genetic associations.

Financing: Coordination for the Improvement of Higher Education Personnel (CAPES, Coordenação de Aperfeiçoamento de Pessoal de Nível Superior, Ministry of Education, Brazil).

224
FF425GH
Area: Biochemistry and Metabolism
Tipo de presentación: Poster en formato PDF
Enviado por: Matias Lastuvka

The role of abscisic acid in kiwifruit seed dormancy

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Kiwifruit (*Actinidia deliciosa* A. Chev. C.F. Liang and A.R. Ferguson) seedling production in the nursery is usually impaired because of low seed germination resulting from primary dormancy. Dormancy of hydrated seeds is alleviated by the perception of a period at low temperatures (stratification), but further incubation under fluctuating temperatures is a requirement for dormancy termination. Some reports have shown that dormancy expression in seeds of some species is associated with abscisic acid (ABA) de novo synthesis and/or a lower rate of ABA catabolism after imbibition, which does not occur in seeds that do not express dormancy. The aims of this work were to determine if dormancy changes of stratified seeds are associated (i) with changes in ABA sensitivity and/or (ii) with changes in endogenous ABA content. Seeds were stratified at 5°C for 0, 14 and 28 days and incubated at 25 and 20/30°C. Part of these treated seeds was exposed to 0, 1, 10, 25, 50 and 100 uM of exogenous ABA to assess sensitivity through germination percentage and the other part was used to measure endogenous ABA content at 0, 24, 120 and 168 hours after imbibition. The results showed that (i) the seeds had a high sensitivity to the inhibitory effect of exogenous ABA prior to stratification which decreases sharply with stratification time, but ii) ABA endogenous content did not change during stratification.

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225
SM489KL
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Lucas Latorre

Role of Nitric Oxide in UV-B induced photomorphogenesis through UVR8 signaling pathway

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UV-B radiation is a component of sunlight, including wavelengths from 280nm to 320nm. The ozone layer filters the UV-B, but a small part reaches the Earth’s surface. This radiation serves both as a stressor and a signal for plants. The protein UVR8 is the plant UV-B receptor.

Nitric oxide (NO) is a signaling molecule that participates in physiological and stress acclimation responses. Our objective was to find the role of NO in the UV-B induced photomorphogenesis. With that goal, seedlings of *Arabidopsis thaliana* wild type (WT) and the UVR8 null mutants *uvr8-1,* were grown 5 days in continuous UV-B (0,5 w/m^2), and endogenous NO was measured by fluorescent probe DAF-FM DA in hypocotyls. Results show that *uvr8-1* mutants did not inhibit elongation of hypocotyl in response to UV-B, and had lower levels of NO compared to WT. Moreover, exogenous application of NO recovered the response to UV-B in the uvr*8-1* seedlings. These results indicate the involvement of UVR8 signaling pathway in the UV-B triggered NO production and its importance in the inhibition of hypocotyl elongation. Our previous results indicate that *nitrate reductase 1* gene (NIA1) which is involved in NO synthesis, is upregulated by UV-B in a UVR8-dependent manner. In addition, *in-silico* analysis of the UVR8 pathway revealed the existence of potentially S-nitrosylable conserved cysteines in COP1, NIA1 and MYB12. Altogether, this evidence aims to a fundamental role of NO in regulation of UV-B induced photomorphogenesis.

226
DG431BH
Area: Developmental Biology
Tipo de presentación: video presentacion
Enviado por: Ignacio Lescano

The DNA glycosylase MBD4L contributes to DNA repair during seed development and germination

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Genome damage accumulates in the embryo of seeds, specially under stressful conditions (i.e. high temperatures) resulting in aged seeds with decreased vigor and viability. In addition, both seed development and germination are coupled with cycles of dehydration and rehydration with increased metabolism and high levels of reactive oxygen species, resulting in oxidation of DNA bases and strand breaks. Consequently, DNA must be repaired prior germination to prevent genomic damage from being fixed after cell division. The base excision repair (BER) system contributes to this end by using DNA glycosylases that excise damaged bases from the genome. Here, we analyzed seed phenotypes associated with the deficiency of the Arabidopsis DNA glycosylase MBD4L (***M**ethyl-**B**inding **D**omain **P**rotein **4**-**L**ike*). Both silique and seed size, as well as the germination rate were decreased in MBD4L mutants (*mdb4l*) compared to wild-type plants. The decreased germination rate of *mbd4l* seeds was exacerbated after long-term aging at controlled conditions or short heat treatments. Germination rate under control and heat conditions were rescued by overexpressing MBD4L isoforms in the mutant background. Interestingly, seeds expressing the shorter isoform presented the highest germination rates. Comet assays and gene expression analysis showed that BER was compromised in *mbd4l* mutants. Moreover, promoter studies indicated that MBD4L expression was higher at early stages of seed development. Our results suggest that MBD4L contributes to DNA repair by activating the BER system prior seed germination to maintain genome integrity, cell viability, and accurate transmission of genetic information.

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227
KN444RH
Area: Signal Transduction
Tipo de presentación: video presentacion
Enviado por: Zenglin Li

The novel phytochrome interacting protein ERF58 is a repressor of light-induced seed germination in Arabidopsis

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Environmental conditions strongly influence the growth and development of plants, and coordinated responses are vital to their survival. Phytochromes function as red/far-red photoreceptors that regulate a variety of responses throughout the lifetime of plants. In a yeast two-hybrid screen, we identified an AP2/ERF transcription factor ERF58 interacts with phyA and phyB. Here, we show that light-dependent seed germination is enhanced in mutants deficient in *ERF58* or the close *ERF58* homolog (*ERF55*), as well as in the *erf5558* double mutant. Light-activated phyA and phyB repress expression of *ERF58*, and we have evidence that phytochromes inhibit ERF58 binding to target promoters, suggesting a potential mechanism for light-regulation of the respective genes by ERF58.

ERF58 overexpressing plants are hypersensitive to ABA and insensitive to GA during seed germination, whereas *erf5558* double mutants are hyposensitive to ABA and hypersensitive to GA. We also found that GA downregulates *ERF58* gene expression levels, while *ABA* upregulates ERF58 transcript and protein levels. In parallel, GA and ABA catabolic/anabolic genes are regulated by ERF58, suggesting a reinforcing feedback mechanism. ERF58 binds directly to the promoters of *PIF1* and *SOM*, which are involved in phyA and phyB mediated seed germination, and the promoter of *ABI5*, an important component of ABA signaling.

In conclusion, we find that phytochromes regulate *ERF58* transcript levels and transcriptional activity to control light-dependent seed germination, and we show that the effect of ERF58 on seed germination is through regulation of ABA and GA anabolic/catabolic genes and ABA downstream signaling components.

228
DK766RP
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Adrya Vanessa Lira Costa

LOCAL APPLICATION OF ABIOTIC STIMULUS INDUCES ROS RESPONSES AT A DISTANCE

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The detection of environmental changes by plants can occur at the level of the entire plant or only locally. The stimulated part (local tissue) responds quickly and activates signals capable of reaching other non-stimulated parts (systemic tissue), causing different molecular, metabolic and physiological responses in these tissues at a distance, resulting in acclimation processes. The participation of different systemic signaling pathways is fundamental for acclimation, and there are several chemical signaling molecules capable of this, including reactive oxygen species (ROS). In this sense, we investigated whether the levels of hydrogen peroxide (H_2O_2), superoxide radical (O^{2-}) and lipid peroxidation in local and systemic leaves of black bean plants (*Phaseolus vulgares*) are altered after local application of 5 and 10 min. stimuli by high light (HL5 and HL10), heat shock by flame (HS) and artificial wounding by scissors cut. The results showed consistent treatment-dependent systemic ROS responses. For the light stimulus, the ROS content varied with the duration of the stimulus. HL5 treatment induced an intense ROS response in local and systemic leaves, and high level of lipid peroxidation only in local leaf, while HL10 induced a reduction in ROS content and peroxidation levels did not differ from control. For the cutting and HS stimuli, a systemic increase in ROS was observed, but not enough to increase the level of lipid peroxidation.

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229
JB516FG
Area: Cell Biology
Tipo de presentación: video presentacion
Enviado por: Ang-Yu Liu

The purple acid phosphatase PAP26 is essential for efficient nucleotide metabolism in the vacuole of Arabidopsis

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Ribosomes are essential cellular components which contain 80% of cellular RNA, yet their turnover is not fully understood. RNS2, one of the *Arabidopsis* T2 ribonucleases, has been shown previously to catalyze bulk RNA degradation in the vacuole. The *rns2-2* mutant accumulates RNA in the vacuole. This mutant also presents upregulation of basal autophagy as a consequence of low TOR activity. This phenotype can be inhibited by treating the plants with inosine, the purine nucleoside precursor. Thus, vacuolar RNA degradation is crucial to maintain cytosolic nucleoside levels. While it is clear that RNS2 initiates RNA degradation, the pathway producing nucleosides in the vacuole remains unclear. We characterized the pathway of nucleotide metabolism and its physiological implications using a combination of in vitro degradation assay and molecular biological analyses. Using recombinant RNS2 and poly(A) RNA as substrate, we showed that RNS2 is able to produce a mixture of 3' NMP and cyclic nucleotides. We also demonstrated that the purple acid phosphatase PAP26 is responsible for 80 % of the acidic phosphatase activity of the vacuole, and the *pap26* mutant display increased basal autophagy that can be inhibited by inosine treatment. Thus, we propose that PAP26 is the major vacuolar phosphatase which catalyzes the production of nucleoside from 3' NMP, the final product of RNS2-dependent RNA hydrolysis. Moreover, PAP26 activity could have an in vivo role regulating RNS2 kinetics by changing the chemical equilibrium through product removal that would increase the efficiency of the hydrolytic step in RNA degradation.

230
FR457DH
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Analía Llanes

New insights into the role of gibberellins in growth responses of the halophytic woody Prosopis strombulifera (Lam.) Benth plants under different sodium salts.

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Phytohormones have essential roles in plant growth responses under salinity. A better understanding of gibberellin (GA) functions in woody plant responses under different sodium salts could help to develop new strategies to improve plant salt tolerance. In this study, *Prosopis strombulifera* plants were grown in hydroponic solutions and exposed to NaCl, Na_2SO_4, or their iso-osmotic mixture at -1.0, -1.9, and -2.6 MPa. Control (without salt) and salt treated plants were sprayed with gibberellin A_3 (GA_3), or chlormequat chloride (CCC), an inhibitor of its synthesis. Growth responses, anatomical alterations and ABA and active GA forms (GA_1, GA_3 and GA_4) and inactive GA forms (GA_8 and GA_{34}) endogenous levels were evaluated. Results showed that GA_3 application increased growth in control plants more than in salt-treated plants. Roots and leaves of salt-treated plants showed high levels of ABA and active GA forms after exposure to GA_3. CCC triggered stress-alleviating responses in these plants, such as an increase in spine length and the number of palisade cell layers, and a reduction in levels of ABA and GA_4. Na_2SO_4-treated plants showed reduced growth, high ABA levels and an active GA metabolism to control the levels of active GA. This study indicates that the suppression of GA signalling would contribute to salt tolerance in the native halophytic woody *P. strombulifera* plants. These findings contribute to the understanding of how gibberellin biosynthesis regulation is involved in the responses to different sodium salts in soils, which could be used as new tools for forest breeding.

Financing: This study was partially supported by Secretaría de Ciencia y Técnica-Universidad Nacional de Río Cuarto (SeCyT-UNRC), Fondo para la Investigación Científica y Tecnológica (FONCyT, PICT 2018-3148) and Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET).

231
MG514PH
Area: Biotic Interactions
Tipo de presentación: Poster en formato PDF
Enviado por: Miguel Lobato-Ureche

Strains 42P4 and 60I1 alleviate NaCl stress in pepper plants

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Environmental stresses have an important role in crop yields of pepper grown in Argentina. Soil salinity is an important agricultural problem in irrigated soil as Mendoza; besides, most crops are sensitive to salinity. Salt stress limits plant growth and development leading to a reduction in crop productivity of pepper. There are numerous reports about the beneficial effects of rhizosphere microorganisms on plant growth. This group including plant growth-promoting rhizobacteria named PGPR. In general, PGPR can improve plant development by producing secondary metabolites as plant growth regulators or phenolic compounds and improving the availability of nutrients such as nitrogen, phosphorus and potassium. The main of this study was to evaluate the effect of the inoculation of pepper plants under saline stress with two native strains isolated from Mendoza. The assay was carried out under greenhouse conditions. A triplicate of randomized design of 5 treatments was established, with 10 plants by treatment. The treatments were: 1) Control, 2) 42P4 + NaCl, 3) 60I1 + NaCl and 4) NaCl. Plants under saline stress were watered with a 150 mM NaCl solution. During the development of the experiment morphological, physiological and biochemical variables were evaluated. The results showed that the 42P4 and 60I1 strains alleviate saline stress by increasing plant height, stem diameter, photosynthetic efficiency, chlorophyll index (SPAD), aerial, and root dry weight, photosynthetic pigment content, and phenolic compound. The results suggest that 42P4 and 60I1 are two native PGPR that alleviating the negative effects of salinity on pepper plants.

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232
NF332RJ
Area: Developmental Biology
Tipo de presentación: Poster en formato PDF
Enviado por: Felipe Lopes

DEVELOPMENT OF ORCHID CACTUS SEEDLINGS IN A SEMI-HYDROPONIC CULTIVATION SYSTEM

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The semi-hydroponic system has advantages over the traditional cultivation and hydroponic system. The orchid cactus (Epiphyllum phyllanthus) is an epiphytic cactus with wide distribution in South America. It is a landscape interesting plant because it has leaves, fruits, and ornamental flowers, plus it has ecological importance, with fruits and pollen edible for wildlife. This study aimed to evaluate the development of orchid cactus seedlings in a semi-hydroponic system with different substrates. In vitro germinated orchid cactus seedlings were planted in pots containing coconut fiber, vermiculite, and a mixture of both in a 1:1 ratio. These seedlings were placed in pools system with nutrient solution composed of commercial reagents soluble fertilizer NPK Hidrogood Fert – 10-09-28 (720g), Haifa Cal GG (540g), and Hidrogood Fert EDDHA iron chelate (40g) diluted in a 1000L water tank. The development was monitored monthly, with the number of cladodes, shoot length, and chlorophyll content being evaluated. Chlorophyll content was measured using the TYS-A chlorophyll meter. The different substrates showed no statistical difference in shoot length and number of cladodes over the period. However, the treatment with vermiculite presented results statistically superior to the others, with the content of total chlorophylls in the first, third, fourth, fifth, eighth, tenth, and eleventh month. The different substrates showed good development in the cultivation of the orchid cactus, but vermiculite is what guaranteed the highest total chlorophyll content in the evaluated plants.

Financing: CNPQ, CAPES and FAPEMIG

233
CL214GG
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Emelí Lopez

Genotype and Environment Affect the Soluble Carbohydrates of the Residual Soybean Seed Component

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Soybean seed is composed of protein, oil, and residual. The residual fraction contains minerals, soluble and insoluble carbohydrates, and lignin. Carbohydrates in the residual fraction are rarely studied because of their low economic and nutritional value, but they can affect the performance and quality of derived protein ingredients. Our objective was to describe how genotypes (G) and environment (E) affect protein, oil, and soluble carbohydrates within the residual fraction of soybean seeds. We evaluated nine commercial genotypes in two environments with contrasting sowing dates (8 Nov. and 19 Dec., 2019) in Zavalla, Santa Fe. The late sowing environment had more protein and slightly less oil concentration, but no significant ($p>0.05$) variation was observed in the residual one. However, observed changes in these three traits were dependent on the specific genotype (significant GxE; $p<0.05$). Significant variation was observed in soluble carbohydrates in the residual seed component for genotypes and environments ($p<0.05$). The later sowing increased seed sucrose (6%) and stachyose concentrations (31%), and reduced the concentrations of raffinose (79%), glucose (33%), and fructose (15%). However, environmental changes were also very genotype specific (significant GxE; $p<0.05$). Our results are highlighting that genotype selection and environment affect not only protein and oil seed concentrations, but also the composition of the residual seed component. Stachyose changes, for example, have important consequences due to their antinutritional effects in monogastric animals and human beings.

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234
GS428NS
Area: Biotic Interactions
Tipo de presentación: Poster en formato PDF
Enviado por: Mariana Melchiorre

Rhizobia strains selection to improve symbiosis with Prosopis alba

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Prosopis alba is a native forest species able to survive in restrictive environments, which has high potential to be used in afforestation and reforestation programs for restoration of degraded areas. In Cordoba Province, it has been suggested as a suitable species to comply with Agroforestry Law N°10467, which obliges farmers to afforest at least 2% of their productive area. *P. alba* can fix N_2 symbiotically associated with nodule inducing rhizobia, contributing to the sustainability of systems. The aim of this work is to characterize the symbiosis between *P. alba* (Origin Salta Province) plantlets grown in a greenhouse, and several rhizobia strains previously selected from Chaqueña Region. The principal component analysis (PCA) of growth parameters in *P.alba* nodulated with five strains, allowed to choose two of them, BP_8 and IC_2.1.7, to perform further trials under diverse nitrate fertilization levels (0; 0.15; 0.25 and 1 mM NO_3). After 90 days and no NO_3 addition, *P. alba'*s height and aerial and root biomass were higher in inoculated plantlets with both strains (BP_8 and IC_2.1.7) compared to control (no inoculation and no NO_3 adition) without differences between strains. Under the highest NO_3 level, nodule weight diminished in both inoculation treatments whereas only in plantlets in symbiosis with IC_2.1.7 lowering in nodule number was observed. However, the symbiosis with both rhizobium strains assayed in presence of any NO_3 level improved the plantlet's growth responses. These responses suggest that *P. alba* symbiosis with either BP_8 or IC_2.1.7 strains could enhance adaptation of plantlets in afforestation procedures.

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235
RC268GM
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Fernando Lorenzini

Evaluation of the effects of different row spacing arrangements in four commercial cultivars of cotton in terms of yield and fiber quality

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Different agronomic practices are carried out in cotton system in order to increase production. One of them is the election of the row spacing arrangement. In Argentina two main spacings are widely used by farmers: Conventional row and Narrow row. The aim of the present work was to evaluate the effects on yield and fiber quality for the two row spacing arrangements commonly used in Argentina, in four commercial varieties of cotton. The experiment was carried out by a split plot arrangement with four replicates for each cultivar per row spacing. The results showed significant statistical differences between row spacings in terms of seed cotton yield (SCY), lint yield (LY), weight per boll (WB) and boll retention (BR), whereas the results did not show differences in fiber quality parameters. In all cases conventional row system achieved the highest values for each recorded variable. Besides, there were significative correlations between WB and SCY, BR and SCY, WB and LY, and BR with LY. In addition, lint percentage was different only between cultivars, being DP 1238 the one that reached the highest value. The increase in WB and BR in Conventional row could explain the increased values of SCY and LY for this arrangement. The present work contributes with knowledge about agronomic management in terms of row spacings used in argentinian cotton production.

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Area: Biotic Interactions
Tipo de presentación: Poster en formato PDF
Enviado por: Laura Medina-Puche

PLASMA MEMBRANE-TO-CHLOROPLAST COMMUNICATION: LEARNING FROM VIRUSES

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Chloroplasts are crucial players in the activation of defensive hormonal responses during plant-pathogen interactions; however, how chloroplasts receive information of biotic threats perceived at the cell surface has so far remained elusive. We have recently shown that a plant virus-encoded protein, C4 from the geminivirus *Tomato yellow leaf curl virus*, re-localizes from the plasma membrane to chloroplasts upon activation of plant defense, which occurs during viral replication. Subcellular compartmentalization of C4 enables its multifunctionality: at the plasma membrane, this viral protein acts suppressing the intercellular movement of RNA silencing; from chloroplasts, it interferes with the chloroplast-to-nucleus retrograde signalling and the subsequent anti-viral salicylic acid (SA) biosynthesis. Strikingly, plant pathogens from different kingdoms seem to have convergently evolved to target chloroplasts and impair SA-dependent defenses following an association with membranes, which relies on the co-existence in their effector proteins of two subcellular targeting signals, an N-myristoylation site and a chloroplast transit peptide. This pattern is also present in plant proteins, at least one of which, Calcium-dependent protein kinase 16 (CPK16), conversely activates SA defenses from chloroplasts. Taken together, our results suggest that a pathway connecting plasma membrane to chloroplasts and activating defense exists in plants and that such pathway has been co-opted by plant pathogens during host-pathogen co-evolution to promote virulence through suppression of SA responses.

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237
DR993QK
Area: Epigenetics, Chromatin, non-coding RNAs, RNA biology
Tipo de presentación: Poster en formato PDF
Enviado por: Sarah Melissa Lugo Caro del Castillo

Differential Association Between Argonaute Proteins and Small RNAs in the Regulation of Legume-Rhizobia Symbiosis

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The symbiotic relationship between Rhizobia and leguminous plants (Legume-Rhizobia Symbiosis or LRS) is a process that has been extensively studied to identify the components that participate in its regulation. One of these components is the regulation induced by small RNAs (sRNAs), which guide gene silencing to modulate numerous processes in most eukaryotes; particularly, the plant-microorganism interactions, including the different stages of the LRS.

Argonaute (AGO) family proteins are crucial for the functioning and action mechanisms of sRNAs, being an essential part of the RNA Induced Silencing Complex. Previously, the role of several differentially accumulated sRNAs in LRS had been identified and evaluated, however, little has been studied about their differential association with AGO proteins in this context.

Furthermore, the preferential AGO loading of sRNAs seems to have a significant impact on gene silencing and potentially influence LRS. For example, mechanisms like “microRNA sequestration” make AGO1 and AGO10 compete for miR165/166 association and therefore impair the regulation of transcripts involved in root development.

In the present work, we selected the model legume *Phaseolus vulgaris* in interaction with *Rhizobium etli* to analyze the differential and preferential loading of sRNAs in AGO1 and AGO10. We observed the AGO loading profile of miR166 when comparing 5dpi inoculated plants with non-inoculated controls, giving rise to further study the functional role of this microRNA in the LRS context.

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238
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Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Andrea Galatro

Phosphorus deprivation in soybean plants induces early acclimation responses and affects endogenous nitric oxide levels

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Nitric Oxide (NO) is known to be involved in plant responses to essential mineral nutrient deficiencies. In this work we evaluated initial changes following phosphorus (P) deprivation in soybean plants focusing on NO levels and the triggering of some acclimation responses. Soybean plants (Glycine max cv. Williams 82) were cultivated in modified Hoagland´s solution containing 500 μM H_3PO_4 (control, +P) or without H_3PO_4 (-P), at 28 °C/22 °C day-night, 400 μmol m^{-2} s^{-1} of PAR, and 16-h photoperiod. Plants were grown under +P condition for 7 d, then a group of plants were moved to -P treatments, and growth and physiological parameters were evaluated up to 96 h of treatment. P concentration decreased 64 % in -P roots and unifoliate leaves, and 40 % in trifoliate leaves respect to control values at 96 h. However, neither growth nor photosynthesis was strongly affected. The decrease in P levels correlated with an increase in NO content in leaves, that was strongly inhibited by treatment with sodium tungstate (an inhibitor of nitrate reductase). Acid phosphatase activity tend to increase in leaves and roots of -P plants, being two-fold higher in roots after 96 h of -P treatment. The levels of organic acids were measured employing HPLC, and malic and citric acid production seem to be stimulated in -P roots.
Overall, the correlation between NO levels and P concentration, and the activation of some acclimation responses might indicate the involvement of reactive nitrogen species in signaling pathways during the first hours of P deprivation.

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FL471NG
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Virginia Luquez

Flooding tolerance during the early stages of growth in 29 willow genotypes (Salix spp.).

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Climate change will increase the occurrence of flooding episodes in several areas of the world. Willow commercial genotypes are usually propagated as unrooted cuttings. During the early stages, cuttings are still developing their root system and leaf area, being more vulnerable to the occurrence of stresses like flooding. In consequence, it is relevant to identify traits correlating to flooding tolerance during the early growth of willows.

We evaluated the flooding tolerance of 29 willow genotypes from the breeding program of INTA. Two-months old plants growing in pots in a greenhouse underwent two treatments: watered to field capacity (control) and flooded (80% of the stem covered by still water) for 41 days. At the end of the stress episode, different traits were measured: height, collar diameter, basic wood density, plant dry biomass and leaf area. A flooding tolerance index for each genotype was estimated as the percent ratio between flooded and control total biomass. There was ample variation in flooding tolerance, with the index ranging from 39% to 117%. Most clones had a reduced biomass accumulation under flooding conditions and only 4 genotypes had similar or higher biomass than control plants. Several traits had a positive and significant correlation (measured with the Pearson correlation coefficient) with flooding tolerance: height ($r=0.69$, $p<0.01$), collar diameter ($r=0.71$, $p<0.01$), plant dry biomass ($r=0.71$, $p<0.01$), plant leaf area ($r=0.49$, $p<0.01$) and basic wood density ($r=0.53$, $p<0.01$).

These traits could be useful to select for increased flooding tolerance in willows during the early stages of growth.

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Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Gabriel Alejandro López

Alternative splicing changes triggered by ferroptosis inhibitors: their putative role in heat stress tolerance.

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Upon heat stress, plant cells undergo an oxidative iron-dependent type of cell death that shows morphological, biochemical and molecular similarities with ferroptosis, an iron dependent type of cell death first discovered in tumor cells. Treatment with canonical ferroptosis inhibitors like CPX, an iron-chelating agent or Fer-1, a lipophilic antioxidant, results in plants that are able to survive otherwise lethal temperatures. As suppressing ferroptosis allows plants to cope with extreme temperatures without previous acclimation, our goal is to investigate if ferroptosis inhibitors trigger a response similar to the one observed after exposing plants to sub-lethal temperatures -a phenomenon known as “acquired thermotolerance”. To get a comprehensive impression of *A. thaliana* transcriptome in response to ferroptosis inhibitors, RNAseq libraries were constructed from plants treated with the inhibitors. We found 64 differentially regulated genes in treated plants, including HS factors and genes related to cell wall modification. Strikingly, we also found that a splicing regulator was strongly induced after treatment, which is in agreement with recent reports that specifically recognized alternative splicing (AS) as a novel component of the heat-stress priming induced memory. Moreover, by using the R package ASpli, we found 178 genes with differential splicing events in treated plants. Our next step is to validate this data via RT-PCR and to study the changes in alternative splicing of genes related to the acquisition of thermotolerance in response to ferroptosis inhibitors.

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LH649PQ
Area: Biotechnology, Research Tools, Resources
Tipo de presentación: Poster en formato PDF
Enviado por: Marlon López

Transcriptional analysis of contrasting coffee cultivars in flowering time regulation

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Coffee flowering is an important physiological step in the transition of vegetative to reproductive phase in worldwide coffee production. Molecular evidence of how this process occurs is scarce. In this study, three coffee cultivars were selected according to their flowering pattern: Acauâ (Late), Oeiras (Early), and *Semperflorens* (Continuous). Molecular analysis (RNA-seq), field evaluations (flower bud development, flowering events) and physiological analysis (Ethylene content evolution and sugar content) were made in march (Flower buds, leaves and Shoot Apical Meristem (SAM)) and August (Leaves). The main objective was to elucidate the molecular and physiological factors influencing the coffee flowering time for each cultivar. Results showed that sugar metabolism could be associated with flowering time since sucrose content was increased in the late cultivar Acauâ before anthesis and sugar transporter genes (Sugar transporter protein 13-like, galactinol-sucrosegalactonyl transferase-like, and bidirectional sugar transporter SWEET 10-like) showed high expression in this period and starch content was higher in *Semperflorens*. Ethylene evolution showed a similar pattern in flowers buds, but Acauâ presented lower content in leaves than Oieras and *Semperflorens*. However molecular analysis in Gene Ontology (GO) showed that others plant hormones could be regulating coffee flowering time. Finally, candidates genes (protein HEADING DATE 3A-like, truncated transcription factor CAULIFLOWER A-LIKE, MAD-box protein SOC1-like, VEIN-like protein 2, two components regulator-like APRR5, protein MOTHER of FT and FTL 1 homolog 1-like and protein EARLY FLOWERING 5-like) associated with endogenous and external stimulus in the flowering time process were selected.

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Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Julio Iehisa

Effect of day length extension on the expression of FT-like genes in two sesame genotypes with different flowering time

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Sesame (*Sesamum indicum* L.) is an important crop species because it represents one of the family farm income sources. Despite being one of the oldest crops, the mechanism involved the variations in flowering time among sesame varieties is still not known. In a previous study, we have found four copies of *FLOWERING LOCUS T* (*FT*)-like genes in sesame. As part of the evaluation of their role in flowering, we analyzed the effect of light phase extension on the expression of four *FT-like* genes (*SiFTL1* to *SiFTL4*) in early- and late-flowering sesame genotypes. It was found that the early-flowering genotype K3 is partially photoperiod insensitive, while the late-flowering genotype NEB is photoperiod sensitive. At a photoperiod of 8 h light and 16 h darkness (8/16), both genotypes presented similar flowering time and as the light phase extends (from 12/12 to 16/8) the days to flowering of NEB greatly increased compared to K3. Among the *SiFTL* genes, *SiFTL1* presented highest expression followed by *SiTL2* and *SiFTL4*. *SiFTL3* was not expressed in our experimental conditions. At a photoperiod of 8/16, the expression of *SiFTL1* was similar between the two sesame genotypes. On the other hand, *SiFTL2* expression was higher in the late-flowering genotype. Extension of a single light period reduced the *SiFTL1* and *SiFTL2* expression in NEB but not in K3. Our results suggest that the major florigen in sesame is *SiFTL1* and at a lesser degree *SiFTL2*, and *SiFTL3* and *SiFTL4* seems not to participate as florigen.

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TJ939DP
Area: Developmental Biology
Tipo de presentación: video presentacion
Enviado por: María Jesús López-Martín

Proliferative Arrest in tomato: searching for mobile signals and genetic factors.

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Monocarpic plants have a single life cycle. The coordinated arrest of all meristems or Global Proliferative Arrest (GPA) takes place after the production of a certain number of flowers and fruits. It is well established that unknown signals from fruit and seed production are major factors controlling GPA in some monocarpic species, including tomato. A genetic pathway regulating GPA in *Arabidopsis* that responds to age-dependent factors has been uncovered and it acts in parallel to seed-derived signals. Two key genetic factors, *FRUITFULL (FUL)* together with miR172, negatively regulates *APETALA2/APETALA2-LIKE (AP2/AP2-like)* expression in the shoot apical meristem and keeps the expression of *WUSCHEL (WUS)* which is essential for meristem maintenance. Tomato homologs of genes involved in the FUL-AP2-WUS genetic pathway are highly conserved. We aim to re-evaluate the role of fruit/seed production, attempting to identify the fruit/seed-derived signals and by assessing the functional conservation of the FUL-AP2-WUS genetic pathway in tomato GPA. Our findings show that complete flower removal maintains GPA indefinitely delayed. Moreover, arrested meristems, can be reactivated by removing the fruits. To identify the signals that trigger GPA in tomato, we developed an efficient method to collect fruit exudates. In these exudates, we identified phytohormones and mobile miRNAs that could be involved in meristematic arrest. In addition, we developed molecular tools to modulate the expression of the sly-miR172 and *FUL* homologs in tomato. This approach will help us to generate biotechnological tools to obtain plants with a longer life cycle and thus increased crop yield.

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Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Ana Karla Lobo

Ion accumulation, PSII quantum yield modulation, and antioxidant enzymes are triggered avoiding photoinhibition in Rhizophora mangle under hypersalinity and non-salt conditions

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Rhizophora mangle, one of the most widespread mangrove species, usually faces salinity and high light conditions, which reduce stomatal conductance and CO_2 assimilation and prone to photoinhibition. The protective mechanisms involved in mangrove species to deal with hypersalinity and non-salt environments are poorly understood. In this study, propagules of *R. mangle* plants were cultivated in a growth chamber and exposed to reference (native environment salt concentration, Ref = 10 g L^{-1} NaCl), non-salt (NS = 0 g L^{-1} NaCl), and hypersalinity (HS = 70 g L^{-1} NaCl) treatments for 30 days. Biometric parameters were similar in Ref and NS plants. However, HS strongly decreased biomass, plant height, leaf area, and the number of leaves, and increased stem diameter compared to Ref plants. HS also reduced leaf water potential, relative water content (especially in leaves), and increased leaf and root membrane damage regarding Ref plants. Though no changes in leaf succulence were noticed. The $[K^+]/[Na^+]$ ratio decreased as the salinity rise. The maximum quantum yield of PSII was not affected by the treatments, but the effective quantum yield, electron transport rate, and open centers of PSII dropped, followed by increases in the non-photochemical quenching in HS plants compared to Ref ones. While the H_2O_2 content and superoxide dismutase and catalase activities were higher in HS plants, they were lower in NS plants compared to Ref plants. These results suggest that *R. mangle* plants trigger ion accumulation, excess energy dissipation mechanisms, and antioxidant enzymes to avoid photoinhibition under hypersalinity and non-salt conditions.

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PD139HS
Area: Biotechnology, Research Tools, Resources
Tipo de presentación: Poster en formato PDF
Enviado por: Oscar A. Ruiz

Study of two paddy field management practices: effects on soil carbon fractions and N-fixing capacity associated with Lotus spp..

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The rice-pasture rotation is the main rice-cultivation system in Entre Ríos where *Vertisol* soils are the most suitable due to the presence of a *Bt* horizon with more than 45% of clay enabling the rice to stay flooded during the whole growing period. The management practices carried out in these ecosystems impact on the edaphic C and N levels and the C storage capacity. In order to account for this, soil C and N contents at two soil depths (0-10 cm and 10-30 cm) of two contrasting rice-production systems (RPR: rice-pasture rotation and RM: rice monoculture), were measured and compared to an undisturbed field (UDF) close to them. The RPR system showed the higher TOC, POC and TN levels and the lowest reductions percentages of the mentioned variables in relation to the UDF. The N-fixing capacity of the legume comprising the RPR system, *L. corniculatus*, was estimated by the ^{15}N isotope abundance technique. In field conditions and when the average value of both reference plants was considered, the %Ndfa resulted to be 77.4 %. In addition, the presence of plant associated P solubilizing and N fixing microorganisms were evaluated. The results obtained show the importance, in terms of ecological and microbiological impact, of including pasture cycles along with rice cycles for achieving an ecologically and economically sustainable rice-production system

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246
RM177KB
Area: Biochemistry and Metabolism
Tipo de presentación: Poster en formato PDF
Enviado por: Mariana Machado

Survival metabolic strategies of Nitzschia palea strains with contrasting growth rates under silicon stress

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Silicon (Si) is an essential nutrient for diatom growth, directly involved in frustule formation. Despite studies analyzing Si stress in diatoms, the association between Si and central metabolism remains poorly understood. Thus, we analyzed the metabolism of two freshwater strains of *Nitzschia palea*, with contrasting growth rates (BR006 and BR022, fast and slow-growing strains, respectively), under different Si concentrations (0, 0.25, 1.25, and 5 mM Si). Despite the differences in growth, both, BR006 and BR022 strains exhibited similar metabolic responses under Si starvation, including high pigment and total lipid content, as well as high primary metabolite accumulation. Nevertheless, the response levels displayed by the strains differed under distinct Si concentrations. Remarkably, the accumulation of triacylglycerol (TAG) in cell was inversely proportional to growth rate. Unlike BR006 strain, the cells from the slow-growing strain (BR022) exhibited high TAG production even under high Si conditions. These results suggest that under optimal Si conditions, in the fast-growing strain (BR006), carbon from photosynthesis is directed toward new cell formation, while in the slow-growing (BR022), carbon is stored as TAG. Based on that, our results indicate that BR006 could be candidate for industry purposes once it respond drastically to stress conditions, increasing the levels of important metabolites such as TAG, fucoxanthin, sugar or PUFA. Meanwhile BR022 is a diatom that could have a great ecological success and outcompete other species during starvation periods.

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Area: Developmental Biology
Tipo de presentación: Poster en formato PDF
Enviado por: Cristian Malavert

Environmental regulation of dormancy in Echinochloa crus-galli seeds

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Predicting weed emergence is of vital importance for weed management, since the seedling stage is the most effective for the application of control practices. In weeds species whose seeds present dormancy, as in *Echinocloa crus-galli* predicting emergence depends on understanding how the environment regulates dormancy level. In the present work, we studied the environmental regulation of dormancy in *E. crus galli* seeds. For this, *E. crus galli* seeds were storage under different conditions: i) 5, 10 and 15ºC (under moist conditions, stratification) and ii) 15 and 25ºC (under dry conditions, after-ripening) for 80 days. During storage, the seeds were tested for germination under a wide temperature range (10-30ºC), light conditions (red light, far-red light and darkness) and different thermal amplitude regimes. The results showed that the changes in dormancy level were associated with a widening of the thermal range permissive for seed germination as consequence of a decrease in its lower limit temperature (T_l). This decrease in T_l was higher when the seeds were stratified at 10ºC than at 5 and 15ºC. Seeds exposed to after-repining conditions showed significant lower rate of dormancy release than those stored under moist conditions at low temperatures (i.e. stratified). Seeds stratified at 10ºC also showed higher germination values under all light conditions and alternating temperatures compared to those stratified seeds at 5 and 15ºC, and to those exposed to after-ripening conditions. Obtained results were used to establish functional relationships to predict emergence of *E. crus-galli* as a function of soil temperature.

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RF987LJ
Area: Epigenetics, Chromatin, non-coding RNAs, RNA biology
Tipo de presentación: Poster en formato PDF
Enviado por: María Florencia Mammarella

Long noncoding RNA-mediated epigenetic regulation of the branching master regulator gene BRC1

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Plant long noncoding RNAs (lncRNAs) have emerged as important and versatile regulators of gene expression, including epigenetic reprogramming of target genes. In Arabidopsis, the intergenic lncRNA *APOLO* was shown to directly regulate a subset of auxin-responsive genes during lateral root development, by sequence complementarity and DNA-RNA duplex (R-loop) formation. In this work we show that *APOLO* is also expressed in the aerial organs of the plant, and that it directly regulates *BRANCHED1* (*BRC1*), a TCP class II transcription factor repressing the outgrowth of axillary buds and plant branching. Upon *APOLO* knock-down (RNAi), CRISPR-mediated knockout and over-expression (35S), *BRC1* epigenetic profile is altered impacting its transcriptional activity. Accordingly, *APOLO* deregulated plants exhibit abnormal branching integrating environmental signals. Moreover, we found that *APOLO*-dependent chromatin 3D conformation of the *BRC1* locus differs between leaves and axillary buds, hinting at tissue-specific chromatin dynamics. Altogether, our results indicate that plant developmental plasticity relies on lncRNA-mediated epigenetic reprogramming of master genes.

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TG378SC
Area: Biotic Interactions
Tipo de presentación: Poster en formato PDF
Enviado por: Carlos Augusto Manacorda

TuMV infection in Arabidopsis: Impact on rosette development and water management

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Characterization of the morphological and physiological outcomes of viral infections is important to objectively quantify the damage caused by them, as well as to envision control strategies that can subsequently be assessed. Due to the importance of water homeostasis and balance during stress, we focused on water management in Arabidopsis under viral infection, a topic that is still poorly understood. Taking into account the interconnectedness of plant tissues, and the spread of virus throughout the entire plant, we studied TuMV impact both at the rosette and root levels. A hydroponic-based system was optimized to gain access to intact root tissue. In this first part of our work we show the main results that were found at the rosette level. Classical morphological parameters were simultaneously assessed by means of PCA, showing a clear separation between treatments. As expected, TuMV arrested rosette growth and PCA demonstrated that not only rosette size but also its shape was affected by the virus. Also, the defense and stress-response hormones SA and ABA overaccumulated under infection. Analysis of physiological parameters showed a decrease of stomatal conductance and water consumption by 40 and 24%, respectively, whereas leaf osmolyte and relative water content increased significantly, suggesting that the viral infection caused a major hydraulic reorganization in the rosette. These results raised the question whether the virus could affect the anatomical and physiological traits of the roots as well. Our findings related to root water management are presented in a separate poster.

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250
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Area: Developmental Biology
Tipo de presentación: video presentacion
Enviado por: Silvia Manrique

HISTONE DEACETYLASE 19 (HDA19) CONTROLS CARPEL MARGIN MERISTEM ACTIVITY BY REGULATING SHOOTMERISTEMLESS (STM) EXPRESSION

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The carpel margin meristem (CMM), formed in the center of the gynoecium in Arabidopsis, gives rise to the placenta, ovules, septum, transmitting tract, style, and stigma, all of which are critical for the reproductive competence of the plant. It is a determined meristem and it disappears when the development of this organ is completed. Therefore, its meristematic activity has to be stopped at a certain point to allow the marginal organs to develop, but how this happens is presently unknown. HDA19 is involved in the maintenance of several meristems and *hda19* mutants display defects in the structures derived of the CMM including a reduced ovule number. Therefore, we hypothesized that HDA19 might be involved in controlling CMM maintenance. Indeed, transcriptomic analysis of *hda19* gynoecium cells revealed that genes involved in meristem maintenance are upregulated in *hda19* while genes involved in the formation of organ primordia are downregulated. In particular, the pluripotency gene STM was upregulated, and ChIPseq revealed an increase in the acetylation at its locus in *hda19* mutants. Reduction of STM levels by RNA interference alleviates the defects in the marginal gynoecium organs in *hda19* mutants, supporting the hypothesis that HDA19 is essential to maintain the balance between meristematic activity and differentiation in the CMM. Additionally, we propose a role for the MADS box transcription factors involved in ovule identity, SEEDSTICK and SHATTERPROOF 1-2, in the regulation of STM mediated by HDA19.

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251
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Tipo de presentación: Poster en formato PDF
Enviado por: Jeremías Mansilla

The cuticle thickness as mechanism of acclimatization to water deficit in olive trees

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The cuticle of the leaves and fruits plays an important role acting as a barrier reducing water loss, controlling temperature fluctuations and participating in the plant-pathogen interaction. Water stress conditions generate morphological changes in plants as a mechanism of response. Under these conditions, there are responses linked to reduce water loss, for example increasing the cuticle thickness. The objective of this work is to evaluate the changes in the cuticle thickness in olive leaves and fruits growing under different levels of water stress. In order to achieve this, an experiment was carried out on productive trees in 'Arbequina' and 'Frantoio' cultivars. Two irrigation treatments were applied according to the maximum crop evapotranspiration: 50% (T_{50}) and 100% (T_{100}) of the ETc, and without irrigation or rain contribution (T_o) during the lipogenesis phase. Leaves and fruits samples were taken when fruit maturity was reached (April). We cut them with a microtome and stained them to measure cuticle thickness. We found that after four months of treatment, fruit cuticle thickness was modified in plants with water restriction. The cuticle of the fruits increased by 27% in 'Frantoio' and by 57% in 'Arbequina' comparing T_o and T_{100} respectively. Leaves cuticle increased by 9% in 'Arbequina', while in 'Frantoio' there was no significant difference. It was demonstrated that the increase in the cuticle thickness is one of the mechanisms of acclimatization to water deficit in olive trees.

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Enviado por: Matías Manzi

Effect of pre-harvest ABA application on postharvest chilling injury of oranges

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Low temperature during the storage is a key tool to maintain fruit quality. However, citrus fruit are sensitive to develop chilling injury (CI) in the peel. It appears as brown sunken spots that eventually may coalesce covering the whole fruit surface, negatively affecting marketability. Factors affecting fruit susceptibility to CI might be pre-harvest (radiation, nutrition, water availability, among others) and postharvest (fruit coatings, pre-conditioning, phytohormones, storage time and temperature). Agricultural practices for the management of postharvest CI are still scarce. The aim of this work was to test the effect of preharvest ABA application (Protone®, Valent Bioscience) on orange fruit susceptibility to develop CI symptoms during cold storage. ABA was applied thrice during fruit development at 500 mg L^{-1} to three different orange cultivars: Salustiana, Navel and Valencia, during two different seasons. Results showed that ABA application promoted cold tolerance in the three cultivars during postharvest storage for 8 weeks at 1.0±0.5 °C. In the cold-tolerant Navel and Valencia (lower CI incidence) there was a decrease in the proportion of fruit with symptoms compared to the control. However, in Salustiana, which showed high CI incidence (>80%) during both seasons, ABA delayed symptoms appearance by two weeks. It is worth noting that in the three cultivars, ABA substantially reduced the proportion of moderate and severe symptoms. In addition, ABA did not affect external (firmness and colour) and internal (total soluble solids and acidity) quality of the fruit, making ABA a suitable tool for its commercial application under field conditions.

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253
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Area: Abiotic Stress
Tipo de presentación: video presentacion
Enviado por: Pedro Augusto Marazzo de Sousa

MORPHOLOGICALLY DISTINCT CYANOBACTERIA DISPLAY DIFFERENTIAL ARSENIC TOLERANCE

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Arsenic (As) is a noxious, nonessential metalloid that has been a priority environmental pollutant. Arsenate [As(V)] can uncouple oxidative phosphorylation and replace phosphorus in DNA, while arsenite [As(III)] reacts with functional groups of cysteine and histidine leading to enzymatic inactivation. Cyanobacteria comprise a diverse morphological group, inhabiting a wide range of environments, including As-contaminated ones. We hypothesized that morphological distinct cyanobacteria show differential strategies to cope with As. Therefore, our main goal was to evaluate the growth responses of three cyanobacterial strains cultivated in As-supplemented BG-11 cultivation media. Two unicellular strains,PCC6803 and CCM-UFV039, which were isolated from freshwater and saline-alkaline lake, respectively, as well as one filamentous homocytous, CCM-UFV065, isolated from an As-contaminated site, were evaluated. Growth curves were carried out for 9 days, applying As(V) and As(III) concentrations of 0, 0.01, 0.05, 0.1, 0.5, 1, 5, 10, 50 and 100 mM. The selected strains were also characterized in a phylogenetic perspective. The phylogenetic analysis corroborated the morphology and the strains CCM-UFV039 and CCM-UFV065 were assigned to the genera *Synechocystis* and *Pseudanabaena*. Growth curves showed similar patterns for unicellular strains, without any growth impairments under As(V), but showing decreasing above 5 mM of As(III). The growth of *Pseudanabaena* sp. was impaired in the presence of 50 and 100 mM of As(V) as well as from 1 mM of As(III). We present evidence that morphologically distint cyanobacteria displayed differential As-tolerance, being As(III) more toxic than As(V). Notably, the ecological origin of the strains is seemingly not an important trait.

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254
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Enviado por: Fernanda Marchetti

PLANT EMBRYOGENESIS AND BEYOND: ROLE OF EMB2217, A MITOCHONDRIAL PENTATRICOPEPTIDE REPEAT PROTEIN CONTAINING SMR DOMAIN.

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EMB2217 is a Pentatricopeptide Repeat containing protein with MutS-related domain (PPR-SMR). PPR proteins constitute the largest protein family in plants and they are involved in the processing of RNA. However, PPR-SMR is a small group with enigmatic function. In Arabidopsis, three PPR-SMR proteins are predicted to localize in mitochondria, being EMB2217 essential for plant embryogenesis. In Maize, its orthologous is related to the splicing of multiple introns of mitochondrial transcripts, which result to be essential for seed development. We study two *EMB2217* Arabidopsis mutant lines (SAIL_639_H09 and SALK_018198). Their siliques show 25% of abnormal seeds, corresponding to homozygous embryos, delayed in early stages of embryogenesis. Complementation with the Wt version of *EMB2217* gene restored the embryo-lethal phenotype. In immature siliques, normal seeds look green while abnormal homozygous seeds look white. In order to rescue homozygous plants, white seeds were transferred to MS medium containing 1% sucrose. After a month, tiny plants were obtained, characterized by curly small leaves. Analysis of the mitotranscriptome will be performed using RNA extracted from this tissue; also from white homozygous seeds. Since PPR-SMR proteins are found in bryophytes, the role of PPR-SMR proteins in mitochondria of non-vascular plants will be studied. Firstly, a putative homologous protein for EMB2217 will be analyzed in *Marchantia polymorpha*. Mutant plants will be created by the CRISPR technique and comparative analysis of mitochondrial transcripts will be performed. Altogether, the results will contribute to understand the role of PPR-SMR proteins as regulator factors of mitochondrial transcripts during land plant evolution.

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255
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Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Ezequiel Margarit

Metabolic and physiological changes during cold acclimation in two eucalyptus species divergent for frost tolerance

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Most *Eucalyptus* species planted for wood and paper in subtropical and temperate regions are highly sensitive to sudden or seasonal frosts. Therefore, selection of genotypes with higher frost tolerance and a quicker acclimation to cold is of major interest. In this work, we studied the basal tolerance and the cold acclimation process in two *Eucalyptus* species (*E. grandis* and *E. benthamii*) by exposing 6-month old seedlings to low temperatures in culture chambers (15/5 °C day/night) for different times (0, 5, 10, 15 and 20 days). Evaluation of lethal temperature 50% (LT_{50}) using leaf disc electrolyte leakage assays pointed to *E. benthamii* as the species with the highest tolerance in control conditions (LT_{50} of -1.9 vs. -1.0 ºC). Also, *E. benthamii* showed a quick rise in tolerance after 5 days of cold treatment (-4.7 ºC), reaching -6 ºC by day 10, while *E. grandis* needed 15 days to reach its maximum tolerance (-3.6 ºC). Physiological parameters such as leaf area, leaf fresh and dry weight, and plant height were also affected by acclimation in *E. benthamii*, where a decrease in area, height, and fresh weight was noted. Leaf metabolome analysis evidenced a rapid increase in sugar contents in *E. benthamii* by day 5, as well as higher accumulation of different protective metabolites during its cold acclimation. Principal component analysis and correlation plots allowed pinpointing metabolites and different parameters related to cold acclimation in both species. Our results showed *E. benthamii* has key traits to breed frost tolerant *Eucalyptus*.

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256
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Area: Signal Transduction
Tipo de presentación: video presentacion
Enviado por: Oriana Mariani

Analysis of the phosphorylation of serine 280 in Arabidopsis thaliana phospholipase C2 (AtPLC2) activation.

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Plants have developed different strategies to respond to external stimuli. Recognition of these stimuli leads to intracellular signaling events via second messengers. Phospholipase C (PLC) are enzymes present in animals and plants that hydrolyze phosphoinositides producing two second messengers: diacylglycerol (DAG) and inositol phosphates (IPs). The structure and function of these enzymes has been extensively studied in animals, but little information is available in plants. The *Arabidopsis thaliana* genome encodes for 9 PLC, which are involved in the response to diverse stimuli both, biotic, abiotic and developing. In particular, our laboratory has proven that AtPLC2 plays a role in the immune response to biotic stress. In addition, phosphoproteomics studies report phosphorylation of S280 in response to the same stimulus. The objective is to determine the role of S280 phosphorylation on AtPLC2 biological activity through computational biology approaches and in vitro activity. The putative orthologues of AtPLC2 were identified by phylogeny, and we found that S280 is not strictly conserved. However, computational studies identified sites located in regulatory regions of the protein that could be involved in membrane location and binding, as well as regulatory processes. This work establishes a basis for designing and carrying out future experiments that would clarify notions not yet studied in plant PLCs enzymes.

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257
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Area: Biotic Interactions
Tipo de presentación: Poster en formato PDF
Enviado por: Facundo Ernesto Marmisolle

Citrus psorosis virus (CPsV) interferes with plant miRNA biogenesis

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Silencing by miRNAs is a fundamental and an evolutionarily conserved mechanism that regulates gene expression in eukaryotes. It also functions as a primary immune defense against viruses in plants. However, plant viruses have developed viral suppressors of RNA silencing (VSRs) to counterattack plant defense and facilitate virus infection. There are numerous reports that indicate alteration in the accumulation of endogenous miRNAs due to viral presence but little is known about how pathogens regulate miRNAs processing and accumulation.

Citrus psorosis virus (CPsV) is a three-partite, non-enveloped, negative-sense, ssRNA virus that encodes 4 proteins: a replicase (RdRp, 280kDa), a small 24kDa protein (24K), an aspartil protease (54kDa) and a coat protein (48kDa). In previous results, we showed that CPsV down-regulates the accumulation of a set of endogenous miRNAs in *Citrus sinensis* plants with a concomitant up-regulation in the accumulation of their target transcripts. Besides, we demonstrated that $24K^{CPsV}$ protein interacts with miRNAs precursors (pre-miRNA) *in vivo* causing a higher accumulation of unprocessed species.

Here, we showed that CPsV-infected citrus plants exhibits a higher accumulation of unprocessed pre-miRNAs compared to healthy plants by RT-qPCR. Besides, we found subcellular co-localization of $24K^{CPsV}$ with different components of the miRNAs biogenesis machinery (DICER-LIKE 1: DCL1; HYPONASTIC LEAVES 1: HYL1 and SERRATE: SE) in D-bodies, forming typical expression pattern. Interaction between $24K^{CPsV}$ and HYL1 or SE was also verified by BiFC and CoIP. These results confirm the interference of $24K^{CPsV}$ with miRNA biogenesis pathway either explained by protein-protein or protein-RNA interaction.

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Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Mailen Ariela Martinez

ABA content and germination in green soybean seed produced under heat-drought stress

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Heat-drought stress during the late-developing (R5-R7) soybean seeds (*Glycine max* (L) Merr.) affects the chlorophyll degradation, resulting in green seeds with low physiological quality. Germination percentages (%G) and times to reach 50 %G (t50) on seeds (S), embryos (E) and, embryonic axes (Ax) were measured to evaluate germination performances. Abscisic Acid content ([ABA]) in Ax, the main germination-inhibitory plant hormone, was also measured. Seeds of SRM 3410 and DM 4214 STS varieties produced under heat-drought stress during the R5-R7 period and, non-stressed seeds of SRM 3410 used as control (C). Stressed seeds classified as green (GS) and yellow (YS). The percentage of GS was 44.8 y 31.9% in SRM 3410 and DM 4214 STS, respectively. The respective %G and t50 of GS (30 and 33%, t50 did not reach), GE (53 and 80%, 58 and 39 h) and, GAx (67 and 83%, 24 and 20 h) were lower than those of YS (77 and 97%, 39 and 31 h), YE (100 and 97%, 13 and 21 h) and, YAx (97 and 100%, 20 and 19 h) and CS (100%, 26 h), CE (100%, 16 h) and CAx (100%, 19 h). The [ABA] in GS of SRM 3410 and DM 4214 STS was 39.7 and 22.3 μg.g DW^{-1}, respectively. By contrast, in YS, [ABA] was 8.1 and 4 μg.g DW^{-1} and, in CS, 1.9 μg.g DW^{-1}. Our results showed that the highest [ABA] could be partially responsible for the low germination performances in stressed seeds (GS and YS).

259
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Area: Developmental Biology
Tipo de presentación: video presentacion
Enviado por: Carmen Martín Pizarro

Identification and characterization of the NAC Transcription Factor FaRIF, a key regulator of strawberry fruit ripening

Identification and characterization of the NAC Transcription Factor FaRIF, a key regulator of strawberry fruit ripening

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Strawberry is becoming a model for studying the molecular mechanism of ripening in non-climacteric fruits. However, a limited number of transcriptional regulators of this process have been identified so far. In this study, we have identified and characterized a gene encoding for a NAC transcription factor (TF), named as *FaRIF* (*Ripening Inducing Factor*).

FaRIF expression presents a fruit-specific pattern, which is upregulated during ripening. In order to functionally characterize this TF, we have generated silencing and overexpressing stable transgenic lines. While the RNAi lines showed an apparent delay of fruit ripening, the overexpressing lines displayed an acceleration of this process. Transcriptomic analysis of the silenced lines showed a significantly altered expression of genes involved in development, hormone metabolism, flavonoid pathway, and cell-wall disassembly, being many of these confirmed by phenotypical and metabolomics analysis. Our results support a main role of FaRIF in the control of relevant ripening-associated processes in strawberry fruit.

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260
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Area: Biochemistry and Metabolism
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Enviado por: Guadalupe Martínez

Sunflower husks: an agroindustrial byproduct enriched in phenolic compounds with antifungal properties

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Plants synthesize diverse types of secondary metabolites, including phenolic acids, terpenes, flavonoids, essential oils and alkaloids, which are involved in protection against fungal infections. Sunflower husks, an under-appreciated byproduct of the oil industry, are enriched in phenolic compounds. The aim of this work was to explore the antifungal potential of sunflower husk ethanolic extracts against different pathogenic fungi of agronomic importance and provide insights on its mechanism of action. Phenolic extracts of sunflower husks (EPC) were prepared by maceration in 80% ethanol. The composition analysis by RP-HPLC showed that the main phenolic compound in the extract was chlorogenic acid. In order to assess the antifungal activity, fungal spores were incubated with increasing doses of EPC and subjected to microscopic observation. EPC 0.4 mg/ml inhibited spore germination of *Sclerotinia sclerotiorum, Fusarium solani, Fusarium oxysporum* and *Verticillium dalhiae*. Further analysis of cell viability by Evans Blue staining revealed the permeabilization of the plasma membrane, suggesting the cytotoxic action of EPC. The fungicidal effect was confirmed by treatment with EPC and subsequent culture on media potato dextrose agar. In addition, using diaminobenzidine to detect reactive oxygen species, EPC-treated spores showed increased endogenous peroxides production. Our findings indicate that EPC displayed antifungal activity on different phytopathogenic fungi through cytotoxic effects mediated by oxidative stress and cell permeabilization. The bioactive properties of EPC contribute to valorize a byproduct of the oil industry that is usually discarded.

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261
MF331KH
Area: Biotic Interactions
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Enviado por: Maria Florencia Martínez

Transcriptome Response to Potato virus X 25K effector in Solanum tuberosum

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Potato (*Solanum tuberosum* L.) is the fourth most important crop worldwide. *Nb* is a single dominant gene from cv. Pentland Ivory that confers hypersensitive resistance (HR) to potato virus X (PVX) strain ROTH1, which carries the 25-kDa effector protein (25K1). The gene *25K* of the virulent strain UK3 (*25K3*) overcomes the HR. The molecular mechanisms governing the incompatible (*Nb*-25K1) and compatible (*Nb*-25K3) interaction are unknown. In this study, an integrated microRNA and mRNA transcriptome analysis of *Nb* potato leaves infiltrated with *Agrobacterium* cultures harbouring pBIN25K1, pBIN25K3 or empty vector was performed. Eleven miRNAs (eight known and three novel), and three miRNAs (one known and two novel) were identified in response to 25K1 and 25K3, respectively. We performed target predictions for differentially expressed miRNAs and correlated their expression levels through mRNA sequencing data. GO analysis of the targets revealed an overrepresentation of genes involved in cell wall reinforcement, oxidative burst, accumulation of phenolic compounds and cell death in the incompatible interaction. The biological processes associated with strengthening of cell wall that involves the miRNAs -stu-*miR397* and stu-*miR408*- which target laccases, were validated by qRT-PCR and histochemical analysis. This study provides a deeper understanding of miRNA dependent regulatory networks in the resistance response to PVX-25K.

262
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Area: Plant breeding
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Enviado por: Carlos Guillermo Bartoli

Increased biotic and abiotic stress tolerance in hybrids between wild and domesticated cucurbit species

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Wild plant species constitute a valuable reservoir of genes contributing to increase the biotic and abiotic stress tolerance in domesticated species. In this study, we generated hybrids between two accessions of *Cucurbitamaxima* subsp. *maxima* var. *Zapallito* (domesticated species) and *Cucurbita ecuadorensis* Cutler y Whitaker accesión Grif 9446 (wild species) and evaluated their performance under stress conditions. Parental and hybrids plants were treated to flooding and recovery conditions in the field what frequently impairs the yield of this species. Hybrids showed higher chlorophyll content (estimated as SPAD units), transpiration (measured with a porometer) and photosynthesis (determined by a chlorophyll fluorometer) leading to a largely increased survival than domesticated parental plants under this stressful environment. In addition, hybrids showed higher tolerance when challenged to virus infections showing only accessions of the domesticated plants symptoms of disease. These results constitute a promising contribution for generating *cucurbit* plants with increased performance when cultivated under an environment restricting crop production.

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QH573SR
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Javier Martínez Pacheco

Apoplastic Class-III Peroxidases COLD1 and COLD2 regulate ROS-homeostasis linked to root hair growth at low-temperature in Arabidopsis thaliana

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Root hairs (RH) growth is under the control of endogenous and external environmental signals that regulate its final cell size. RHs are part of the active surface root area crucial for nutrient uptake and water absorption. Previously, we have determined that the low-temperature treatment at 10°C is able to trigger, unexpectedly, an exacerbated RH growth compared to the room-temperature. This conditional RH growth at low-temperature was linked to a reduced nutrient availability in the media. Here, we explore the molecular basis of this strong RH growth response by using the Genome Wide Association Studies (GWAS) approach on *Arabidopsis thaliana* accessions. We identified an uncharacterized PEROXIDASE COLD1 as a key protein triggering the end of conditional growth under a moderate temperature stress. In addition, we also identified a related PEROXIDASE COLD2 to be associated to this growth condition. Double *cold1/cold2* mutant and the overexpressor COLD1 and COLD2 lines showed contrasting RH phenotypes, peroxidase activities and $_{\text{cyt/apo}}$ROS levels. Collectively, both COLD1 and COLD2 are key apoplastic PRXs that modulates ROS-homeostasis linked RH elongation at low-temperature.

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264
KB453QJ
Area: Biochemistry and Metabolism
Tipo de presentación: video presentacion
Enviado por: Félix Juan Martínez-Rivas

Strawberry fruit FaCXE2 carboxylesterase is involved in the catabolism of volatile esters during the ripening process.

Strawberry fruit FaCXE2 carboxylesterase is involved in the catabolism of volatile esters during the ripening process.

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Consumers appreciate strawberry fruit because of its unique flavor and nutritional quality. As part of a variable diet, strawberry is becoming one of the most considerable fruit in the world. Strawberry ripening culminates as the flesh softens, volatile emission peaks, and sugars accumulate. The content and balance of those compounds would define their taste. Strawberry volatiles are mainly composed by esters, which are synthetized by alcohol acyltransferases and are broken down by carboxylesterases. While two-alcohol acetyltransferase have been identified, so far, no carboxylesterases have been characterized in strawberry. Here, we report the biochemical and functional characterization of FaCXE2, mainly expressed during the fruit ripening specifically expressed in the fruit and responding to the key hormones, auxins and abscisic acid, which control this process. Our results show that FaCXE2 is able to hydrolyze artificial ester substrates *in vitro* that are similar to those produced by ripe strawberry fruit. The transiently transgenic fruits, knocking-down the
expression of *FaCXE2* exhibited a concomitant increase of esters, as methyl hexanoate, methyl butanoate and ethyl hexanoate, among others as well as the decrease of alcohols, hexenol and linanool, providing evidence that FaCXE2 plays a role regulating volatile content in strawberry having a role in the ester metabolism in ripe fruit. Additionally, this work enhances our understanding of the molecular basis of fruit volatiles production so that relevant genes can be introduced into common selections, producing better flavored fruits. The identification of relevant genes provides strong tools to breeders to ease the selection of new varieties.

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265
SG361BS
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Daniel Matsusaka

Mapping flowering time in a new RIL Population between Col-0 and Patagonia Arabidopsis accessions

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Adaptation enables plants to successfully grow and reproduce, even under transient unfavorable conditions. One important developmental stage of this process is flowering, which integrates various environmental inputs. Plants evolved complex regulatory networks for transitioning from vegetative to reproductive stages, essentially matching the developmental shift with the best possible prospective environment. Temperature is a major seasonal cue that can be sensed and integrated. Exposure to weeks of cold accelerates the transition to flowering and is called vernalization. In *Arabidopsis thaliana*, flowering is controlled through a cascade of key transcription factors: *FRI* gene up-regulates *FLC*, which represses the expression of *FT* and *SOC1.* Vernalization impacts this hierarchical ladder epigenetically repressing *FLC*, thus activating flowering. Although major causative players driving this process have been already uncovered in *A. thaliana*, knowledge of all flowering genetic natural variants enabling quick adaptation is still in its infancy. Here, we took advantage of QTL mapping —a genetic strategy that associates genotype to phenotype in bi-parental experimental crosses —, to score flowering using an informative mapping population between Col-0 and Patagonia (Pat) *A. thaliana* accessions. With QTL mapping, we associated a novel region in chromosome V to flowering time after vernalization under both short and long days growth, representing a new *VERN1* QTL which is not revealed when plant are not vernalized. We confirmed this QTL with two recombinant-inbreed-lines, showing that Pat allele shortens the flowering time. Our observations suggest that an undescribed rewiring of flowering regulation may underlie the quick adaptation of *A. thaliana* to Patagonian steppes.

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MD162RP
Area: Plant Physiology and Ecophysiology
Tipo de presentación: video presentacion
Enviado por: Maria Lucia Mañueco

Effect of the water logging of the root zone on the development of cherries cv Santina/Santa Lucia 64 in the Alto Valle of Río Negro and Neuquén

Effect of the water logging of the root zone on the development of cherries cv Santina/Santa Lucia 64 in the Alto Valle of Río Negro and Neuquén

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The Alto Valle of Rio Negro and Neuquén (AVRN&N) is an intensive irrigated fruit producing area. The existence of a shallow water table causes a capillary rise that modifies the water content in the soil profile, generating waterlogging and salinization, influencing the water balance and occasionally jeopardizing the growth and development of fruit trees. The aim of this trial included the assessment of the performance of cherry cv. Santina/Santa Lucia 64 in the season 2015-2016. Soil water content was measured with a FDR sensor at three depths: 0.30 m, 0.60 m and 0.90 m and the water table level was regularly monitored. The fruit trees response was evaluated by gaging xylem water potential and stomatal conductance in four opportunities: after stone hardening, at mid-stage III, at harvest time and after fruit harvest. The measures were correlated to vapour pressure deficit and soil water content. A detrimental effect was observed in crop development, causing stomatal conductance to be lower in spring in contrast to January. Fruit quality was not affected but the yield was lower than expected, due to plant mortality induced by successive events of spring waterlogging. It can be concluded that water table fluctuation in spring added to the recharge caused by spring frost control causes a waterlogging condition in the root zone that should be prevented during long periods with adequate drainage systems.

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MF225FF
Area: Biotic Interactions
Tipo de presentación: Poster en formato PDF
Enviado por: Laura Medina-Puche

MOLECULAR DETERMINANTS UNDERPINNING THE DYNAMIC DUAL LOCALIZATION OF A VIRAL PROTEIN IN THE PLANT CELL

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A growing body of evidence points at the targeting of several subcellular compartments as a strategy deployed by proteins to achieve multifunctionality. In the case of plant viruses, which have limited coding capacity, this strategy becomes crucial. One example is illustrated by the C4 protein encoded by the geminivirus *Tomato yellow leaf curl virus* (TYLCV). C4 contains two overlapping localization signals, namely an N-myristoylation motif for plasma membrane (PM) tethering and a chloroplast transit peptide (cTP) for chloroplast targeting (Rosas-Diaz et al., 2018). PM localization of C4 requires myristoylation; at the PM and plasmodesmata (PD), C4 interacts with the receptor-like kinases BAM1/2 and hinders the cell-to-cell spread of RNAi (Rosas-Diaz et al., 2018; Fan et al., 2021). Following activation of defense, triggered by the presence of the virus-encoded Rep protein during the viral infection, by the bacterial pathogen-associated molecular pattern (PAMP) flg22, or by the plant immunogenic peptide Pep1, the PM-associated C4 is translocated to the chloroplast, where it interacts with the Calcium Sensing Receptor (CAS) and interferes with SA-dependent defense responses. Our results indicate that PM release of C4 requires active phosphorylation, while its chloroplast import depends on a functional protein import TOC/TIC complex (Medina-Puche et al., 2020). Our results demonstrate that a wide range of immunity-activating signals modulate the dynamic PM-to-chloroplasts localization of C4, and illustrate how C4 hijacks plant modification and intracellular trafficking pathways and acquire multifunctionality. In addition, this work sheds new light onto the molecular and cellular events connecting PM and chloroplasts during defense responses.

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268
LC396RQ
Area: Biotic Interactions
Tipo de presentación: Poster en formato PDF
Enviado por: Laura Medina-Puche

EXPLORING THE SUBCELLULAR LANDSCAPE OF THE ARABIDOPSIS CALCIUM-DEPENDENT PROTEIN KINASES (CDPKs) AND ITS ROLE IN PLANT IMMUNITY

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Plants are under constant adaptation to the surrounding environment. To face those challenges, plants have evolved a signal transduction network. The information encrypted by calcium, the most important secondary messenger, needs to be decoded and relayed by calcium binding proteins to be converted into biological responses. One of the calcium sensor families is the calcium-dependent protein kinases (CDPKs). This family in *Arabidopsis* is represented by 34 members, some of them play important roles in development, abiotic stress responses, and immunity. Most AtCDPKs have a predicted N-myristoylation site involved in membrane targeting. To stabilize the membrane tethering, a second post-translational modification is frequently required, such as a reversible palmitoylation. Strikingly, we have identified the presence of a chloroplast transit peptide (cTP) overlapping with the N-myristoylation site in four AtCDPKs (CPK3, CPK16, CPK24 and CPK28). Recently, we have shown that CPK16 re-localizes from the PM-to-chloroplasts upon treatment with the bacterial elicitor peptide flg22 to promote chloroplast-dependent defenses. Surprisingly, unpublished work from our lab shows that although CPK28 does not accumulate in chloroplasts following flg22 treatment, a recently described alternative splice variant produced upon DAMP treatment unable to be myristoylated does. Unexpectedly, we also observe that the non-myristoylable version of CPK18, that together with CPK16 and CPK28 form the subgroup IV, constitutively localizes in chloroplasts despite lacking a predicted cTP. Considering these results, suborganellar targeting could provide an additional layer of regulation to enable CDPK-mediated fine-tuning of plant immune responses and where chloroplasts could emerge as a central subcellular compartment to CDPK function.

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QL138RB
Area: Systems, Synthetic, and Computational Biology
Tipo de presentación: Poster en formato PDF
Enviado por: Devang Mehta

Closing the protein gap in plant chronobiology using time-course BoxCarDIA proteomics

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Over the last decade transcriptomics technologies have powered a revolution in our understanding of the plant circadian clock and chronobiology in model plants and crop systems. This includes a clearer picture of anticipatory (circadian) and reactive (diel) changes in plant gene expression as well as the role of core clock transcription factors. However, transcript-level data is inadequate to provide a complete description of circadian regulation and can mask protein-level events that directly impact plant physiology. Indeed, initial proteomics data from wild-type Arabidopsis plants have found an intriguing lack of protein-level oscillation at the same scale as transcriptional oscillation. Phosphoproteomics studies have also found large diel changes in global protein phosphorylation suggesting that circadian post-transcriptional and post-translational mechanisms (PTMs) play a key role in regulating plant circadian outcomes. Here we present data from a large-scale study profiling the diel proteomes of wild-type and circadian clock mutants of Arabidopsis for the first time. In order to execute such complex multivariate time-course experimentation we also developed a new label-free proteomics workflow called BoxCarDIA that enables us to achieve complete protein profiles without the use of data imputation. Finally, our results provide a first look at the impacts of the core clock components at the protein-level revealing new insights into disconnects between the circadian transcriptome and proteome. Our results argue for greater focus on protein and PTM-level circadian dynamics in order to close the protein gap in plant chronobiology.

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Area: Biotic Interactions
Tipo de presentación: Poster en formato PDF
Enviado por: Mariana Melchiorre

Genetic polymorphisms of rhizobia nodulaing Prosopis flexuosa in saline environments in Chaqueña Region

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In the salt flates, Pipanaco (Catamarca) and La Antigua (La Rioja), Parque Chaqueño, *Prosopis flexuosa* provides the ecosystem services and contributes with soil fertility by fixing N_2 in symbiosis with soil rhizobia. The aim of this work was to characterize genetic diversity and symbiotic performance of indigenous rhizobial populations able to nodulate *P. flexuosa*. Soils samples were collected from four locations which showed different electric conductivity, and used to sown *P.Flexuosa* seeds as trap plants in order to recover soil rhizobia. The conductivity in samples from Pipanaco_1 and Pipanaco_2 was 25 and 20 dS/m, whereas in samples from La Antigua_1 and La Antigua_2 were 9.7 and 62.5 dS/m respectively. *P. flexuosa* cultivated in soils from La Antigua_1 showed the highest leave and nodule number, on the contrary no nodules and the lowest plant height and leave number were observed in plants grown in extreme salinity (La Antigua_2). Nodules were collected and crushed to isolate rhizobia. From 73 strains, DNA was obtained and used to analyze genetic polymorphisms from BOX A1R PCR amplification. Cluster analysis was performed with the UPGMA algorithm using the binary matrix based on DNA BOX A1R electrophoretic patterns. Principal coordinate analysis (PCO) was performed. Strains from La Antigua_1 had the highest variability, almost homogeneously distributed along both PCO axes, whereas the strains from Pipanaco_1 and Pipanaco_2, were grouped on the left of the orthogonal axis in PCO1. These results showed that rhizobia diversity as well as their contribution to *P. flexuosa* growth were negatively affected by salinity increases.

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271
RK711MM
Area: Epigenetics, Chromatin, non-coding RNAs, RNA biology
Tipo de presentación: Poster en formato PDF
Enviado por: Regina Mencia

Transcriptionally regulation of the Arabidopsis EFR gene by siRNA-induced chromatin conformation changes associated with pathogen resistance

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Plant genomes are largely composed of transposable elements (TEs), reaching up to 90% of some grasses' genomes. In the model plant *Arabidopsis thaliana*, 20% of its genome is composed of TEs and other repetitive elements. To keep transposition under control, plants rely on the RNA-dependent DNA methylation (RdDM) pathway to transcriptionally silence TEs. As a side effect, the silencing of TEs can also impact the transcription of neighboring genes. Here we identified a TE-derived inverted repeat element (IR) adjacent to de 3' UTR of the Arabidopsis *EF-Tu RECEPTOR (EFR)* gene. This element's transcript is further processed into 24 nucleotides siRNAs that trigger DNA methylation at its loci. Such DNA methylation induces a change in the chromatin folding, creating a short-range DNA loop that comprises the coding region of *EFR*. EFR is a pathogen-associated molecular patterns (PAMPS) receptor that's able to trigger PAMP-triggered immunity (PTI) and, by this, acting in the front line of plant-pathogen responses. We found that the identified IR can dynamically affect *EFR* expression, but also that this element is not conserved across Arabidopsis accession. The variability in the IR's content across accessions correlates with a variation in the local chromatin topology, *EFR* expression, and response to the model pathogen *Pseudomonas syringae.* Our findings represent a unique case of potential adaptive evolution to pathogens caused by TEs movement and chromatin alteration.

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Area: Abiotic Stress
Tipo de presentación: video presentacion
Enviado por: Francesco Mignolli

Flooding increases respiration and sugar content in the tomato stem: survival strategy or “aimless” response?

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With flooding being one of the numerous challenges that ecosystems face throughout the world, plants are obliged to adopt plastic responses in order to cope with it. When flooded, the tomato hypocotyl undergoes profound changes that entail rearrangements in its physiology and metabolism. In this work, we observed that, although soil flooding markedly dampens root respiration, the submerged hypocotyl surprisingly enhances oxygen consumption in spite of hypoxic conditions. Several pieces of evidence indicate that the respiratory pathway is indeed promoted in submerged stems. Besides, underwater hypocotyls are shown to accumulate sugars. Girdling and feeding experiments revealed that leaf-derived sucrose is metabolized and channelled to maintain respiration in underwater hypocotyls. Our data suggest that high respiration is required for sucrose unloading from phloem, since inhibition of hypocotyls respiration significantly prevents sugar build-up. As substrate availability increases, respiration is fuelled even more, leading to a sustained allocation of sugars to flooded hypocotyls.

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273
LG789KN
Area: Developmental Biology
Tipo de presentación: video presentacion
Enviado por: Virginia Miguel

The transcription factors AtHB6 and AtHB16 modulate light responses in Arabidopsis development

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Plants' development is affected by light which is a regulating signal in multiple developmental events. AtHB6 and AtHB16 are transcription factors encoded by paralogous genes belonging to the homeodomain-leucine zipper I family. These proteins were associated with plant development in response to environmental factors, in particular to light conditions. However, functional studies are scarce or directly null for these genes. To elucidate their role, we generated overexpressor and silenced plants, as well as transgenics carrying both promoters driving the expression of the *GUS* reporter gene. GUS staining was evident in 3-day-old seedlings for both genes, especially in cotyledons in dark conditions. *AtHB16* overexpressor seedlings (OX16), grown in complete darkness, exhibited open cotyledons and apical hook with an increased aperture angle. However, they had no chloroplasts and did not develop them even after several days in normal illumination conditions. Moreover, these plants did not present the ethylene triple-response. The cotyledon bleaching was more severe in the presence of $AgNO_3$, an inhibitor of ethylene sensing. Plants overexpressing *AtHB6* exhibited a similar phenotype in darkness, but this differential phenotype reverted after placing the plants in the light, whereas *AtHB6* silenced plants (*amiR6*) showed the opposite phenotype. Notably, *COP1*, *PIF1*, and *EIN3* transcript levels were significantly reduced in OX16 plants, suggesting a loss in the protection to deal with oxidative damage. The repression of these targets could explain the bleaching observed in light by these plants. Altogether, the results indicated that these transcription factors are involved in seedlings' development in response to light conditions.

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274
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Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Javier A Miret

High temperature impacts and plastic responses to sustain yield. Temperature-breaking points and season-critical periods on common bean heat-tolerant germplasm

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Common bean is a global food security staple as a source of affordable protein and micronutrients. Climate change will not only increase average growing season temperatures, but also frequency and intensity of heatwaves. To investigate the impacts of heat stress on common bean (Phaseolus vulgaris), we characterised the response of the best available sources of heat tolerant germplasm to both chronic (season-long) higher temperatures and acute 24h heat periods thorough the season. We observed different genotypic breaking points for chronic high temperatures, beyond which yield was compromised. However, two compensatory strategies emerged. Mesoamerican interspecific crosses maintained yield until a higher temperature by developing a more indeterminate habit, staying green and flowering for longer, thus generating enough sinks to partition into seed. Meanwhile, bushy Andean genotypes presented more losses, while maintaining fewer but bigger seeds. 24h-periods of high temperature caused dramatically different effects, because of the dynamic balance of adverse impacts and positive plastic responses as the plant growths. We characterised a critical period for yield determination at 6 to 7 days before anthesis, defined by a developmental window when plastic compensatory responses are reduced as plants get bigger, but still present a large proportion of sensitive small buds. To rise to the challenge of hotter and more variable seasons, we need to identify and exploit both functional and developmental plastic phenotypes from diverse germplasm to develop climate-smart and nutritive crops.

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275
CM716KK
Area: Plant Physiology and Ecophysiology
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Enviado por: Andrea Miserere

Response of oil accumulation dynamics to elevated temperature in olive fruit (Olea europaea).

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Olive crop expansion to new, warmer growing regions and climate change have reinforced the need for manipulative field experiments to better understand the physiological responses to elevated temperature. Thus, the aim of this study was to evaluate the response of oil accumulation dynamics including accumulation rate, duration, and maximum oil concentration to a moderate temperature increase in young trees of two cultivars (‘Arbequina’, ‘Coratina’). Two- or three-years-old potted trees were actively warmed by 3-4 °C from final fruit set to the end of the oil accumulation phase (December to early May) in one season using open top chambers under outdoor conditions or grown at near-ambient temperature in similar control chambers. Oil accumulation dynamics were determined from successive fruit samplings. Oil concentration was determined on a dry weight basis by nuclear magnetic resonance. Fruit oil accumulation dynamics were explained by a bi-linear function. In both cultivars, the sustained warming reduced the final oil concentration due to a strong reduction in oil accumulation rate (% day^{-1}), while the duration of the oil accumulation period (in days) was unaffected. In a similar manner, the decrease in final fruit dry weight in response to warming was associated with reductions in fruit growth rate (g day^{-1}) and generally not the duration of fruit growth. As a result, oil content per fruit (g fruit^{-1}) was severely reduced by warming. These insights should be considered to improve current predictive models of climate change impact on olive production.

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276
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Area: Abiotic Stress
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Enviado por: LAXMI Mishra

The plastid-localized AtFtsHi3 pseudo-protease of Arabidopsis thaliana has impact on plant growth and drought tolerance

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While drought severely affects plant growth and crop production, the molecular mechanisms of the plant´s drought response remain unclear. Here we demonstrate for the first time the pseudo-protease AtFtsHi3 of *Arabidopsis thaliana* to affect overall plant growth and to be involved in drought tolerance. An *AtFTSHi3* knockdown mutant *(ftshi3-1(kd))* displayed a pale-green phenotype with lower photosynthetic efficiency and Darwinian fitness compared to wild-type. An observed delay in seed germination of *ftshi3-1(kd)* was attributed to over-accumulation of ABA; *ftshi3-1 (kd)* seedlings showed partial sensitivity to exogenous ABA. Being exposed to similar severity of soil drying *ftshi3-1(kd)* was drought-tolerant up to 20-days after the last irrigation, while wild-type plants wilted after 12 days. Leaves of *ftshi3-1(kd)* contained reduced stomata size, density and a smaller stomatic aperture. During drought stress, *ftshi3-1(kd)* showed lowered stomatal conductance, increased intrinsic water-use efficiency and slower stress acclimation. Expression levels of ABA-responsive genes were higher in leaves of *ftshi3-1(kd)* than wild type; *DREB1A*, but not *DREB2A*, was significantly upregulated during drought. However, although *ftshi3-1(kd)* displayed a drought-tolerant phenotype in aboveground tissue, the root-associated bacterial community responded to drought.

Financing: I am a last year PhD student from Umea University, highly motivated to present at the meeting and would appreciate a free registration.

277
RN748GQ
Area: Developmental Biology
Tipo de presentación: video presentacion
Enviado por: Chiara Mizzotti

Identification of genes involved in fruit development and senescence in Arabidopsis thaliana

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Fruits represent the key of the successful evolution and spread of angiosperms. They play a fundamental role in the worldwide economy, directly affecting the global market, and provide essential nutritional elements for the human consumption. Fruit yield and quality are therefore key features to be controlled in the agricultural production, and improvements of fruit characteristics depend on the comprehension of the mechanisms controlling their development and maturation. In order to identify genes involved in such processes, an RNA sequencing on the fruit of the model plant *Arabidopsis thaliana*, called silique, was performed. In order to cover the entire fruit formation and maturation, different developmental stages were considered, from the initial development to the final senescence stage. Bioinformatics and statistical analyses of the data led to the identification of about thousand genes differentially expressed between early and late stages of development. In order to find genes involved in the regulation of such a process, we focused our attention on a family of transcription factors known to be involved in fruit growth and maturation: the NAC (NAM, ATAF, CUC) family of transcription factors. We selected some NAC genes from the transcription factors resulted to be differentially expressed, and we characterized the corresponding mutant lines in Arabidopsis. Our data indicate that an intricate network of NAC proteins modulates the correct silique maturation.

278
LR334JC
Area: Biochemistry and Metabolism
Tipo de presentación: video presentacion
Enviado por: Francisco Javier Molina Hidalgo

The R2R3-MYB transcription factor FaMYB123 regulates anthocyanin and flavonol biosynthesis in strawberry fruit.

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Using transcriptomics and metabolomic approaches, we have identified and functionally characterized an R2R3 MYB transcription factor, FaMYB123. Like most genes related to fruit ripening, the expression of *FaMYB123* is ripening-related, receptacle-specific and antagonistically regulated by both abscisic acid and auxin. When *FaMYB123* expression was knocked down by RNAi in ripe strawberry fruit receptacles, the expression of genes that encode enzymes involved in the final steps of anthocyanin/flavonoid biosynthesis were down-regulated. These fruits showed a concomitant decrease in total anthocyanin and flavonoid content, noticeable in malonyl derivates of pelargonoidin and cyanidins. Additionally, in the transgenic receptacle, the metabolomic results showed an accumulation of proanthocyanidin, propelargonidins and other condensed tannins, which is characteristic of green receptacles. These results indicate that FaMYB123 is a transcription factor involved in the anthocyanin/flavonoid production in ripe fruit receptacles along the ripening stages, regulating key enzymes of these pathways, such as FaANS, FaUFGT and FaMalTransf. Transient expression assays in *Nicotiana benthamiana* leaves revealed that FaMYB123, in coordination with FabHLH3, is able to transactivate the expression of the GUS reporter construct containing around 2000-bp promoter region of *FaMalTransf*. Altogether, these results provide evidence that FaMYB123 plays a regulatory role in late steps of flavonoid pathway. Besides, for the first time in plants, it is demonstrated that a R2R3MYB TF regulated the expression of a gene that encode a malonyl transferase responsible for the biosynthesis of cyanidin and pelargonoidin malonyl derivatives.

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279
KB582TR
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Nidia Helga Montechiarini

Early proteome profile of soybean embryonic axes germination.

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Seed germination implies restarting of embryonic axis growth, with cell expansion defining radicle protrusion. Isolate soybean embryonic axes (Ax) [*Glycine max* (L. Merr)] start expansion from 10 h, completing germination at 12 h of water incubation. The present work aimed to evaluate the early proteome profile promoting Ax germination. One hundred Ax were incubated for 9 h in distilled water at 27 ± 1 ºC and in the dark. Samples of 1 g Ax were powder in liquid N2, homogenized in 5 mM NaAc pH 4.6 buffers containing Sucrose gradients (0.4–1) M, followed by sequential extraction in 0,2 M CaCl2 (Ca), 2 M LiCl (Li) and Urea buffer (U) and final precipitation in TCA 100 %. A total of 40, 103 and 946 unique proteins with at least two high confidence peptides (Uniprot and Phytozome), of which 5, 33 and 888 were exclusively identified in Ca, Li and U. The total exclusive proteins localized (TargetP) as Secretory (118), Mitochondrial (161) Chloroplastic (156) and unknown (491). The gene ontology classification (AgriGO) for orthologue proteins of *Arabidopsis thaliana* showed enrichment in translation and gene expression processes, catabolism and energy, and embryo development ending in seed dormancy. These results evidenced a great cellular activity associated with early events defining soybean embryonic axes germination.

280
QH518SJ
Area: Biochemistry and Metabolism
Tipo de presentación: Poster en formato PDF
Enviado por: Eduardo Monteiro

Respiratory activity during cell viability loss in mesocarp of grape berries

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Xylematic connections between fleshy fruits and the mother plant are disconnected on the ripening of grape berries, resulting in a physiological event known as “hydraulic isolation”. Our research group showed that this event starts in Vitis labruscana var. 'Niagara Rosada' promptly after the veraison, concomitantly with the loss of cell viability of the mesocarp. This cellular event is inconsistent with other Vitis varieties evaluated so far, including Vitis vinifera var. 'Chardonnay'. We hypothesised that the hydraulic isolation could result in cell death, using the respiratory and ATPase activities as parameters. We demonstrated the maintenance of mitochondrial membrane potential (by means of viable mitochondria) and respiratory activity (activity of F1-ATPase and oxygen consumption by the Electron Transport Chain) during the ripening of berries of var. ‘Niagara Rosada' and 'Chardonnay'. Moreover, dehydrogenase activity was present in the mesocarp of 'Niagara Rosada' berries, even in the final stage of maturation. Our results have shown that mesocarp cells do not die; they undergo structural and functional changes instead.

Financing: Faperj, Cnpq

281
DC733NG
Area: Other
Tipo de presentación: Poster en formato PDF
Enviado por: Mariela Monteoliva

Market research for non-transgenic drought-tolerant wheat in Argentina

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Wheat is a grain crop with the highest commercial importance in the world (currently 28% of the world cereal production). In the context of climate change, droughts are more frequent and intense, reducing agricultural production. With the increase in food demand due to the growth of the human population, the current rise in wheat production is mostly due to the expansion in the cultivated area. However, this is not sustainable in long term. Another possible strategy is to develop more drought-tolerant crops, and due to the current controversy about the introduction of new transgenic crops for human consumption, here we evaluate the viability to develop, register, and commercialize a new non-transgenic drought-tolerant wheat, from pre-existing genotypes generated by INTA. We describe the limitation for wheat production in Argentina, the regulations to release new cultivars, the companies able to commercialize, and the regulation to export to Brazil, the most important destination of Argentinian wheat. The potential new cultivar, as it is a non-transgenic genotype, will take a relatively short time to be approved and released, and enhance wheat production in Argentina.

Financing: Proyecto INTA 2019-PE-E6-I115-001

282
PT496CQ
Area: Plant Physiology and Ecophysiology
Tipo de presentación: video presentacion
Enviado por: Mariela Monteoliva

Biochemical responses to the combined stress by drought and fungal infection in peanut

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In Argentina, peanut (*Arachis hypogaea* L.) production is mostly affected by seasonal droughts (up to 30% of yield reductions) and peanut smut, caused by the fungal pathogen *Thecaphora frezii*. Both factors may occur simultaneously in the same season. Our group has been studying biochemical responses to drought for several years. Drought stress in peanut induces changes in chlorophylls (related to the photosynthetic capacity of the plant and yield), proline (as part of the osmotic response), and redox status (total non-enzymatic capacity -FRAP- and oxidative membrane damage -MDA-). Recently we found that dry years increase the severity of the disease, but biochemical and physiological responses to the combination of drought and the pathogen have not been addressed yet. We aimed to evaluate if the presence of the pathogen under drought accentuates or reduces the known responses to water deficit. We grow peanut plants in the greenhouse until all the pots were flowered (~30 days). Then water was reduced until the soil humidity reached 30% of field capacity. The soil was maintained at 30% for 30 days when leaves samples were collected. Proline, chlorophylls, FRAP, and MDA were measured in pools of at least 3 leaves from different pots for each treatment. Relative water content was measured to check the efficiency of the treatment. We found notable changes in proline and chlorophylls, which were differentially induced by the presence of the pathogen, suggesting the fungus might be favored by the typical responses associated with drought tolerance in groundnut.

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283
NJ197KM
Area: Biochemistry and Metabolism
Tipo de presentación: Poster en formato PDF
Enviado por: Mickaela Moreira

Phloem unloading influences the accumulation of sugars in Vitis vinifera and Vitis labruscana berries.

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Grapes are unusual fleshy fruits because, unlike other fruits, their ripening period is associated with the second phase of expansive growth. In this phase, the berry development is associated with the accumulation of sugar, resulting in high phloem activity, though variable during the ripening stage. Based on differences in *Vitis* species, this work aimed to understand how phloem unloading influences the way that sugars are accumulated during the ripening stage. For this purpose, *Vitis labruscana* (var. Niagara rosada) and *Vitis vinifera* var. Chardonnay were assayed for analyzes such as SST and ATT, deformability, dry weight and fresh weight. To track changes in solute composition during berry ripening, the apoplastic sap was extracted with a Scholander pressure pump and used to measure apoplastic and vacuolar pH, and the quantification of soluble sugars on HPLC. The activity of soluble and insoluble acid invertase was measured, indicating the way the phloem unloading proceeds at berry development. Our results showed that qualitative analyzes illustrated the physiological changes in the mesocarp while the berry passed form pre-*veraison* to post-*veraison* stage. In Chardonnay, insoluble invertase showed no decrease in post-*veraison*, and in Niagara Rosada, soluble invertase activity was reduced. Overall, we found a contrasting pattern of sugar unloading via phloem during berry ripening, with *V. labruscana* using preferentially the apoplastic path and *V. vinifera* preferentially the simplastic path.

Financing: UENF, FAPERJ

CP535SJ
Area: Biochemistry and Metabolism
Tipo de presentación: video presentacion
Enviado por: Juan Camilo Moreno Beltran

Tyr-Asp inhibition of glyceraldehyde 3-phosphate dehydrogenase affects plant redox metabolism

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How organisms integrate metabolism with the external environment is a central question in biology. Here, we describe a novel regulatory small molecule, a proteogenic dipeptide Tyr-Asp, which improves plant tolerance to oxidative stress by directly interfering with glucose metabolism. Specifically, Tyr-Asp inhibits the activity of a key glycolytic enzyme, glyceraldehyde 3-phosphate dehydrogenase (GAPC), and redirects glucose toward pentose phosphate pathway (PPP) and NADPH production. In line with the metabolic data, Tyr-Asp supplementation improved the growth performance of both Arabidopsis and tobacco seedlings subjected to oxidative stress conditions. Moreover, inhibition of Arabidopsis phosphoenolpyruvate carboxykinase (PEPCK) activity by a group of branched-chain amino acid-containing dipeptides, but not by Tyr-Asp, points to a multisite regulation of glycolytic/gluconeogenic pathway by dipeptides. In summary, our results open the intriguing possibility that proteogenic dipeptides act as evolutionarily conserved small-molecule regulators at the nexus of stress, protein degradation, and metabolism.

285
KB566TG
Area: Other
Tipo de presentación: video presentacion
Enviado por: Juan Camilo Moreno Beltran

Single gene bioengineering as starting point to produce a new generation of super crops with enhanced photosynthetic efficiency, stress tolerance, plant yield, and nutritional content in plants

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Climate change affects soil properties and the atmospheric conditions of our planet, causing dryness and salinity in the soil, and ultimately affecting crops and food production. Together with the concomitant increasing world population, this will have a direct impact on food demand and require a sustainable increase in crop productivity. Here, we describe a single gene manipulation in a carotenoid biosynthetic gene that enhances pro-vitamin A content, photosynthesis, photoprotection, abiotic stress tolerance (high light, salt, drought, oxidative stress), biomass, and yield in tobacco and tomato by modulating carotenoid and hormone contents. Because carotenoid pathway is present in all plants, our findings serve as a solid ground to design the next generation of super crops able to cope with climate change-related environmental issues, enhanced nutritional content (pro-vitamin A), and crop productivity.

286
GT254KL
Area: Plant breeding
Tipo de presentación: Poster en formato PDF
Enviado por: Robertino J. Muchut

Development of a segregating population for QTL mapping in cotton (Gossypium hirsutum L.)

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There are few commercial varieties of cotton available in Argentina and consequently low genetic variability. Thus, being necessary the development of new cultivars with improved agronomic characters that allow to be more competitive worldwide. In this context, a segregating population (F_2) derived from a cross between two elite and contrasting parents for fiber quality was carried out to map QTL (Quantitative Trait Loci). Parent 1 (P_1) has low lint percent (LP) and high fiber quality (FQ) (length, strength and micronaire, among others) whereas parent 2 (P_2) has high LP and low FQ. The F_2 population, together with the parents and F_1, were subjected to a phenotypic evaluation for LP and FQ parameters. Broad sense heritability (h^2) was estimated from the variance components of the non-segregating generations (P_1, P_2 and F_1) and the F_2 segregating generation. Levene´s test was performed to confirm homogeneous variance in non-segregation generations, while normal distribution was confirmed by the Shapiro-Wilks´s test. The h^2 values were 0.83, 0.72, 0.59 and 0.58 for LP, fiber length, micronaire and strength, respectively. These results show high ratio of total genetic variation (additive and non-additive component) to the total phenotypic variation in the evaluated parameters. The high genetic component that underlie these agronomic characters, together with the identification of polymorphic molecular markers will allow us to detect QTLs for assisted breeding selection in the cotton crop.

Financing: INTA (PEI 119 - PEI113)Convenio INTA-APPA (Asociación para la Promoción de la Producción Algodonera)CONICET

287
JL142GF
Area: Signal Transduction
Tipo de presentación: Poster en formato PDF
Enviado por: Maria Noelia Muñiz García

The catalytic subunit c2b of protein phosphatase 2A (StPP2Ac2b) regulates tuber sprouting in Solanum tuberosum Spunta.

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Once harvested, potato tubers undergo a period in which their buds are not able to grow, called dormancy, whose duration depends on genetic and environmental factors and is controlled by hormonal balance. The concentration of abscisic acid (ABA) increses after harvest, inducing and maintaining dormancy. However, its levels decrease during tuber storage, while the levels of gibberellins (GA) and cytokinins increase, triggering the reactivation of dormant meristems. Tuber dormancy break implies a rearrangement of sugar metabolism, from a reserve-synthesis metabolism to its degradation. Initially, tuber soluble hexoses and sucrose are transported to the shoot to initiate the dormancy break. But then tuber starch degradation will support the supply of energy to the developing shoot, where sucrose, after being transported and hydrolyzed will be used to sustain growth. Serine/threonine protein phosphatase type-2A (PP2A) are involved in several physiological processes in plants. We developed potato plants overexpressing the catalytic subunit c2b (StPP2Ac2b) (StPP2Ac2b-OE). In this work the role of StPP2Ac2b in potato tuber dormancy and sprouting was studied. Sprouting progression, variation of glucose, sucrose and starch levels, as well as invertase and amylase activity and the expression of genes controlling the balance of ABA/GA hormones were evaluated. StPP2Ac2b overexpression delays the start of tuber sprouting and modifies the sprout growth pattern, by a mechanism involving changes in the regulation of sucrose/starch metabolism as well as GA/ABA balance. These results point out that PP2A is involved in the signaling and regulation of tuber dormancy and shoot growth.

288
NT431LH
Area: Biochemistry and Metabolism
Tipo de presentación: video presentacion
Enviado por: Pilar Muñoz del Río

Quantitative trait loci (QTL) analysis identified genomic regions and candidate genes associated with L-ascorbic acid content in strawberry fruit

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(2) Finca el Cebollar, IFAPA Centro las Torres, Huelva, Spain
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(8) Research Institute of Horticulture, Department of Breeding of Horticultural Crops, Skierniewice, Poland
(9) Forschungszentrum Juelich GmbH, Juelich, Germany
(10) INRA, UMR 1332 Biologie du Fruit et Pathologie, Villenave d'Ornon, France
(11) Unidad Asociada de I+D+i IFAPA-CSIC Biotecnología y Mejora en Fresa, Málaga, Spain.

Strawberry (*Fragaria ×ananassa*) fruits are an excellent source of vitamin C or L-ascorbic acid (L-AA), which is a powerful antioxidant both for plants and humans. However, L-AA content in plants is affected by environmental factors and by genotype, varying widely between different strawberry cultivars. In this study, we aim to unravel the genetic architecture of L-AA accumulation in strawberry fruit and estimate the environmental effect. We have quantified L-AA content in fruits of a F_1 population of 122 lines derived from parental lines 'Candonga' and 'Senga Sengana', adapted to contrasting Southern and Northern European areas, respectively. The F_1 population was grown and phenotyped during two seasons in five locations across Europe (Poland, Germany, France, Italy and Spain). Variation in L-AA content ranged from 18 to about 97 mg/100 g FW or 2 to 12 mg/g DW and had significant genetic and environmental components. Phenotypic data from the 5 countries and the average in all of them was used in combination with a linkage map of 6,974 SNPs for QTL analysis. Stable QTLs, detected in at least two countries, were detected in linkage groups LG3-4, LG5-1, LG5-3, LG6-3 and LG7-1. In agreement, QTLs using the average content were detected in overlapping regions. Nine candidate genes were identified within stable QTL intervals based on annotated function and physical position in the *F.* × *ananassa* genome. Five of them showed significant expression in ripe fruit based in RNA-seq data and they are currently being functionally validated using F_1 lines with contrasting L-AA content.

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289
BT886FC
Area: Other
Tipo de presentación: Poster en formato PDF
Enviado por: Robert Márquez Gutiérrez

Identification of orthologs to Flowering locus T in the hop genome (Humulus lupulus L.) and in silico analysis of cis-regulatory elements

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Florigen is a phosphatidylethanolamine-binding domain protein that in plants is encoded by the *Flowering Locus T* (*FT*). In plants with photoperiod requirements, the expression and subsequent translation of *FT* is a critical step for the beginning of the reproductive phase. Hop is a short-day plant, and it only blooms if the photoperiod conditions are less than 16.5 h of light. Therefore, this plant appears to depend on FT-dependent signaling. Through phylogenetic análisis, six homologs to FT or HD3A were identified in the hop genome. Two homologs clustered in the same clade as AtFT and AtTSF, while three members are homologs to HD3A. However, a homolog shares the same common ancestor with all analyzed proteins, indicating the ancestry of this gene. The cis-regulatory elements analysis showed that four members have the I-box and the REalpha-box, both domains responsible for the interaction with phytochromes. While, only three members contain the CCAAT-box responsible for the interaction with CONSTANS (CO) through the NF-Y complex. Moreover, promoters of four FT homologs in hop present the E-box, which is the binding site of bHLH proteins such as CIB1 that upregulate *FT* expression in response to blue light. Taking into account the size of the protein that acts as a possible FT in hop and the parameters of cis-regulatory elements, at least one possible member in hop could act as ortholog to FT, being that also contains the amino acids characteristic of FT funcion.

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290
QM846MQ
Area: Developmental Biology
Tipo de presentación: video presentacion
Enviado por: Ana Lucía Méndez

MtSUPERMAN is a pandora box during reproductive development in M. truncatula

Ana Lucía Méndez[1], Edelín Roque[1], Rim Hamza[1], Concepción Gómez-Mena[1], Yosapol Harvanichvech[2], Dolf Weijers[2], José Pío Beltrán[1], Luis A. Cañas[1]
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Legumes have distinctive features, such as compound inflorescences, complex floral ontogeny, and the production of nutrient-rich seeds. Thus, the study of regulatory genes in these species during reproductive development is essential to understand their role in the evolutionary origin of developmental novelties. The *SUPERMAN* (*SUP*) gene encodes a C_2H_2 zinc-finger transcription factor that plays key roles during reproductive development in the floral meristem termination, floral organogenesis, and gynoecium development in *Arabidopsis thaliana*. In this work, we present the functional characterization of the *Medicago truncatula SUPERMAN* (*MtSUP*) based on gene expression analysis, complementation and overexpression assays, and reverse genetic approaches. Our findings provide evidence that *MtSUP* is the orthologous gene of *SUP* in *M. truncatula*. We have unveiled novel functions for a *SUP*-like gene in eudicots. *MtSUP* regulates the activity of the secondary inflorescence meristem and common primordia thus controlling the number of flowers and petals/stamens produced. Furthermore, *MtSUP* has a critical role during early embryogenesis impacting the seeds production in *M. truncatula*. Our work provides insight into the regulatory network behind compound inflorescence, flower development, and embryonic development in this angiosperm family.

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291
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Area: Developmental Biology
Tipo de presentación: Poster en formato PDF
Enviado por: Michele Carla Nadal

Cattleya walkeriana in vitro flowering induction at different temperatures

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Orchids are widely distributed around the world and have different flowering control mechanisms between the genera. The *in vitro* orchids flowering has been the object of study of several international research. The study aimed to investigate the temperature effect on the *in vitro* flowering induction of *Cattleya walkeriana*. The plants were exposed to average temperatures, representative of the climatological data of the natural occurrence region of the species (Lavras, Minas Gerais, Brazil). For three months, the plants remained in BOD at 24°C, 20.5°C, 17°C, and the control were present in the growth room at 26°C. Knudson medium, 2% sucrose, 5.5 g L^{-1} agar, 1% activated charcoal was used. The plant material came from in vitro sowing. The photoperiod was fixed at 16 h and light intensity of 27 µmol m^{-2} s^{-1}. Plants cultivated at 17°C and 24°C presented *a, b*, and total chlorophyll and carotenoid contents higher than the other treatments, however, at temperatures studied in isolation they did not induce the *Cattleya walkeriana* flowering. For some species, temperature and vernalization are described as possible flowering process inducers. However, similarities are not always found between the effects of these factors in plants cultivated *in vitro* compared to that cultivated *ex vitro*.

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292
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Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Vitor Nascimento

Manganese foliar application increases rice grain production through changes in morphophysiological traits

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Rice (*Oryza sativa*) is an important annual crop, one of the world's most-produced cereals. Except for Asia, Brazil is the largest producer and consumer of this crop. Manganese (Mn) is a micronutrient that acts physiologically linked to proteins as a catalytically active metal or an enzymatic activator. Mn foliar supplementation is a promising way to boost rice yield, but the understanding of how such management affects the morphophysiological, nutritional, and agronomic traits in this crop is still incipient. This study was conducted at Universidade Federal do Tocantins, Gurupi *campus*, with rice plants growing in pots during the 2018-2019 crop season. We evaluated 37 morphophysiological, nutritional, and agronomic traits. Statistical analysis was performed using the R software, ggplot2 package, for principal component analysis (PCA), and ExpDes, for descriptive statistics. Outputs from PCA delineated two major components (PC1 and PC2), which explained over 65% of the total variation within 26 variables. Based on the PCA biplot, a remarkable separation between Mn-treated and control plants was evidenced by the PC1 (51%), and shortly after by PC2 (14%). Overall, the groups mainly differed as growth-related rather than physiological traits. Plants Mn-treated presented improved plant height, root length, root, shoot and total dry mass, and number of tillers. Regarding grain yield and other agronomic traits, Mn-treated plants developed more spikelets and grains per panicle, coupled with reduced sterility and increased size of flag leaves. Mn application increases rice yield mainly through increases in plant growth at the vegetative stage without major changes in physiological parameters.

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293
LK212ND
Area: Biotechnology, Research Tools, Resources
Tipo de presentación: Poster en formato PDF
Enviado por: Andres Nejamkin

Expression of NO synthase with a globin domain shift nitrogen metabolism increasing tuber yield in potato

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Nitric oxide (NO) is a second messenger in phytohormone-regulated developmental processes, also a player in biotic and abiotic stresses. In animals, the enzyme NO synthase (NOS) catalyzes the biosynthesis of NO from arginine and modulates many pathophysiological processes. There has not been described any NOS-like in higher plants. We identified and characterized a new type of NOS from the cyanobacteria *Synechococcus* PCC 7335 (SyNOS). SyNOS possesses the oxygenase and reductase domains like animal NOS, but it has a third domain encoding a globin at the amino terminus. The globin domain of SyNOS appears to function in the hemoglobin/NO cycle, in which NO is oxidized to NO_3^-. Thus, NO_3^- would enter in the nitrogen (N) assimilation pathway, contributing to amino acids generation. Since arginine is the main organic N storage in plants, our hypothesis states that SyNOS expression would allow the mobilization of N from arginine into NO and NO_3^-, improving N use in higher plants. Transgenic potato plants expressing SyNOS constitutively were generated and grown in sufficient (60 mM) or deficient (5 mM) NO_3^- availability under *in vitro* conditions. In N deficiency, wild type (wt) potato plants present reduced levels of photosynthetic pigments, while SyNOS-transgenic plants keep pigment levels stable. Besides, SyNOS expression induces glutamine synthase expression and nitrate reductase activity in both treatments. Moreover, SyNOS transgenic lines produced 50% more tubers than wt when grown in pots containing either sufficient or deficient nutrient conditions. In potato, SyNOS expression could allow an increase of tuber yield in poor soils.

294
QK386JM
Area: Plant breeding
Tipo de presentación: Poster en formato PDF
Enviado por: Catarina Neves

CRISPR-based functional analysis of SlGRAS9 and SlGRAS10 genes in tomato fruit ripening.

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Fleshy fruits, like Solanum lycopersicum (tomato), comprise an indispensable commercial and nutritional food commodity, being an important crop in agriculture worldwide. Tomatoes are climacteric fruits, and these fruits continue their fast process of ripening after harvest making it much more difficult to store and distribute, compared to other fruits. These processes of ripening and post- harvest decay are very complex. The trigger to the reprogramming of fruit development and ripening comprises several transcription factors with GRAS as putative regulators. These transcription factors are plant-specific and involved in plant growth and development. However, their role in fruit development is not fully understood yet. Recent genome-wide analysis of the *GRAS* gene family in tomato showed that the duplicated genes *SlGRAS10* and *SlGRAS9* might be involved in tomato fruit ripening.

In this study, we have first developed *SlGRAS10* mutant plants using CRISPR/Cas9 which generated mutations in two different regions of the *SlGRAS10* gene. Phenotypically, no major differences were found in mutated fruits compared with wild type fruits. However, molecular analyses using RT-qPCR genes showed that genes involved in the ripening process were differentially expressed in the mutated fruits compared to the wild type, in particular, *RIN*, *ACS2* , *ACO1*, *PYL9 and PSY*. Currently, we are quantifying carotenoid accumulation in order to integrate with this information that suggests a role of the *SlGRAS10* in tomato ripening. Additionally, we have developed double mutants for *SlGRAS10* and *SlGRAS9* that may exhibit functional redundancy and/or neofunctionalization.

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295
NN981FL
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Gabriela Niemeyer Reissig

Effect of moderate magnetic field on the antioxidant system of tomato fruits subjected to a calcium channel inhibitor (La3+)

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There are many studies showing the influence of the magnetic field (MF) on the antioxidant system (AS) in plants, but little is known about the mechanisms behind it. Among some possibilities, calcium transmembrane dynamics is a likely candidate in mediating responses of ROS to MF. Thus, the use of calcium channel inhibitor lanthanum (La^{3+}) could bring evidence that the plasma membrane is a primary target of the MF effect. The objective was to investigate the effect of the moderate magnetic field (MMF) on the AS of tomato fruit using La^{3+}. Mature green tomato fruit (*Solanum lycopersicum* var. cerasiforme) were subjected to the following treatments: Control - distilled water 12 hours; La - 10 mM $LaCl_3$ 12 hours; MF - distilled water 12 hours and MMF (200 mT); MF+La - 10 mM $LaCl_3$ 12 hours and MMF. When the first treatment achieved fully red color, all samples were stored at −86 °C. We evaluate hydrogen peroxide (H_2O_2) and anion superoxide (O_2^-) content, as well as the activity of superoxide dismutase, catalase, ascorbate peroxidase, and guaiacol peroxidase. The results showed a higher content of H_2O_2 and O_2^- under MF treatment. In the presence of $LaCl_3$ (MF+La), the concentration of H_2O_2 and O_2^- decreased 67%, approximately. Regarding antioxidant enzymes, interestingly, MMF and La showed greater activity separately. Also, the control showed 2-fold higher activity than the other treatments, demonstrating that MMF and La decreased the enzymatic activity. The effect of the MMF in the AS is probably associated with calcium channels in fruit.

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296
DR888FJ
Area: Epigenetics, Chromatin, non-coding RNAs, RNA biology
Tipo de presentación: Poster en formato PDF
Enviado por: Marcelo Nogueira do Amaral

Epigenetic changes in leaves of different rice genotypes subjected to salt stress

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Soil salinization is one of the main environmental factors that negatively influence productivity, particularly in rice cultivation. Epigenetic mechanisms, such as DNA methylation, act in coordination to influence chromatin structure and gene expression in response to stress. These DNA methylation levels are modulated by the action of DNA methyltransferases and demethylases. Therefore, in this study, the expression of genes involved in the process of DNA methylation and demethylation were evaluated, as well as the global levels of DNA methylation (% 5-mC) in leaves of four rice genotypes (BRS 358, BRS Bojuru, BRS Pampa CL and BRS Pampeira) subjected to salt stress (150mM) at stage V3 for 11 days. The results clearly demonstrate an increase in gene expression values in response to salt stress. The highest expression values were found for the *DRM1a* and *DRMA1b* genes in the BRS 358 genotype, and *CMT1* in the BRS Pampa CL and BRS Pampeira genotypes, while the lowest values were for *MET1-1* and *DRM3* for the BRS Pampa CL and BRS Pampeira genotypes, respectively. Regarding the global levels of DNA methylation, only BRS Bojuru did not show any significant difference. In the other genotypes there was an increase in methylation levels under salinity conditions compared to the control condition. Therefore, according to these results, salt stress triggers genotype-dependent alterations in the expression of genes involved in the DNA methylation process, as well as in the global levels of 5-mC.

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297
BP973GD
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Stefânia Nunes Pires

PHYSICAL RICE GRAINS QUALITY PRODUCED IN LOW LUMINOSITY ENVIRONMENT

Stefânia Nunes Pires[1], Bruna Evelyn Paschoal Silva[1], Caroline Hernke Thiel[1], Cleiton Brandão[1], Bruna Regina Souza Alves[1], Pedro Augusto Bianchini Schena[1], Kauana De Andrade Pereira[1], Sidnei Deuner[1]
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Light is the main source of energy for plant photosynthesis, thus, light intensity an important component for plant development and consequently for the physical characteristics of grains. This study aimed to evaluate the physical characteristics of rice grains, cultivar IRGA 424 RI produced in a greenhouse under 35% light restriction during the reproductive phase. The plants were exposed to light restraint during the stages R0-R4, and R4-R9, keeping them as control plants without the restriction of brightness. After physiological maturity, the harvest was carried out and the grains were evaluated for transparency, whiteness, and chalky. In the control condition, the whiteness and the degree of polishing were superior to the light restriction treatments in both periods, whereas the chalkiness degree was greater for the treatment where the restriction occurred in the R4-R9 stage. Adverse environmental conditions are among the possible causes of grain opacity, and these results show that grains produced under light restriction during the R4-R9 stage have a higher percentage of chalky grains when compared to the control condition. Also, the transparency and whiteness values for this treatment were lower, a fact justified by the gypsum process of the grain, which causes its opacity, preventing the passage of light, which reduces its translucency.

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Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Ellen Rayssa Oliveira

Growth rate of sunflower intercropped with forage in the ILP system

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The crop growth rate is defined as the increase in total plant dry matter mass per unit of time, which corresponds to an indicator of the plant's productive capacity, through the accumulation of dry matter mass. The objective of this study was to evaluate the intercropped sunflower, cultivated in the integrated crop-livestock system through the physiological index of the crop growth rate. The experiment was installed at the Experimental Farm of the Federal University of Recôncavo of Bahia, in the city of Cruz das Almas - BA. The experimental design used was a randomized block design in a 3x3+1 factorial scheme. The treatments consisted of three intercropping of sunflower and forage (sunflower + *Urochloa ruziziensis*, sunflower + *Panicum maximum* cv. Tanzania, sunflower + *Urochloa ruziziensis* + *Cajanus cajan*), sowed in three different ways (simultaneous sowing, delayed sowing and simultaneous sowing with application of herbicide/gramicide), with single sunflower as a control in four replications, studied in three agricultural years. Based on the total dry matter mass and the leaf area of the sunflower plants, the crop growth rate was determined. Data were subjected to analysis of variance and adjusted by exponential equation ($\mathrm{Ln}(y) = a + bx^{1.5} + cx^{0.5}$) representing growth as a function of time. Sunflower has higher crop growth rates in delayed sowing and with herbicide/gramicide application. The intercropping sunflower + *Urochloa ruziziensis* and sunflower + *Urochloa ruziziensis* + *Cajanus cajan* promote higher sunflower performance in this system.

299
JQ616RM
Area: Other
Tipo de presentación: video presentacion
Enviado por: Fabiana Mara de Oliveira Fabiana

ANATOMIA DA CASCA CAULINAR DE Cedrella fissilis Vell. SUBMETIDA AO ALAGAMENTO

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Espécies arbóreas são utilizadas para reflorestamento em áreas sujeitas ao alagamento, mas estas plantas podem não tolerar as inundações sofridas. Com o intuito de buscar informações para que sejam utilizadas espécies tolerantes ao alagamento, o presente trabalho teve como objetivo analisar as alterações anatômicas do caule da espécie arbórea *Cedrela fissilis* Vell. submetida à diferentes saturações hídricas. O experimento foi realizado em casa de vegetação com duração de 90 dias, as plantas foram cultivadas em bandejas contendo substrato composto por vermiculita e areia lavada, sendo submetidas a três disponibilidades hídricas: capacidade de campo, substrato alagado e o terceiro com a lâmina de água formada a três centímetros de altura em relação ao substrato. Ao final do experimento, foram coletadas e fixadas em F.A.A$_{70\%.}$ Fragmentos do caule foram emblocados em historesina e submetidos a seções transversais em micrótomo rotatório. As lâminas foram coradas com azul de toluidina e lugol e imagens foram obtidas em microscopia de luz. As imagens foram analisadas no software ImageJ. O delineamento experimental foi completamente casualizado com três tratamentos e nove repetições. O alagamento promoveu uma redução da espessura da periderme, um aumento dos espaços intercelulares corticais, aumento na quantidade de grãos de amido na medula e córtex e redução no número de elementos de tubo crivado do floema. A formação de espaços intercelulares pode auxiliar na difusão de gases sendo uma modificação importante para ambientes alagados, mas as alterações de outros tecidos podem indicar limitações para o seu crescimento e desenvolvimento em condições de alagamento.

Financing: nenhum

300
TG148JK
Area: Biochemistry and Metabolism
Tipo de presentación: Poster en formato PDF
Enviado por: Patrícia Mara de Oliveira patymarha

TOLERANCE AND DROUGHT SENSITIVITY ARE RELATED TO REMOBILIZATION OF CARBOHYDRATES IN SUGAR CANE?

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Brazil is the largest producer and exporter of sugar and the second largest producer and exporter of ethanol. However, the water deficit causes losses of up to 60% in production causing economic losses. Therefore, this study aimed to evaluate the carbohydrate metabolism in two varieties of sugarcane (Saccharum ssp.) subjected to drought and analyze its relationship with tolerance and sensitivity strategies to water stress. The experiment was carried out in a greenhouse, with two sugarcane varieties (RB855536-drought-sensitive and RB867515-drought-tolerant), planted in 3.8 liter pots. 91 days after planting, the seedlings were subjected to the following treatments: (i) Irrigation and (ii) water deficit (DH), imposed with suspension of irrigation for 8 days, followed by rehydration. Two collections were performed, the first during the period of maximum stress (ME), and the second after rehydration (REC). Growth analysis was performed weekly, daytime CO2 assimilation (A), water potential (w), relative water content (RAC) and macromolecules determination (Total soluble sugars -AST, reducing sugars-AR, sucrose-SAC, starch- A and total protein-PT) in leaf, stem and root tissues in both collections. For the biometric variables analyzed, the genotype did not promote better performance during water stress. Plants under maximum stress, variety RB867515, had higher sucrose and starch content after recovery than variety RB855536. These results indicate that the variety RB867515 was more tolerant to drought than the RB855536 when subjected to water deficit, because after rehydration it showed better recovery due to carbohydrate translocation.

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301
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Area: Biochemistry and Metabolism
Tipo de presentación: Poster en formato PDF
Enviado por: Santiago Nicolás Otaiza González

FB1-INDUCED PHYTOTOXICITY: REDOX STATE OF DIFFERENT INTRACELLULAR COMPARTMENTS AND THEIR CORRELATION WITH AUTOPHAGY.

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Mycotoxin FB1 is an important pathogenicity factor in the *Fusarium verticillioides*-plant interaction and alone induces many of the phytopathological signs observed in infection.

The aim of the work was to correlate the role of autophagy and redox changes in different intracellular compartments in a model of acute phytotoxicity induced by FB1.

Arabidopsis Col-0, atg7 mutant seedlings were grown with FB1 (0-1 μM). At 7 days after planting, cell death was determined by electrolyte leakage (EL) y and ratiometric redox-sensitive GFP (roGFP) expressed in different compartments (cytoplasm, mitochondrion, peroxisome and chloroplast) of the plant, were observed by confocal microscope and analyzed with FIJI ImageJ software.

FB1 induced different EL profile in atg7 with respect to Col-0 (decrease and increase at low and high concentrations of FB1, respectively). Also, a different oxidation level was observed in the cytoplasm in atg7 at 0.1 μM (decrease) and 1 μM (increase) of FB1 with respect to Col-0.

Our preliminary results suggests that autophagy induces death at low concentrations of FB1 and inhibition at high concentrations of the mycotoxin. Likewise, cell death is correlated with a higher level of oxidation in the cellular cytoplasm.

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Area: Plant Physiology and Ecophysiology
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Enviado por: Daniela Pacheco

Evaluation of crop forcing technique in Syrah (Vitis vinífera L.) to increase wine quality

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High temperatures during the ripening of red winegrapes varieties, reduce anthocyanin content and color of the wines. The aim of this study was to assess the effect of crop forcing technique on phenology, yield and wine quality of Syrah, trained on a vertical trellys system, in San Juan-Argentina. The experiment was conducted in 2016, and consisted of one Control (with traditional winter pruning) and two forcing treatments applied on 18 november (CF1) and 6 december(CF2), In the forced vines, the canes were pruned to seven nodes, and the leaves, the lateral growth and clusters were removed. Ripening in the Control occurred from december to february, while in forced treatments from february to april(CF1) and from march to april (CF2). Yield per plant was similar in Control (5.35kg) and CF1(4.93) and lower in CF2(1kg). The number of clusters followed the same trend with 42, 58 and 15 clusters respectively for Control, CF1 and CF2. The clusters of forced vines were smaller than that of the Control. Forced treatments increased anthocyanins content(mg/L), total polyphenol index and color intensity of wines when compared to Control. Results showed that the best forced treatment was in november, and that crop forcing in Syrah increased wine quality.

303
BQ717BH
Area: Biotic Interactions
Tipo de presentación: Poster en formato PDF
Enviado por: Ricardo Padilha

Fruit herbivory induces systemic antioxidant response in different organs of tomato plant

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Understanding plant-herbivory interactions is of extremely importance, considering that one of the greatest challenges is to produce food efficiently and with the least possible impact on the environment. Here, we investigated whether tomato fruit (*Solanum Lycopersicum* cv. Micro-Tom) under caterpillars' (*Helicoverpa armigera*) herbivory is capable of signaling to other parts of the plant, generating a systemic response. To accomplish this task, components of the antioxidant system and reactive oxygen species (ROS) were analyzed. Red ripe tomato fruit were exposed to caterpillars for a period of 24 h. Soon after, fruit and leaves were collected and immediately stored at −86◦C for further biochemical analysis. After 48 h, more fruit and leaves were collected and stored under the same conditions. We evaluate hydrogen peroxide (H_2O_2) and anion superoxide (O_2^-) content, as well as the activity of superoxide dismutase, catalase, ascorbate peroxidase, and guaiacol peroxidase. Regarding ROS, H_2O_2 content was 85% (fruit) and 41% (leaf) higher after 24 h of fruit herbivory, compared to control. Ascorbate peroxidase activity was higher in the leaves, both in 24 h (53%) and 48 h (54%) of fruit herbivory. Guaiacol peroxidase activity was 59% higher in the fruit compared to control. Interestingly, in leaves, activity decreased 49% after 48 h of herbivory compared to 24 h. Herbivory on the fruit has led to a response in different organs, showing the importance of studying and understanding the signaling that can be generated from the fruit.

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304
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Area: Biochemistry and Metabolism
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Enviado por: Maria Ayelen Pagani

The rubredoxin domain of HSCB modulates Fe-S synthesis and Fe translocation from roots to shoots in Arabidopsis

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In yeast, flies and vertebrates there is an intimate connection between Fe homeostasis and Fe-S cluster formation, however in plants this link is not so clear yet. We have shown that altered levels of HSCB (co-chaperone, involved in the Fe-S cluster biogenesis) affect iron translocation from roots to shoots in Arabidopsis. In this work we analyzed the role of the HSCB rubredoxin domain, suggested to bind Fe ions or Fe-S clusters, by overexpressing rubHSCB –the truncated form of the protein-in wild type and *hscb* genetic backgrounds, *rubHSCB-wt* and *rubHSCB-hscb* respectively. Under Fe sufficient conditions, there were alterations in root and shoot Fe contents in both *rubHSCB-wt* and *rubHSCB-hscb* lines, however these changes were milder than in *hscb* knockdown or complete HSCB overexpressing plants. Expression and activity of the main Fe uptake system were correlated with the altered Fe contents. Shoot activities of the Fe-S enzymes ACO and SDH in *rubHSCB-wt* and *rubHSCB-hscb* lines were lower than in *wt* lines, but higher than in knockdown or HSCB overexpressing lines. All these changes point to a regulatory effect of the rubredoxin domain over HSCB activity. We confirmed, by recombinant expression and *in vitro* reactions, that rubHSCB protein induced a lower ATPase activity in its partner protein of the Fe-S biosynthesis pathway –the chaperone HSCA1- than the complete HSCB protein.

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305
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Area: Other
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Enviado por: Alejandro Palavecino

Structural characterization of the GRF-GIF regulatory module: understanding function from structure.

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Growth-regulating factors (GRF), GRF-interacting factors (GIF) and miR396 are part of a complex regulatory module that plays a major role in plant growth and development. The interaction of GRF transcription factors with GIF transcriptional co-regulators in combination with GRF post-transcriptional silencing by miR396 affects key biological processes such as cellular proliferation, leaf longevity and organ development. GRFs are characterized by the presence of the QLQ and WRC domains which are evolutionary conserved throughout plant species. Whereas the QLQ domain mediates GRF-GIF complex formation by interacting with SNH domain of GIFs, the WRC has been proposed as a putative zinc finger domain responsible for target DNA recognition. Moreover, QLQ domain is also present in essential core ATPase subunits of the chromatin remodeling complex of the BRAHMA (BRM) family. Despite the importance of these proteins in plant development, information on the nature of GRF-GIF and the GRF-DNA recognition remains scarse. In this work, we present the first structural characterization of the QLQ:SNH complex of GIF1 and GIF2 with the QLQ domains of GRF1 and BRM from *Arabidopsis thaliana* using NMR and explore the Zn^{2+} and DNA binding properties of the WRC domain from GRF7.

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306
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Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Darshan Panda

Contribution of phytochrome A in the regulation of sink capacity, starch biosynthesis, grain quality, grain yield and related traits in rice

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Field experiment was conducted on the effect of LL intensity and subsequent exposure to natural light on *japonica* rice cultivar *Akitokomachi* (WT) and its phytochrome A mutant(*phyA)* to understand the role of phyA in the regulation of sink capacity, starch biosynthesis, grain quality, grain yield and related traits during wet season of 2018. Leaf soluble protein, photosynthetic CO_2 assimilation rate, leaf non-structural carbohydrate content, sink capacity, grain quality traits such as hulling percentage, milling percentage, head rice recovery, water uptake, volume expansion, alkali spreading value, gel consistency, grain breadth, grain starch content, amylose content and yield attributes such as grain yield, panicle fertility, 1000-grain weight, panicle per plant, spikelets per panicle and grains per panicle along with the expression of starch biosynthesizing enzymes such as such as ADP-glucose pyrophosphorylase (AGPase), starch synthase III (SSIII) and granule bound starch synthase I(GBSSI) were reduced significantly in *phyA* than WT plants. However, % of grain chalkiness, length and amylopectin content increased in the *phyA* than WT plants. This study indicates the possible role of phyA in the regulation of source-sink communication, starch biosynthesis and grain quality in rice. Presumably, by participating in the control of several starch synthesizing pathways in the grains, phyA play a crucial role in the regulation of grain quality of rice which depends on the availability of the light intensity during grain-filling stage.

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307
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Area: Cell Biology
Tipo de presentación: Poster en formato PDF
Enviado por: Rosario Pantaleno

The role of mitocondrial H2S in stomatal immunity response

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Stomata are microscopic structures responsible for gas exchange regulation between plant and the environment. They are formed by a central pore delimited by pairs of specialized cells, the guard cells (GCs), which sense different stimuli and integrate them into a signalling network that controls pore size. Stomatal pores, as natural openings, are the entry gate for microorganisms and pathogens, therefore, stomatal closure is considered the first mechanical barrier to prevent infection.

The signalling molecule hydrogen sulfide (H_2S) is a low-weight gas that belongs to the group known as gasotransmitters. H_2S is endogenously synthesized in plant mitochondria, by the activity of the enzyme ß-Cyanoalanine Synthase (CAS-C1), which catalyzes the reaction between cysteine and CN^- to form ß-Cyanoalanine and H_2S (H_2S_m). However, the function of $H_2S_m$is mostly unknown.

Currently, we are studying the role of mitochondrial H_2S in GCs during pathogen induced stomatal closure. Results obtained so far showed that mitochondrial-targeted H_2S donors (AP123, AP39 and RT01) induce stomatal closure in a dose-dependent manner, requiring the normal activity of complexes I an IV of mitochondrial electron transport chain (mETC) to trigger this response. On the other hand, treatment of the mutant *cas-c1* with the bacterial elicitor flagellin (flg22), showed a lower apoplastic ROS production and an impaired stomatal closure. The latter response was restored with the addition of exogenous H_2S_m (AP39).

Altogether, data indicates that H_2S donors targeted to mitochondria induce stomatal closure needing mETC normal activity, and suggests that H_2S_m participates in the flg22-induced stomatal immunity.

308
CQ221MB
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Sofia Papu

Differential protection mechanisms against water stress of Araucaria araucana seedlings from contrasting pluviometric provenances

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Water stress triggers acclimatization responses and/or cause damage in plants, which varies according to local adaptation of species to certain climatic conditions and stress level. Ongoing climate change is projected to result in longer and more intense water stress conditions leading to an alarming increase in drought-induced forest decline. The aim of this study was to evaluate the physiological responses of *Araucaria araucana* pot-grown three-year old seedlings, originated in mesic environments (~2000; Verde Chico), intermediate (~1200; Villa Pehuenia) and xeric (~600 mm year-1; Lonco Luan). Plants were subjected to moderate and severe water restriction regimes and compared to well-watered controls during 120 experiment days. Origin-dependent defense strategies were observed, evidenced by a differential behavior of xeric site seedlings under water stress: (i) relative water content did not markedly decrease, while growth was practically stopped, (ii) a higher leaf temperature and a lower decrease in matric potential was related to lower leaf transpiration, (iii) photosynthetic pigments had a low degradation values, (iv) monoterpenes concentration remained low, (iv) sesquiterpenes and total terpenes concentration dropped drastically, (v) a larger synthesis of the amino acid L-proline was produced, and (vi) seedlings did not exhibit a marked trade-off between growth and defense. This differential behavior would indicate that *A. araucana* is a great physio-ecological amplitude species, allowing to classify xeric individuals as "water-saving" plants and mesic individuals as “water-wasters”. Those responses could be intensified in a context of decreased precipitation and increased temperature, causing physiological imbalances, especially in mesic sites plants with higher water requirements.

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309
HD292MN
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Lucas Giovani Pastore Bernardi

Use of coating particle film to modulate leaf temperature and heat stress on citrus trees

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Climate changes promote extreme weather conditions, with increased irradiance and air temperature. Those affect citrus trees impacting fruit yield and quality. The citrus industry is important in the world agriculture and requires high production efficiency within high levels of sustainability. Under excessive air temperature and UV radiation, plants increase the production of reactive oxygen species (ROS) that damage tissues and physiological processes. Coating particle films have been developed to minimize these losses and optimize production in the field, given such climate change scenario. Leaf temperature and net photosynthesis changes under different environmental conditions were evaluated in plants exposed to: T1: full sun light (control tree sprayed with water), T2: full sunlight and kaolin [wettable powder, 1 µm (30 g L^{-1})] sprayed tree, T3: full sunlight and calcium carbonate [wettable powder, <1 µm (30 g L^{-1})] sprayed tree, T4: reduced irradiance control, under protective net and, T5: reduced irradiance control, under anti-UV transparent plastic, with 6 repetitions per treatment. Climate data was recorded in each treatment condition with an automatic weather station. Leaf temperature was measured with an infrared thermometer and superficial images were recorded with a thermal camera. Our results demonstrate that the T2, T3, T4 and T5 avoided leaf temperature peaks on the course of the day, with T2 and T3 exhibited higher photosynthesis after one month of leaf spray compared to the control treatments. These results point out to a likely improvement in plant’s adaptation to high irradiance conditions when particle films are used in the field.

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310
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Area: Plant Physiology and Ecophysiology
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Enviado por: Rebeca Patrícia Omena Garcia

The physiological bases of high photosynthetic activity in a Solanum pennellii chromosome 2 QTL under high CO2 levels

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Higher photosynthetic efficiency can be achieved by genetic approaches through the identification of natural genetic variation. By using two *Solanum pennellii* introgression lines (ILs), we previously demonstrated that IL2-5 and 2-6 exhibit high photosynthetic efficiency associated with altered biochemical components of photosynthesis, such as higher RuBisCO levels under non-photorespiratory conditions. In order to understand the physiological bases of these traits, we characterized plants from introgression Sub-lines (Sub-ILs) of *Solanum pennellii* (Sub-ILs 2-5-2, 2-5-6, 2-5-12, 2-6-1, 2-6-3, 2-6-6) and the parental M82 under ambient and high [CO_2], 400 and 800 ppm CO_2, respectively. As expected, the Sub-ILs 2-5-2 and 2-5-6 exhibited higher photosynthetic capacity compared to M82 in both ambient and high [CO_2], accompanied by increases in total biomass production under high [CO_2]. These Sub-ILs also showed high biochemical capacity (maximum carboxylation velocity by RuBisCO and maximum electron transport rate) specially under ambient [CO_2]. The Sub-IL2-5-12 stood out for exhibiting high water use efficiency under high [CO_2], with reduced net photosynthesis without changes in stomatal conductance compared to M82. Together, these results suggest that the biochemical and photochemical components are the physiological bases to the high photosynthetic rates observed in plants from the studied Sub-ILs.

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311
TS281RM
Area: Biochemistry and Metabolism
Tipo de presentación: Poster en formato PDF
Enviado por: Tatiana Pavlovic

DIFFERENTIAL MATERNAL SUPPLY OF AMINO ACIDS SPECIFIES CONTRASTING COMPOSITION IN SOYBEAN SEEDS

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Soybean is one of the most important oilseed crop, providing large amounts of vegetable protein and oil as feedstocks for food, feed, and industrial applications. The biosynthesis of seed reserves or filling depends on the transport of several carbon and nitrogen compounds generated through photosynthesis, which are received and metabolized by the developing embryo. The translocation is via phloem, but then the substrate transfer is apoplastic since there is no vascular connection between the seed coat and the embryo. Here, we report a comparative characterization of the content of amino acids in the nutrient supply from the seed coat of two soybean recombinant inbred lines with different level of protein at the seeds. For this, the embryo was replaced *in planta* by sterile agar and the amino acid profile was assessed by phenylisothiocyanate derivatization followed by reverse phase-high performance liquid chromatography. Despite having similar genetic background, the contrasting lines exhibited differential amino acid composition throughout development. Most amino acids presented higher contents in the high-protein genotype than in the low-protein genotype. The largest supply of amino acids in the high-protein genotype could be supporting an enhanced synthesis of proteins for embryo development and reserve accumulation. This, together with the varying amino acid composition may partly explain the different strategies that each genotype has to obtain its contrasting amounts of reserves. Gain understanding on how the plants regulate the carbon flux to synthesize storage compounds is esential in order to provide biotechnological tools for obtaining high-quality soybean genotypes.

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312
DG451LQ
Area: Abiotic Stress
Tipo de presentación: video presentacion
Enviado por: Necla Pehlivan

Plastic Pollution Facts: Impact on Plants

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One of the greatest ecological challenges of our time appeared more than half a century ago. Production in the 1950s which was 1500 metric tons(mt), has reached about 350000 mt whose toxic footprints found even in the polar regions today. This is due to the increasing public preference for plastics in every aspect of our daily lives. Climate uncertainty and global population growth dramatically turned the issue into a planet crisis. The crisis is being tried to solve by inventing plastivor bugs or bioplastics. However, even biodegradable ones, such as bamboo-based organic plastics, have recently been reported to not different than synthetic ones and not safe at all. Plastic polymers are the carriers of more than one chemical additive (the combination is usually kept as a confidential commercial formulation) used in industry to change their mechanical features to meet the growing demand. Additives are bioavailable when leaked into the water and reported to cause acute or sublethal toxicity to algae and mussels. Accordingly, plastic pollution has become a priority for the aquatic system and is mainly discussed in marine pollution studies. However, chemical pollution does not only occur in the oceanographic zones but also in agricultural soils occupied by plants. Some work has explained the physiological effects in a few plants, but there are still research gaps, especially impacts on major crops. To this end, we comprehensively analyzed the possible phytotoxicity at the gene and physiological levels in maize. Our data so far, will be discussed during the presentation.

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313
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Area: Biotic Interactions
Tipo de presentación: video presentacion
Enviado por: Micaela PEPPINO MARGUTTI

Differential expression of BNT1 splice variants during the Arabidopsis defense responses

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Nucleotide-binding leucine-rich repeat receptors (NLRs) are key sensors of the plant immune system, conferring resistance to diseases. NLRs have been found to act from several compartments inside the cell. However, NLRs have never been described as functioning from plastids, which are essential organelles for a successful defense against pathogens. Interestingly, results from our group showed that the Arabidopsis NLR called BNT1 localize in this organelle. We also predicted that three variants of *BNT1* could be generated by alternative splicing, with only one of them displaying a complete plastid targeting signal. Thus, the activation of different BNT1 isoforms could be related to the well-known defense responses associated to plastids. Here, we confirmed the presence of the *BNT1* variants transcript and analyzed their localization. Moreover, we found that the expression of the *BNT1* splice variants differentially change under conditions/treatments that affect chloroplast normal function and during the induction of defenses. Consistently, our preliminary results show that *bnt1* mutant plants have an anormal resistant to pathogens and altered expression of biotic and oxidative stress marker genes. Together, our findings suggest that BNT1 immune function(s) are mediated by the plastids activity. The elucidation of the role of BNT1 variants and its regulation could represent a new paradigm to understand the function of NLRs located at different subcellular compartments.

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314
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Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Francisco Percio

A peek at ER-Golgi contact sites proteins: Arabidopsis and Tomato SMP-containing proteins

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(2) Sin Afiliación

An essential aspect of lipid homeostasis is the non-vesicular transfer of lipids between membranes from different organelles. This transfer occurs in membrane contact sites (MCS), which are regions where two membranes are close, but they do not fuse. The synaptotagmin-like-mitochondrial-lipid binding protein (SMP) domain targets proteins to organelle contact sites in eucaryotes. Proteins containing this domain act as tethers of these MCS and as lipid transporters between apposed membranes. In particular, a family of proteins have been identified in Arabidopsis (SYT family) where SYT1 is the best characterized member. This protein transfer glycerolipids in the ER-PM MCS. However, aside from it, little is known about other SMP-containing proteins in plants.

In our studies, human E-Syt1 was used to retrieve the remote orthologues in plants, and they were double-checked by using other SMP-containing proteins from human and yeast. Subsequent in silico analysis allowed us to stablish different groups among SMP-containing proteins, with the highlight that some subfamilies of proteins are plant exclusive (SYT6, NTMC2T5 and NTMC2T6). Our next step was to understand their subcellular localization by transient expression in Nicotiana benthamiana followed by confocal microscopy. We have found that both SYT6 and NTMC2T6 subfamilies localise in ER-Golgi contact sites, alongside TEX2 (which has a human ortholog). Further studies showed that Arabidopsis mutants for those genes had an altered root growth, lower seed germination rates and altered fully expanded cotyledons rate in media supplemented with salt or ABA, which suggest these proteins might be implicated in abiotic stress and signalling through ABA.

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315
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Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Eduardo Pereira Shimoia

Co-inoculation of seeds with Bradyrhizobium and Azospirillum attenuates the oxidative stress in roots and nodules of soybean plants exposed to flooding

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The oxidative stress induced by hypoxia affects the integrity of cell membranes in plants exposed to flooding. Here, we evaluated if the co-inoculation of soybean (*Glycine max*) seeds with diazotrophic bacteria improves the antioxidant system of soybean plants submitted to flooding. Prior to sowing, seeds were inoculated with *Bradyrhizobium elkanni* and *B. japonicum* or co-inoculated with *Azospirillum brasilense* (strains Ab-V5 and Ab-V6) + *B.elkanni and japonicum*. Then, plants were cultivated in a greenhouse and irrigated with a nutrient solution without N until theV8 stage, in which plants were exposed to flooding. After eight days of flooding, roots and nodules were harvested and the levels of hydrogen peroxide (H_2O_2) and lipid peroxidation, and the activity of antioxidant enzymes were accessed. The co-inoculation increased the H_2O_2 levels in the roots of flooded plants, while lipid peroxidation decreased. However, co-inoculation did not change the root activity of antioxidant enzymes. Similarly, the co-inoculation increased the accumulation of H_2O_2 in nodules with no change in lipid peroxidation levels. However, the co-inoculation increased the activity of catalase and ascorbate peroxidase in nodules. In conclusion, the co-inoculation of seeds with *B. japonicum* and *A. brasilense* contribute to plant tolerance to flooding by a decrease of lipid peroxidation in roots and nodules of plants exposed to flooding throughout the enzymatic or non-enzymatic system.

Keywords: abiotic stress; antioxidant system; diazotrophic bacteria; *Glycine max*; hypoxia.
Financing: Funding: Coordenação de Aperfeiçoamento de pessoal de Nível Superior (CAPES), Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), Fundação de Amparo à Pesquisa do Estado do Rio Grande do Sul (FAPERGS), Stoller and NovaTero.

316
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Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Marcos Sebastian Pereyra

GENOTYPE-DEPENDENT RESPONSE STRATEGIES OF THREE ARGENTINIAN OREGANO CULTIVARS EXPOSED TO MODERATE AND SEVERE WATER STRESS

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The responses of oregano genotypes to water stress are still poorly understood. 21-days pot experiments were performed to evaluate the response of three Argentinian oregano cultivars (*O. vulgare* subsp. *vulgare* ‘Don Bastías FCA-INTA’, *O. vulgare* subsp. *hirtum* ‘Alpa Sumaj FCA-INTA’ and *O.* x *majoricum* ‘Aguanda FCA-INTA’) subjected to two stable-water stress levels (MS-moderate: -6b and SS-severe: -12b). Twenty-six traits from five clusters were measured: *i)* water relations, *ii)* plant architecture and development, *iii)* light interception and resources use efficiency, *iv)* biomass and biomass partitioning patterns, *v)* growth rate. Water stress induced alterations throughout all evaluated traits. Moreover, drought stress triggered genotype-depending adaptive response strategies. Aguanda showed more adaptation to water stress. Total biomass was only reduced under SS although it was the highest between genotypes in this water scenario. Aguanda preserved water uptake and photosynthetic capacity by sustaining partition toward roots and leaves and maintaining higher values of leaf area, chlorophyll content and net assimilation rate. Furthermore, it exhibited higher stomatal regulation and water use efficiency (WUE). Don Bastías displayed two stress-level dependent strategies. Under MS, the maintenance of photosynthetic capacity by partitioning to leaves (higher leaf area ratio) with elevated water consumption (lower WUE) was highlighted. In contrast, transpiration rate was decreased under SS by reducing leaf area causing an improvement of WUE. Last, Alpa Sumaj was the most sensitive to water stress. The strategy pointed since MS to maintain water balance by reducing water consumption through morphological, developmental, and physiological changes that sharply decreased the aerial biomass yield.

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Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Adriana Quiriban

Differences in the accumulation of osmolytes at lower water availability during stem elongation in wheat.

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The objective of this study was to evaluate the response to the low availability of water at the beginning of stem elongation in wheat (*Triticum aestivum* L.), in the content of osmotic metabolites, in order to characterize them as biochemical markers of stress tolerance. We worked in a greenhouse, in pots, with two contrasting wheat genotypes in drought tolerance, ACA 315 (resistant) and Buck Arriero (sensitive), subjected to suspension of irrigation for 0, 5, 10 and 15 days. Before the suspension of irrigation, the ACA 315 genotype expressed mechanisms that allowed it to maintain turgor with respect to Buck Arriero, shown in the higher value of relative water content (RWC) and osmotic adjustment. ACA 315 expressed greater accumulation of sucrose, glucose and fructose, and a lesser proportion proline. Thus, the greater availability of sugars in the tolerant genotype could indicate that its greater capacity for osmotic adjustment is due to these biomolecules and to a lesser degree to the proline content. The sensitive genotype Buck Arriero, showed an increase in the proline content higher than ACA 315 and this coincided with the lowest values of RWC, equal to days of suspension of irrigation. In addition, ACA 315 showed an increase in proline prior to Buck Arriero, which coincided with a decrease in RWC after 5 days of suspension of irrigation. Therefore, the accumulation of proline in addition to its function as an osmolyte, can also be considered an early metabolic indicator of water availability.

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LD282SG
Area: Signal Transduction
Tipo de presentación: video presentacion
Enviado por: Enzo Perk

The Isothiocyanate sulforaphane induces RBOHD-dependent reactive oxygen species production and enhances expression of plant biotic and abiotic related genes.

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Abstract

Sulforaphane (SFN) is an isothiocyanate-type phytomolecule present in crucifers, which is mainly synthesized in response to biotic stress. In animals, SFN incorporated in the diet, has anticancer properties. The mechanism of action and signaling are well described. However, little is known about SFN signalling and mechanism of action in plants. The goal in the present study was to elucidate components of the SFN signaling pathway, particularly the production of hydrogen peroxide (H_2O_2), and its effect on the transcriptome.

Our results showed that in Arabidopsis, SFN causes H_2O_2 production exclusively through the action of the NADPH oxidase RBOH isoform D. On the other hand, we used the RNAseq technique, in order to analyze the effect of SFN on the transcriptome. We observed a large increase in the expression of heat shock proteins (HSP) genes and also on genes associated with the response to oxidative stress. The upregulation of several genes linked to the biotic stress response, confirms the interplay between SFN and biotic stress. In addition, SFN increases the levels of transcripts related to the response to abiotic stress, as well as related to various phytohormones.

Taken together, these results indicate that SFN induces an oxidative burst, leading to signaling events and gene expression. This oxidative burst may cause the increase of the expression of genes such as heat shock proteins to restore cellular homeostasis. We also obtained many upregulated genes that codifies for possible components of the signalling pathway and putative effectors.

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319
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Area: Developmental Biology
Tipo de presentación: video presentacion
Enviado por: María Florencia Perotti

The transcription factor AtHB23 controls root development in response to salinity

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Roots are the anchorage organs responsible for plant water and nutrient uptake. The root system exhibits high plasticity, which is governed by physiological, genetic, and epigenetic programs. Hormone-responsive transcription factors (TFs) are crucial players in determining root developmental flexibility and architecture. AtHB23 is a TF belonging to the *Arabidopsis thaliana* homeodomain-leucine zipper I family. It is directly activated by the auxin-regulated TFs ARF7/19 and it acts as a direct regulator of the auxin carrier *LAX3* and the TF *LBD16.* In this work, we report that *AtHB23* is negatively regulated by NaCl in roots. In response to salt, *AtHB23* knockdown triggered a strong reduction of primary root length and affected the gravitropic response, whereas the opposite phenotype was observed in overexpressor plants. Moreover, *amiR23*-silenced plants showed a low survival rate under salt stress, compared to wild-type. Additionally, Lugol staining followed by TEM analyses revealed that *amiR23*-silenced plants exhibited degraded amyloplasts in high salt concentrations, and were unable to recover when transferred back to normal conditions. Accordingly, the expression of several genes involved in starch degradation is altered in *AtHB23-silenced and overexpressor plants.* Furthermore, the AtHB23-target *LAX3* was repressed by NaCl in the tip of the main root, remaining unaffected in higher order roots, whereas GUS staining was significantly decreased in the root tip of *PromLAX3:GUS x amiR23* crossed plants. Altogether, our results indicate that AtHB23 is vital for plant survival and adaptation to salinity stress conditions, and that it participates in the root gravitropic response mediated by amyloplasts turnover.

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320
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Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Alejandra Peruzzo

Use of tetrazolium test in artichoke seeds (Cynara cardunculus var. scolymus) as an alternative to classic germination test

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The artichoke crop is commonly propagated by offshoots, but this vegetative form has sanitary and productive problems. Thus, producers are moving to seed-propagated cultivars, where the use of high quality seeds is an important point for a good establishment of the crop. To measure seed quality, various seed tests are used. However, not all physiological tests are standardized for artichoke. The objective of this work was to evaluate the correlation between tetrazolium (not standardized) and germination (standardized) tests to replace the latter with a faster evaluation. Germination test was performed using 200 seeds (4 replicates/50 seeds) from two seasons. Seeds were placed in three layers of paper previously moistened with distilled water. The material was kept in a climate-controlled chamber (20°C, continuous light) during 21 days. Percentage of normal seedlings (NS) was recorded using a seedling evaluation manual. For tetrazolium test, 2 replicates of 100 seeds of each season were soaked in water for 18 hours, cut longitudinally through the embryon axis and kept in darkness in tetrazolium 1% for 6 hours at 30°C. The results were registered as percentage of viable seeds (VS). Pearson coefficient correlation was calculated using Infostat software. The results obtained from germination test showed an average of 69% NS, while tetrazolium test exhibited a mean of 56% VS. Comparing both tests, no correlation was found ($r=-0.99$; $p=0.008$). Thus, tetrazolium test is not a feasible alternative to replace germination test for this crop under those procedures. More studies should be performed to understand its possible variations.

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321
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Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Julieta Pesqueira

Waterlogging does not affect plant dry-mass or root carbohydrates of Chloris gayana and Panicum coloratum, but it does induce a decrease of leaf-chlorophyll content.

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The hypoxia induced by waterlogging normally generates changes in the carbohydrate metabolism of plants unless strategies are developed to maintain aerobic conditions within the root. With the objective to evaluate the effect of waterlogging on plant dry-mass, shoot-root ratio, root content of starch and sucrose and chlorophyll content (measured as SPAD index), plants of *Chloris gayana* 'Finecut' (CgF) and *Panicum coloratum* 'Klein Verde' (PcKV) were grown six weeks in pots with alkaline-sodic soil (pH=8.3; CE_s=0.93 dSm^{-1} and ESP=26.2 %) at field capacity and then they were subjected during 26 days to two water conditions: waterlogging (pots were immersed in tap water up to 3 cm above the ground, 5.8 % O_2) and field capacity (control). Statistical design consisted of DCA with a factorial arrangement of 2 species x 2 water conditions. When ANOVA detected significant differences between the means, these were separated using the DGC test (α= 0.05). Total dry mass per plant (mean±SEM, g) of CgF (9.72±1.3) was higher ($p \leq 0.0001$) than that of PcKV (3.6±0.52), but waterlogging did not affect plant dry-mass or shoot-root ratio of either of the two species. Sucrose and starch contents of roots (mean± SEM, mg g^{-1} dry mass) were similar for plants of CgF (1.7±0.52; 25.7±2.28) and PcKV (1.24±0.1; 29.53±4.08) grown in soils at field capacity (1.03±0.06; 27.05±2) or under waterlogging (1.91±0.49; 28.18±2.3). Even though, leaf chlorophyll-content (mean±SEM, SPAD units) was lower (p=0.0049) for waterlogged plants (7.40±0.56) than for the controls (10.05±0.66).

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322
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Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Lídia Pessanha

XYLEM SAP TRANSPORT IN Vitis labruscana PLANTS AFTER BUD BREAK IN CONTRASTING SEASONS

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In tropical climates, photoperiod reduction in the autumn appears to induce endormancy in buds even in a low latitude region (21°S). Non-uniformness in bud break is usual in vineyards pruned during the warm winters with insufficient winter chilling, even with the use of a chemical dormancy-breaker, the hydrogen cyanamide. So, the aim of this work was to record the xylematic sap transport and correlate this with the dormancy state in two contrasting seasons: summer (non-dormant buds) and winter (dormant buds). We observed that the discrepant pattern of the BR50 index between the seasons showed that bud endodormancy was inducted when photoperiod was naturally reduced in the autumn. Additionally, sprouts and young branches showed lower growth rates in the winter, possibly due to the mild temperatures of this season (22°C+-X). The xylem sap showed significant differences in the total volume collected (four times higher in the summer), but not in the specific mass. Interestingly, hydraulic conductance was similar between the seasons. The non-correlation between total volume of xylem sap and the number of days for the 1st bud break shows no effect of the xylem sap on bud break. Such results lead us to conclude that endodormancy occurred in the autumn and that xylem sap is not apparently involved with bud break.

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323
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Area: Biochemistry and Metabolism
Tipo de presentación: video presentacion
Enviado por: María Victoria Petreli

Exploring natural variation and reverse genetics to unveil the genetic regulation of flower and seed abortion in Arabidopsis thaliana.

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Crop improvement is essential to meet rising food demand and combat changing climate. This involves identifying alleles that improve stress adaptation and yield potential. Yield is severely impacted by flower and seed abortion due to carbon shortfall early in the reproductive phase (Lauxmann et al., 2016). Here we combine both, the analysis of a core set of accession to identify natural variation and a screening of a mutant population targeting genes involved in central metabolism regulation to identify genetic factors involved in the process of seed and flower abortion. We phenotyped for this trait a core set of 40 accessions belonging to the diversity panel (Horton et al., 2010) and a group of 30 SALK lines. Accessions and mutants were grown under normal conditions (i.e., long day: 16h light/8 h dark). A group of plants from each line was subjected to abiotic stress (i.e., 4 days of extended darkness) at the beginning of the reproductive phase, and then returned to normal growth condition. Silique and flower abortion was scored at day 15 after the stress treatment. A differential response was observed for natural accessions after stress. Mutants targeting a gene involved in the regulation of fructose metabolism showed less flower and seed abortion than wild-type plants, growing them either under control or after stress conditions. Overall, these findings indicate both that GWA can be applied to identify genes involved in the regulation of flower and seed abortion, and that carbon metabolism is highly influencing sink strength under abiotic stress.

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324
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Area: Developmental Biology
Tipo de presentación: video presentacion
Enviado por: Rosanna Petrella

WUSCHEL-RELATED HOMEOBOX 9/STIMPY (WOX9/STIP) is important for ovule development and female germline progression in Arabidopsis thaliana

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WUSCHEL-RELATED HOMEOBOX (WOX) genes encode for a family of transcription factors, sharing important roles in a wide range of processes during plant development. In *Arabidopsis thalianaWOX9/STIP* gene is reported to be necessary for the correct patterning of the embryo and for the shoot apical meristem maintenance. We have investigated the role of *WOX9/STIP* in ovule development by the analysis of *loss-of-function* and *gain-of-function* mutant alleles. Our results showed that *WOX9/STIP* is required for the correct patterning of the outer integument and the anatropy of the ovule. In fact, knockout mutant of *WOX9/STIP* is characterized by severe defects in outer integument development, hence determining a radialized ovule phenotype. In addition, alteration of *WOX9/STIP* expression in the ovule affects the correct differentiation and progression of the female germline.

Our results unravel an important role of *WOX9/STIP* during ovule development and female germline progression, contributing to better dissect and reconstruct the regulatory networks determining ovule development.

325
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Area: Developmental Biology
Tipo de presentación: Poster en formato PDF
Enviado por: Georgina Pettinari

Roles of autophagy in growth and development under optimal and nutrient-deprived conditions in the moss P. patens

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Autophagy (ATG) is an evolutionarily conserved cellular process that involves sequestration, degradation, and recycling of cytoplasmic components, thus constituting a fundamental mechanism for the maintenance of cellular homeostasis in eukaryotic organisms. Most knowledge and major contributions in the field of plant autophagy arise from studies in seed plants. However, our research is focused on bryophytes, the earliest diverging group of terrestrial flora, using the moss *Physcomitrium patens* as a model system that allows us to dive into evolutionary aspects regarding the autophagic process and specie-specific roles of this mechanism.

In this study, we explore the involvement of autophagy in growth and development under optimal and nutrient-deprived conditions (carbon and nitrogen starvation) in *P. patens.* We describe the autophagic response of wild type, *atg5*,and *atg7* knock-out lines by phenotypic characterization, *PpATG8a-f* gene expression analysis, combined with autophagic flux assay and visualization of autophagic vesicles using a *PpATG8b::GFP-PpATGb* reporter line. Both *atg* lines showed accelerated senescence under both carbon and nitrogen deficiencies and optimal growth conditions, highlighting that the protective role of autophagy is conserved in *P. patens*. In addition, *atg* mutants are characterized by shorter protonemata cells and impaired apical caulonema cell growth rate, and the spread of the colony through protonema growth is prioritized at the expense of a reduction in buds and gametophore development. Taken together, our results show that autophagy highly contributes to the progression of *P. patens* life cycle in optimal and nutrient-deprived conditions and suggests a role in sustaining the growth of caulonema cell type.

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326
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Tipo de presentación: video presentacion
Enviado por: Kellen Kauanne Pimenta de Oliveira

Characterization of a novel microRNA responsive to heat stress in Coffea sp.

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Warmer global temperatures are inevitable throughout the next years. This warming impacts agriculture. Thus, it is mandatory to understand biological responses to heat for direct breeding programs. MicroRNAs are small molecules that regulate gene expression. However, there are very few studies about the role of microRNAs in coffee heat stress. The objective of this study is to characterize a novel coffee microRNA and to describe its function in heat stress. To conduct the experiment, firstly, a pipeline was used to identify novel microRNAs in the Coffee canephora genome. Secondly, an alignment of microRNAs precursors was made using heat stress libraries of RNA-Seq. Then, one microRNA was selected for gene expression analysis based on three contrasting genotypes (Coffea arabica cv. Mundo Novo and Catuaí vermelho and Coffea, canephora cv. Robusta tropical), and considering different temperatures. MicroRNAs targets were identified using psRNAtarget. GO terms were analyzed by the Singular Enrichment Analysis method. In summary, it was observed that the expression of this novel microRNA increases in response to warm temperatures for all genotypes. Interestingly, microRNA gene expression was lower in Coffea canephora, when compared to the others genotypes that are considered sensitive to heat stress. It suggests an interspecific transcriptional difference. In addition, a GABA transporter, a molecule related to abiotic stress, was identified as a target of this microRNA. Finally, GO terms directly related to the GABA transporter were also found, which suggests a possible function of the microRNA for heating stress regulation.

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327
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Tipo de presentación: Poster en formato PDF
Enviado por: Paula Pimentel

Phenotyping of root system architecture in Prunus rootstocks

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Root system architecture (RSA) is defined by structural features such as number and length of roots of different orders, distribution area, density, among others. These traits or phenes exhibit a phenotypic plasticity that can respond to environmental stresses. As an initial step in the phenotyping of roots in *Prunus* species, the RSA of six rootstock genotypes was evaluated. The 1-year-old seedlings were planted in rhizoboxes (60x40x3 cm) in a peat:perlite mixture (2:1) supplemented with controlled release fertilizer and regularly watered every third day until the end of the assay (48 days after planting (DAP)). The images of the radical systems were acquired on five dates. Captures were processed with Root Image Analysis-J (RIA-J) software. This analysis revealed that it is possible to differentiate the root systems of *Prunus* spp. based on phenes mainly associated with the distribution of roots, where 'Rootpac 20' (R20) showed the widest root system. Likewise, this hybrid rootstock showed to have the longest root length, which, added to the above, gave it the largest convex hull area but the lowest exploration ratio due to its lower root density. Furthermore, it was possible to demonstrate the growth dynamics over time by identifying ‘Mariana 2624’ (M2624) as the rootstock with the highest speed of root generation per unit of time. Finally, these results demonstrate the applicability of this root phenotyping method to fruit tree species in early development stages, which will allow studying the phenotypic plasticity of their root systems in the face of environmental stress conditions.

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328
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Enviado por: Gabriela Pittaro

Morphophysiological responses to defoliation frequencies in two cultivars of Cenchrus ciliaris L. under field conditions

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Subtropical pastures grazing frequency based on leaf lifespan (LLS), instead of the traditional livestock management, entails an increase in its nutritional quality, affecting animal performance and, consequently, the whole system productivity. However, there is scarce information regarding morphological and physiological responses to grazing frequencies, particularly those related to pasture organic reserves and its influence on forage accumulation patterns and persistency. The objective of this study was to evaluate morphological and physiological variables, and its relationship with reserves compounds accumulation, in two cultivars of *Cenchrus ciliaris* L. (Lucero INTA-Pemán and Orión INTA) and two defoliation frequencies, 250 GDD (LLS) and 450 GDD (traditional management), under field conditions. Three and six defoliations every 450 GDD and 250 GDD, respectively, were carried out. The performance of photosystem II was evaluated in different leaves at the end of the growing season as reserves accumulation. While no differences were found between the two cultivars, defoliation frequency affected pasture production, height, and cover (450 GDD > 250 GDD), as well as its nutritional quality in terms of leaf: stem ratio (250 GDD > 450 GDD). The JIP test results, corresponding to the sward upper stratum, showed a better performance of photosystem II electron transport in plants defoliated at LLS than traditional management, as well as a greater non-structural carbohydrates accumulation in root reserves. No differences were found in protein and total soluble sugars reserves between treatments. These preliminary results would indicate that *C. ciliaris* management based on LLS would not negatively affect pasture organic reserves.

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RT157HN
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Natalia Podio

Effects of a new fluorinated fungicide on the seed germinations of corn (Zea mays) and chicory (Cichorium intybus).

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The goal of this work was to compare the effect of cyproconazole (CYP) and a new fluorinated derivative (CF) on the germination stage of corn and chicory. Three treatments were used: Control (0.1% methanol), 3.4 mM CYP, and 3.4 mM CF. Five corn or 20 chicory seeds were added to the Petri dish with 4 layers of paper and incubated, after adding treatment solutions, in the dark for 6 days. Five Petri dishes were used for each treatment. The experiment was repeated 3 times. After 6 days, germinated seeds were harvested, dissected into the root, shoot, and cotyledon. Germination rate and lengths were recorded for each harvested seed. After that, cotyledons, shoots, and roots from each Petri dish were pooled and dried at 90 ºC for 48 h to measure dry biomass, moisture, and specific lengths. CF showed a less phytotoxic effect on corn and chicory germinations than CYP. A negative effect of CF was found in the specific lengths of root and cotyledon in corn, and in the length and the specific length of root in chicory with respect to controls. On the other hand, CYP showed significant disparities in root length, specific root length and shoot moisture in both species, and negative effects on cotyledon in corn. Length, biomass and the specific length of shoot were also affected in chicory. These results indicate that CF is less phytotoxic than its precursor CYP and the differences observed between them could be related to the log K_{ow} values.

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330
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Area: Abiotic Stress
Tipo de presentación: video presentacion
Enviado por: Douglas Antônio Posso

Lactate dehydrogenase activity in roots and shoot of soybean plants during soil flooding

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Soil flooding impairs the respiration in soybean roots due to hypoxia. To alleviate the hypoxia-induced ATP shortage, the fermentative pathway is induced in plants during soil flooding. This study aimed to evaluate the lactate dehydrogenase (LDH) activity in roots and leaves of two soybean sister-lines with differential tolerance to hypoxia. Soybean plants were cultivated in a 100 L plastic container under field conditions. At the R3-R4 stage (pod filling), plants were subjected to soil flooding. After 11 days of hypoxia, roots and leaves were sampled and the LDH activity was determined. The LDH activity was higher in the tolerant than in the sensitive sister-line in both, roots and leaves. This indicates that, at least part of lactate produced in the roots during flooding is transported to the leaves to be metabolized. The product of the foliar lactate degradation can possibly be redirected to the hypoxic roots contributing to higher carbon cycling and hypoxia tolerance.

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331
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Area: Biochemistry and Metabolism
Tipo de presentación: Poster en formato PDF
Enviado por: Delphine Pott

Exploring the effects of contrasting climates on the fruit metabolite composition of different raspberry genotypes

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Red raspberry (*Rubus idaeus L.)* fruit consumption is increasing due to its remarkable flavor and its well-known positive implications for human health. One of the main objectives of present-day breeding programs is to improve the fruit sensorial and nutritive characteristics, by developing new genotypes with enhanced quality traits and which are adapted to the current changing climatic conditions triggered by global warming. Here, we compare the fruit metabolic profiling of four commercial raspberry cultivars (‘Glen Ample’, ‘Schönemann’, ‘Tulameen’ and ‘Veten’) grown in different European climates (Norway, Germany and Poland), using a combination of liquid or gas chromatography coupled to mass spectrometry.

Although the cultivars evaluated here appear to be better adapted to North-Europe growing conditions (Norwegian location), multivariate statistical analysis allowed us to outline important genotype-dependent differences based on the profiles of important flavor- and health-related compounds. Indeed, ‘Schönemann’ and ‘Veten’ were characterized by high levels of polyphenols (anthocyanins and ellagitannins, respectively) and high antioxidant activity, and ‘Schönemann’ was furthermore highlighted for its peculiar aroma. On the other hand, ‘Tulameen’ was distinguished for its high acidity, and ‘Glen Ample’ for its high content of sucrose and β-ionone, two of the main raspberry taste and aroma contributors, respectively. Taken together, our results may facilitate the development of new raspberry genotypes, which will combine high levels of metabolites involved in the fruit health properties with enhanced flavor.

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Area: Biotechnology, Research Tools, Resources
Tipo de presentación: Poster en formato PDF
Enviado por: Nicole Pretini

Detection of QTL for spike fertility related traits in two doubled haploid wheat (Triticum aestivum L.) populations

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In breeding programs, the selection of cultivars with the highest yield potential consisted in the selection of the yield *per se*, which resulted in cultivars with higher grains per spike (GN) and occasionally increased grain weight (GW). In this study, we used two doubled haploid (DH) populations (Baguette Premium 11 x BioINTA 2002 and Baguette 19 x BioINTA 2002) which were genotyped with an iSelect SNP 90K array and phenotyped in 4 and 5 environments respectively. Quantitative trait loci (QTL) for GW, GN and spike fertility traits were mapped using the QTL Cartographer 2.5 software. In total 305 QTL were identified for 14 traits, out of which 12 QTL were identified in more than three environments and explained more than 10% of the phenotypic variation in at least one environment. Eight hotspot regions were detected on chromosomes 1A, 2B, 3A, 5A, 5B, 7A and 7B in which at least two major and stable QTL sheared confidence intervals. QTL on two of these regions (R5A.1 and R5A.2) have previously been described, but the other six regions are novel. Based on the pleiotropic analysis within a robust physiological model we conclude that the hotspot genomic regions R5A.1 and R5A.2, together with the *QGW.perg-6B* are of high relevance to be used in marker assisted selection in order to improve the spike yield potential. All the QTL identified are the first step to search for their candidate genes, which will allow their better manipulation in the future.

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333
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Area: Evolution, Ecology, or Genetics
Tipo de presentación: video presentacion
Enviado por: Santiago Prochetto

Transcriptional dynamics and gene expression profiles along the foliar gradient in C3 and C4 grasses

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C_4 photosynthesis has allowed plants to adapt to high temperatures and solar radiation through better use of water and nitrogen. Despite the fact that only 3% of angiosperms use the C4 cycle, these species are among the most important crops on the planet (e.g. corn, sugar cane, sorghum) and cover about 25% of the Earth. In addition, species with C_3-C_4 intermediates photosynthesis are usually found near the C4 lineages. Indeed, current models indicate that the assembly of C4 photosynthesis was a gradual process that included the relocation of photorespiratory enzymes, and the establishment of intermediate photosynthesis subtypes.

Interestingly, more than 1/3 of the C4 origins occurred within the grass family (Poaceae). In particular, the Otachyriinae subtribe (Paspaleae tribe) includes 35 American species from C_3, C4 and intermediates taxa resulting in an interesting lineage to answer questions about the evolution and optimization of photosynthesis.

To explore the molecular mechanisms responsible for the evolution of C4 photosynthesis, the transcriptional regulation of genes along leaf development was comparatively studied among Otachyriinae non-model species. For this, leaf transcriptomes were sequenced, de novo assembled and annotated. Then, transcriptional dynamics and gene expression along the foliar gradient were investigated. We found that genes associated with photorespiration and the C_4 cycle are differentially expressed between C_4 and C_3 species, whereas their expression patterns are well preserved throughout leaf development.

334
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Tipo de presentación: Poster en formato PDF
Enviado por: Álvaro Quijano

YIELD AND MORPHO-PHYSIOLOGICAL PARAMETERS OF TWO SOYBEAN SIBLING LINES DIFFERING IN INTERNODE LENGTH

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Differences in plant structure can affect canopy light distribution, producing changes in morpho-physiological parameters related to seed yield. Plant structure can be modified by internode elongation, a typical shade avoidance response that presents genetic regulation. Soybean plants with longer Internode Length (IL) have less lodging resistance, and yield (Y) is reduced when sown at high densities. Two soybean sibling lines differing in IL: FV-N9_30 (short IL) and FV-N9_114 (long IL) were sown in high (HD) and low (LD) density during 2019/20 growing season. At full flowering, light interception (LI), leaflet angle (LA) and relative chlorophyll content (CC) at different canopy strata were measured. At maturity, plant height (PH), stem diameter at soil level (SD), stem angle inclination (SI), main stem partition (MSP), harvest index (HI), Y and Y components were determined. Less light reached deeper canopy stratum in FV-N9_114 than in FV-N9_30 ($P<0.01$), but no differences were observed in LA and CC. At maturity, parameters were affected by genotype, but not by interaction with density. FV-N9_114 showed higher PH, IL and thinner SD ($P<0.05$) than FV-N9_30 causing agreater SI in in the first (43,7° vs. 62,3°, respectively, $P<0.05$). FV-N9_114 presented higher MSP (0.34 vs. 0.24, $P<0,0001$) and lower HI (0.45 vs. 0.52, $P<0.0001$). FV-N9_30 yielded more than FV-N9_114 (435 vs. 388 $g.m^{-2}$, $p=0,07$) because of its higher seed number (25%), pod number (15%) and branch pod number (25 %). Results demonstrate that genetic variability in IL can be exploited in order to reduce lodging and increase Y in soybean.

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335
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Area: Plant breeding
Tipo de presentación: video presentacion
Enviado por: Jesica Raineri

From sunflower HaHB11 gene to remote sensing in the field

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HaHB11 is a sunflower transcription factor belonging to de HD-Zip I family. It was previously described that transgenic maize plants expressing this gene exhibited increased biomass and seed yield compared to controls. We evaluated the phenotype of two independent events in greenhouse and field conditions using as controls null segregants. In this work, we tested such plants in front of waterlogging stress using two genetic backgrounds: B73 lines and B73 x Mo17 hybrids. Under waterlogging, transgenic plants developed longer roots showing more xylem vessels, less ROS, and radial loss oxygen than controls. Moreover, they had increased leaf area, stomatal conductivity, and augmented the number of vascular bundles in stems, having more phloem cells than controls. Genes involved in sucrose fermentation (*ADH*, *GAPDH*, and *G6PI*) were differentially regulated, and in agreement, transgenic plants had more sucrose content at the beginning of the treatment and glucose in leaves after 4 days of stress. They also kept a higher starch amount in roots than controls. After recovery, transgenics yielded more biomass and seeds than nulls. These beneficial traits were observed at similar extents after defoliation assays, both in the greenhouse and the field. Finally, canopy spectral reflectance data were taken in the VIS-NIR during field assays in three different moments. Such data allowed determining biomass, chlorophyll, and stress indexes. Interestingly, most of them correlated with the manually phenotypical observations.

Altogether, the results indicated the potential of HaHB11 to improve stress tolerance and the use big data to distinguish transgenics from controls.

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336
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Area: Developmental Biology
Tipo de presentación: Poster en formato PDF
Enviado por: Betina Lorena Raminger

The transcription factor AtHB5 is a negative regulator of carbohydrate transport

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AtHB5 is a transcription factor belonging to the homeodomain-leucine zipper I family. It was previously reported as repressed during stem maturation, being the only member of this family to show such behavior. To elucidate the role played by this protein, we obtained mutant (*athb5*) and overexpressor (AT5) plants, as well as plants in which the *AtHB5* promoter drives GUS expression. The reporter expression was evident in hypocotyls and vascular tissues. Mutant plants exhibited wider stems with increased lignification, phloem, and xylem vessels, both in leaves and pedicels vascular tissues, whereas AT5 showed the opposite phenotype. Notably, staining leaves with aniline blue revealed callose deposition in OE leaves, suggesting a defective carbohydrate transport. This observation was in agreement with the increased starch content in rosette leaves compared with those of WT plants that could be explained by the altered expression levels of several enzymes involved in starch synthesis and degradation. Although we were could not detect GUS expression in roots, these organs exhibited a differential phenotype depending on AtHB5 and illumination conditions. Mutant plants had longer roots, whereas AT5 shorter ones compared with the WT. Such differential phenotype was observed in seedlings grown under a long photoperiod regime, or in the dark but when the medium was supplemented with sucrose. Moreover, an assay performed with the tracer CFDA, mimicking carbohydrates, revealed a lower transport speed in AT5 plants than in controls.

Altogether the results suggested that AtHB5 is a negative modulator of the source-to-sink carbohydrate transport.

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337
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Area: Biotic Interactions
Tipo de presentación: video presentacion
Enviado por: Romina Nair Ramos

SlWRKY22 and SlWRKY25 are positive regulators of plant immunity

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Plants defend themselves against pathogens using a two-layered immune system. Pattern-triggered immunity (PTI) is activated upon recognition of microbe-associated molecular patterns, such as flg22 epitope from flagellin. Virulent bacteria as *Pseudomonas syringae* pv. *tomato* (*Pst*), can deliver effector proteins into the plant cell to promote susceptibility. However, some plants possess resistance proteins that recognize specific effectors leading to the activation of effector-triggered immunity (ETI). Resistant tomatoes such as Río Grande-PtoR recognize two *Pst* effectors (AvrPto and AvrPtoB) through Pto/Prf complex, activating ETI.

Previously, we found that WRKY22 and WRKY25 transcription factors (TF) participate in plant immunity against bacterial and non-bacterial pathogens in *Nicotiana benthamiana*. Using CRISPR-Cas9, we generated 3 tomato lines to knock-out these TFs (simple and double mutants). Higher *Pst* DC3000 ∆*avrPto*∆*avrPtoB* titers and reduced callose deposition associated to PTI induction, were observed in knock-out plants. We found that both SlWRKY22 and SlWRKY25, have a nuclear localization. Transcript abundance analysis, indicated that *SlWRKY22* is induced earlier than *SlWRKY25*, suggesting a possible co-regulation, considering both genes have predicted WRKY binding sites (W-box) in their promoter regions.

We identified a set of genes with expression patterns most similar to *SlWRKY22-25* and selected those with W-box in their promoter regions. Out of 7 candidates, we found 1 that was induced by ETI in wild type but not in double mutant plants, indicating this could be a gene participating downstream of the TFs understudy.

Our results confirm the involvement of both WRKY TFs in plant immunity and contribute to identifying components acting downstream.

338
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Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Isabella Rampoldi

Developmental plasticity confers adaptive traits to Argentinian weedy rice to become extremely successful weeds.

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Agricultural weeds are responsible for a large proportion of crop yield losses worldwide. In particular, weedy rice (a closely related weed to rice, *Oryza sativa*) can cause complete loss of the crop and lead producers to abandon weed-infested fields for years when left unattended. In Argentina, weedy rice invades the whole rice producing area, imposing the need for more effective management strategies for local producers in the short term. Therefore, understanding local weedy rice characteristics is of importance to develop more sustainable weed control programs. Using four weedy biotypes and two cultivated genotypes, we evaluated weedy rice developmental plasticity (flowering time and seed production) under two contrasting environments (control and high temperature), and assessed progeny seed germination. Flowering time significantly differed between the weedy biotypes and the cultivated genotypes. Even more, weedy rice plants showed a longer flowering period than the cultivated genotypes (~1 month vs 1 week, respectively). The environment during the reproductive stage did not affect seed production of both cultivated and weedy genotypes. However, the environment during reproductive growth influenced the germination response of progeny seeds of cultivated and weedy genotypes in a pattern dependent on genotype and incubation temperature (significant Maternal Environment x Genotype x Incubation Temperature interaction). Nevertheless, weedy rice seeds showed higher variability in dormancy levels. Altogether, our results show that Argentinian weedy rice biotypes have increased developmental plasticity that may result in extremely adaptive phenotypes, suggesting their control would soon require multiple and potentially more expensive management programs in the region.

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Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Mariana Andrea Reginato

STRONG GROWTH INHIBITION UNDER Na2SO4 SALINIZATION IN THE HALOPHYTE PROSOPIS STROMBULIFERA IS RELATED TO CHANGES IN PSII PROTEINS

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Prosopis strombulifera (Lam.) Benth. is a halophytic shrub found in highly saline soils in Argentina and Chile, with high tolerance against NaCl but strong growth inhibition by Na_2SO_4. In the present study, the differences in growth response, ABA levels and PSII proteins caused by NaCl, Na_2SO_4 and the iso-osmotic combination were analyzed. Na_2SO_4-treated plants were the most affected by salinity, showing a significant decrease in several growth parameters with visible toxicity symptoms: chlorosis, necrosis and, finally, leaf abscission at high salinity (Ψo = -2.6 MPa). Accordingly, Na_2SO_4-treated plants showed the highest leaf ABA levels, with a significant increase in the three osmotic potentials tested (-1.9, -2.24, and -2.6 MPa), in relation to control and the other salt treatments. Western Blot analysis indicated important differences in the composition of PSII and related proteins between the different saline treatments. Important changes were observed in the Lhcb2 (LHCII type II chlorophyll a/b-binding protein), PsbA / D1(Protein Photosystem II protein D1) and PsbH (Photosystem II reaction center protein H) proteins in plants treated with Na_2SO_4. These changes were in correlation with the evaluated photosynthetic parameters and the strong growth inhibition observed in these plants. The results show for the first time that the SO_4^{2-} anion is triggering damage in the photosynthetic apparatus and consequently affecting the photosynthetic process, which may explain the strong growth inhibition in these plants at high salinity.

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340
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Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Silvana Boggio

The involvement of ER-sHsp21.5 in the tomato development and postharvest chilling tolerance

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Tomato (*Solanum lycopersicum*) fruit is a valuable horticultural crop worldwide. Usually, non-freezing low-temperature storage is applied after harvesting. However, the production yield and the fruit quality can be severely impaired by chilling injury. A previous study showed transcriptional up-regulation of genes coding for small heat shock proteins (sHsps) associated with postharvest chilling tolerance. sHsps are proposed to act as molecular chaperones to protect other proteins from stress-induced damage and in plants are remarkably diverse and numerous. This diversity comprises classes including proteins targeted to the cytosol, nucleus, endoplasmic reticulum, chloroplast, mitochondria, and peroxisome. To explore the role of endoplasmic reticulum-located small heat-shock proteins 21.5 (ER-sHsp21.5), we constructed Micro-Tom transgenic plants overexpressing and silencing the *ER-sHsp21.5* gene under the control of the fruit specific phosphoenolpyruvate carboxylase isoform gene (*PPC2)* promoter. The phenotypic characteristics of the silenced and overexpressing plants, seeds, and flowers indicate that ER-sHsp21.5 participates in the plant development processes. Both the overexpressing and the silenced fruits were more susceptible to postharvest chilling than the wild-type fruits, showing that the ER-sHsp21.5 concentration should be optimal to develop postharvest chilling tolerance. Also, the color and pigment content analyses showed that ER-sHsp21.5 has a possible role in regulating the β-carotene and lycopene synthesis and protecting the post-chilling color development process. These results show that the ER-sHsp21.5 roles in the plant are diverse and complex.

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341
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Enviado por: Maria Ines Zanor

Genome-wide characterization and analysis of the CCT motif family genes in the Solanaceae family

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The group of genes that encode proteins with a conserved motif called *CCT* (*CONSTANS*, *CONSTANS-like* (*CO-like*), and *Timing of CAB expression1*) participate in the regulation of flowering and circadian rhythm. CCT proteins can be divided into three groups, the CMF (CCT motif factor) group that has a single CCT domain, and the CO-like and the PRR group that besides the CCT domain have a B-Box or a pseudoresponse regulator domain, respectively. Recent progress in the characterization of some CCT proteins showed that they regulate not only plant growth and development but also stress tolerance. Because of limited information about *CMF* gene function in the *Solanaceae* family and especially in tomato, here we report a comprehensive characterization. Our results indicate that in tomato the family is relatively small. A detailed analysis including gene and protein structures, mRNAs expression, and regulatory sequences was done. Also, by using correlation analysis we identified possible genes that co-express with the different tomato *CMF* genes. Among them, genes encoding proteins closely related to early fruit development such as *STAY-GREEN-like protein* and the transcription factor *RIPENING INHIBITOR* (*RIN*) were found. Another group of genes found is related to stress tolerance such as *jasmonic acid 1*, which encodes a transcription factor involved in plant defense and a gene encoding a plant type 2C phosphatase protein that is a negative regulator of the stress response. These results, can serve as a strong foundation for further elucidation of the physiological functions and biological roles of the members of this family.

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342
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Area: Plant Physiology and Ecophysiology
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Enviado por: Thales Ribeiro

Transcriptome analyses suggest that changes in fungal endophyte lifestyle could be involved in grapevine bud necrosis

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Grapevine bud necrosis (BN) is a world-wide spread disorder that affects Vitis vinifera L. The vineyards in Brazilian southeast are particularly affected by this disorder which severely reduces its yield. To investigate this phenomenon at the molecular level, we have sequenced the transcriptome of necrotic and non-necrotic buds from plants of the Syrah variety in two different seasons of a year grown in a commercial vineyard in the municipality of Três Corações, Minas Gerais State, Brazil. Bioinformatic analyses showed that genes related to cell death induced by endophytic microorganisms were more expressed in the necrotic buds when compared to health ones. Additionally, we could identify thousands of transcripts belonging to endophytic fungi such as Alternaria alternata and Pyrenochaeta sp in both necrotic and non-necrotic tissues. However, in the necrotic tissues those endophytes were expressing genes responsible for the metabolism of toxic compounds at a enhanced level when compared to non-necrotic buds. From these findings we propose a model in which under unfavourable conditions, such reduced carbohydrate level, buds can become necrotic as an effect of biotrophic endophytes turning their lifestyle to necrotrophic.

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343
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Area: Developmental Biology
Tipo de presentación: Poster en formato PDF
Enviado por: Jonata Alex Ribeiro Christino

Root photomorphogenic development dependency on the flavonol pathway in Arabidopsis thaliana

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Light perception by the shoot activates the primary root development underground. Genes from the flavonol biosynthesis pathway have their expression increased by shoot illumination. Previous works in the model species *Arabidopsis thaliana* have shown several potential light signaling components involved in root development, such as sugars, auxin and the transcription factor Elongated Hypocotyl 5 (HY5) HY5 is a positive regulator of photomorphogenesis, controlling the transcription of several light regulated genes, including many belonging to the flavonol biosynthesis pathway such as *chalcone synthase* (CHS), *chalcone isomerase* (CHI), *flavanone 3-hydroxylase* (F3H) and *flavonol synthase* (FLS1). Ultimately, HY5 functions communicating roots of the light signal perceived by shoots and inducing flavonol biosynthesis in the roots by increasing gene expression. The loss of function mutant for F3H (*tt6*) produces more lateral roots, a characteristic that is also observed in the *hy5* mutant. This shared root phenotype suggests a link between HY5 and flavonols during lateral root growth. Hence, our goal is to evaluate whether lateral root formation depends on flavonols accumulation promoted by HY5. Currently, we are establishing reporter lines and crosses of selected mutants to identify if flavonol accumulation affects auxin and ROS distribution in roots and its dependence on HY5 abundance.

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344
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Area: Biochemistry and Metabolism
Tipo de presentación: Poster en formato PDF
Enviado por: Simone Ribeiro Lucho Simone

Insights into the role of PpSnRK1-TOR in sugar driven signaling in “Myrobalan 29C” shoots in vitro-grown

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SnRK1 (Snf1-related protein kinase 1) and TOR (target of rapamycin) are evolutionarily conserved protein kinases that lie at the heart of plant cell energy sensing, playing a central and antagonistic roles in the regulation of sugar metabolism. SnRK1 is activated in response to energy decline; conversely, TOR is activated and promotes growth and biosynthetic processes in high-energy availability. However, it is not known exactly how sugar availability affects SnRK1 and TOR activity. Thus, the aim of this study was to establish a connection among the *PpSnRK1–TOR* expression, energy status (low and high sucrose availability) and in vitro shoot development. Explants of “Myrobalan 29C” plum rootstock with approximately 2.0 cm were cultivated in flasks containing 40 mL of MS medium and different concentrations of sucrose (15, 30 and 60 g L^{-1}), supplemented with 0.4 mg L^{-1} BAP, 0.05 mg L^{-1} AIB and 0.3 mg L^{-1} GA_3, 7 g L^{-1} agar and pH 5.2. After 30 days, the explants were sectioned at base and apex (with and without contact with the medium, respectively). Exogenous supplementation of 15 g L^{-1} sucrose up-regulated *PpSnRK1* gene (4.05±0.04), and decreased the carbohydrate content and some growth parameters (explant length and apex fresh weight). Furthermore, shoots in vitro-grown with 60 g L^{-1} sucrose showed the highest carbohydrate content, which may be the signal for the activation of *PpTOR* gene, which was up-regulated more than two-fold. Overall, the results support the globally antagonistic roles of the SnRK1-TOR in modify growth and developmental in response to sugar signal.

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345
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Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Camila Alejandra Rios Rios

Auxin inhibitory effect on stomatal closure requires jasmonate signaling

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Both auxins and the active form of jasmonate (JA), JA-Ile, or its structural analog coronatine, inhibit stomata closure triggered by ABA or bacteria. The effect of these compounds depends on the presence of components of their respective signaling pathways. In this work we observed that *tir1-1* and *aux1* mutants are insensitive to inhibition of ABA-induced stomatal closure by the auxins indoleacetic acid (IAA) and naphthaleneacetic acid (NAA), but also to reopening of stomata by coronatine-producing *Pseudomonas syringae* pv. *syringae* DC3000 (*Pst* DC3000). Conversely, coronatine-insensitive mutants *coi1-16* and *anac019/anac055/anac072*, affected in JA signaling, were not only insensitive to stomata reopening by *Pst* DC3000, but also to inhibition of ABA induced stomatal closure by IAA and NAA. In addition, other mutants previously shown to have stomatal insensitivity to coronatine, *lecrkVI-2.1*, *mpk3*, *mpk6* and *rbohd*, were also resistant to inhibition of ABA induced stomatal closure by IAA. Given that coronatine was previously shown to inhibit reactive oxygen species synthesis, we are currently studying if auxins inhibit stomatal closure through a similar mechanism. Inhibition of stomatal closure by auxins should allow the plant to enhance carbon fixation.

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346
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Area: Signal Transduction
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Enviado por: Claudia Rivera-Mora

Identification of Calmodulin-binding Transcription Activator (CAMTAs) genes in raspberry

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Raspberry (*Rubus idaeus* L.) is a crop of economic interest for its fruits consumed worldwide due to its high antioxidant compounds, vitamins and minerals. The Calmodulin-binding Transcription Activator (CAMTAs) is a transcription factors family characterized by binding to calmodulin, and it is one of the most studied regulators of calcium signaling in multicellular eukaryotic organisms. In plants, CAMTAs has been identified and characterized in different species of economic interest, describing their participation in growth, development and stress tolerance processes. However, their role in fruit ripening is unknown and have not been identified in raspberry. Therefore, this study aims to identify and evaluate the expression of CAMTAs transcription factors in raspberry.

In this study, four CAMTAs genes (*RiCAMTA1*, *RiCAMTA3*, *RiCAMTA4* and *RiCAMTA5*) were identified in two transcriptomes and a raspberry genome draft. Gene structure of the *RiCAMTAs* was determined, and the protein sequences were analyzed, identifying the characteristic CAMTAs domains and motifs in these sequences (CG-1, ankyrin repeats, IPTG and IQ). Bioinformatic prediction of the sub-cellular location indicated that CAMTAs localization in the nucleus and three-dimensional protein models show that all CAMTAs proteins present a tertiary structure with a high number of alpha-helices connected by loops or turns. In addition, differential relative expression of *RiCAMTAs* -in both drupelets and receptacles of fruits- was found in different fruit ripening stages of both tissues and leaves.

This study provides valuable information for future investigations of the role of CAMTAs transcription factors in raspberry fruit ripening.

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347
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Enviado por: Claudio Rivero

ARFA1 and its interacting protein FIP2 mediate bacterial infection and the formation of nitrogen-fixing nodules in Medicago truncatula

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Legume plants have the capacity to incorporate atmospheric nitrogen by establishing an endosymbiotic interaction with soil bacteria that result in the formation of nitrogen-fixing nodules. Bacteria are internalized through a tightly regulated process that requires membrane remodeling and vesicle trafficking, leading to the formation of a tubular structure referred to as the infection thread. Considering that the ARF family of monomeric GTPases mediates vesicle budding in a wide number of biological processes, we focused our studies on the role of a member of the ARF family, ARFA1, during the root nodule symbiosis in *Medicago truncatula*. Overexpression of constitutively active or dominant negative mutant versions of ARFA1 affected root development and bacterial infection. Supporting the role of ARFA1 in bacterial infection, immunolocalization assays showed that ARFA1 localized around infection threads. A yeast two-hybrid screening using ARFA1 as bait identified FIP2, a protein with a BTB/POZ domain that acts as a substrate-specific adaptor of the E3 ubiquitin ligase CUL3. The interaction occurs both in the cytoplasm and in punctuated structures, in an independent manner to the ARFA1 GTP-association state. Using fluorescent cell markers, we found that these punctuate structures correspond to late endosome vesicles. FIP2 and ARFA1 showed a similar expression pattern in the different nodule zones. Overexpression of FIP2 resulted in an increased number of nodules, indicating a role of FIP2 in nodule organogenesis. Altogether, these results support a role for ARFA1 and FIP2 in the vesicle trafficking required for bacterial infection and the formation of nitrogen-fixing nodules.

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Enviado por: Rosa M Rivero

Abiotic stress combination induced a specific metabolism disruption in ABA-deficient mutants ‘flc’ as compared to single stress application

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Current climate change predictions point to an increase in environmental temperature that will act synergistically with an increase in the salinity of the irrigation water due to the rising in the sea level. With the objective of shed some light on the specific ABA interaction mechanisms under abiotic stress combination *Solanum Lycopersicum* L. (cv. Micro-Tom) ABA deficient plants (flacca, *flc*), and wild type (Wt) were subjected to single stress (100 mM NaCl or 35ºC) and their combination. Stomatal responses were highly inhibited in *flc* plants, showing opened stomata under any stress applied and the concomitant reduction in the CO_2 assimilation rate, being heat treatment the most dramatic treatment. The ABA deficiency in *flc* was highly correlated with an increase in JA and its precursors, which was more evident under the combination of salinity+heat. These mutants also exhibited a significant accumulation in Zn, Cu and Mn under stress conditions respect to Wt. The expression of the ABA synthesis pathway-related transcript indicated an overexpression of SAM and ABA2 in *flc* under salinity+heat. ABA deficiency in *flc* was correlated with a higher and accumulation in ROS and NO as compared to Wt under the combination of salinity and heat due to a strong upregulation of *Cu/ZnSOD* and GSNOR genes as compared to Wt under these conditions. Our results showed that stress combination induced a specific stress response in Wt plants, but more importantly, that this specificity is truncated in ABA-deficient mutants, showing the importance of this hormone in the stress combination-related signaling mechanisms.

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349
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Enviado por: Luciana Robuschi

A bioinformatic insight into the Arabidopsis phospholipase C 2 (AtPLC2) interactome

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Phosphoinositide-specific phospholipase C (PI-PLC) plays an important role in signal transduction during plant development and in the response to various biotic and abiotic stresses. However, how PI-PLCs are regulated and how they control these processes remains to be fully understood. In Arabidopsis, the PI-PLC gene family is composed of nine members (AtPLC1 to AtPLC9), being AtPLC2 the most abundant isoform. AtPLC2 is involved in plant defense responses, stomatal closure, gametophyte development and embryogenesis and is rapidly phosphorylated following flagellin recognition. To gain insights into PLC-regulators, we characterized the interactome of AtPLC2. TurboID proximity-dependent biotin labeling was used to identify AtPLC2 associated proteins. A total of 167 candidates were enriched in the AtPLC2 interactome from Arabidopsis cell suspension culture. Gene Ontology classification revealed multiple AtPLC2-mediated biological processes including actin-filament-based movement, vesicle-mediated transport, exocytosis, brassinoesteroid mediated signaling pathway, in addition to signal transduction. Regarding molecular functions, AtPLC2-asociated proteins were mainly related to protein kinases. Moreover, pathway analysis showed that regulation pathways such as protein modification, calcium regulation and receptor kinases were significantly enriched. Taken together, this work presents valuable information for the identification and functional elucidation of AtPLC2-associated proteins, and provides a reference to identify critical regulators of AtPLC2-mediated signaling.

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Area: Signal Transduction
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Enviado por: Carla Roda

The P cyclin PvCYCP, a direct target of the symbiotic transcriptional complex NF-Y, is required for nodule organogenesis

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Legume plants are able to associate with nitrogen-fixing bacteria from the soil. The presence of the bacteria in the rhizosphere triggers a developmental program in the plant required for nodule formation. Members of the Nuclear Factor Y (NF-Y) family of transcription factors (TFs) have been implicated at different stages of the root nodule symbiosis. We have previously shown that NF-YA1 and NF-YC1 play crucial roles during nodulation, modulating the expression of G2/M transition cell cycle genes. To identify direct targets of these TFs we performed a chromatin immunoprecipitation (ChIP) assay followed by PCR of the CCAAT-boxes regions in the promoters of cell cycle genes, such as *CDC25*, *CDC2*, *CYCP,* and *CYCC*. A region of the promoter of the cyclin P was enriched in the ChIP samples from roots expressing FLAG-NF-YC1 as compared to the control roots transformed with the empty vector) suggesting that PvNF-YC1 directly binds the promoter region and might modulate the expression of *PvCYCP*. The ortholog gene of *PvCYCP* in *M. truncatula* is mainly expressed in the nodule meristematic zone and it could be implicated in the cell cycle reactivation that initiates nodule organogenesis. Knock-down of *PvCYCP* in *P. vulgaris* roots led to a marked reduction in the number and size of nodules formed by *R. etli,* and negatively affected the frequency of infection events. These data suggest that *PvCYCP* might play a role in the activation of the cortical cell divisions required for nodule development and rhizobial infection.

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Enviado por: Carla Roda

Silencing of the PvIDN2 protein involved in the RdDM pathway affects root infection and proper nodule development in common bean

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Plants have the capacity to sense and recognize the bacteria present in their environment and adjust expression of their genetic programs accordingly. The perception of bacteria molecules is essential for the establishment of nitrogen-fixing symbiosis, to initiate the infection process by suppressing defense responses, and the organogenesis of the nodule. To investigate the role of bacterial signaling molecules in the activation of symbiosis response genes, we have performed a transcriptional profiling study analysis using roots of *Phaseolus vulgaris* inoculated with mutant strains of *Rhizobium etli* defective in the synthesis of Nod Factor, exopolysaccharides, or lipopolysaccharides. This approach identified differentially accumulated transcripts modulated by this signals at early stages of symbiosis. A gene associated with the regulation of gene expression mediated by small RNAs, which encodes an XH/XS domain protein, was identified. This gene is orthologous to the Arabidopsis *IDN2* gene (*INVOLVED IN DE NOVO 2*), a double-stranded RNA-binding protein involved in RNA-directed DNA methylation pathway. To gain insight into the role of *PvIDN2* during root infection and nodule organogenesis, we carried out a functional analysis of XHXS using an RNAi approach. Phenotypic analysis showed that plants with reduced *PvIDN2* mRNA levels exhibited a reduction in the number of nodules formed by *R. etli* as compared with control roots. Moreover, the frequency of infection events was affected by *PvIDN2* silencing. These results suggest that *PvIDN2* might play a role in the rhizobial infection and nodule organogenesis in *P. vulgaris* roots.

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352
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Enviado por: Daniel Rodela Rodrigues

Cover crops affect proline content and cotton yield in a sandy soil

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Cover crops can improve water storage in sandy soils and mitigate the effects of dry spells on following cash crop yield. The objective was to evaluate the leaf proline content, yield components and cotton yield grown in different crop rotations in a sandy soil. The experiment was carried out in Presidente Bernardes-SP, Brazil. Treatments were: *Urochloa ruziziensis,* millet+velvet bean, millet+*U. ruziziensis*, millet+velvet bean+U. ruziziensis (MIX) and fallow. Leaf sampling (fifth leaf) was carried out at 70 DAE, 5 days after the last rain (10 mm). Plant height and number of nodes were measured, and the bolls in two linear meters from each plot were hand-picked to evaluate yield components (number of bolls and average boll weight) and fiber yield. Cotton leaf proline content in the system with millet+velvet bean was 35% higher than in cotton grown after *U. ruziziensis*. Boll weight and plant height were not affected by the cover crops, but the boll number was higher in the MIX, which was similar to U. ruziziensis, with an increase of 21.6 bolls m^{-2} over the other treatments. The combination of millet+*U. ruziziensis* and fallow had a higher number of nodes compared with MIX. Gin turnout was higher in treatments with grass and legume associated. Fiber yield was similar on MIX and U. ruziziensis rotations and these treatments yielded 381 kg ha^{-1} more than the other systems. An increase in the proline content in the millet + velvet bean treatment did not result in a higher yield in a year of high rainfall.

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Area: Abiotic Stress
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Enviado por: Florencia Sol Rodriguez

CHARACTERIZATION OF NUCLEASE ACTIVITY IN QUINOA ROOTS UNDER SALINE STRESS

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The increase in soil salinity due to global climate change affects plants' biological processes causing great losses in crop productivity. Quinoa (*Chenopodium quinoa* Willd.) is a native crop from the Andean region capable of tolerating high concentrations of salt, which is a great agronomic advantage. The aim of this work was to characterize the nuclease activities in Quinoa roots from seedlings growing under saline stress. To this end, an in-gel assay was used to detect nuclease activity using single-stranded DNA (ssDNA), and RNA as substrate. The results revealed 5 different bands of nuclease activity when RNA was used as a substrate, having different pH-dependent and cofactor-dependent activation patterns. An increase in nuclease activity was observed when seedlings were exposed to 24 or 48 hs under 300 or 500 mM NaCl. Nuclease activity was not detected using DNA as a substrate. In addition, a bioinformatic search was performed and 24 possible ribonucleases were identified in the Quinoa genome. All the 24 sequences found showed CASI and CASII motifs, and the conserved cysteine and histidine residues that are commonly present in ribonucleases. A phylogenetic tree was elaborated, and 20 of these sequences were grouped into Class I, which has been previously reported to be involved in the response to stress and the maintenance of cell homeostasis. Our results suggest that ribonucleases may play an important role in nucleic acid metabolism during radicle growth. On the other hand, according to our results, Programmed Cell Death (PCD) could be triggered under severe stress.

355
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Area: Cell Biology
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Enviado por: Diana Rosa Rodriguez

KDEL-Cysteine-EndoPeptidases CEP1 and CEP2 is involved in EXTensin mediated root hair polar-growth in Arabidopsis thaliana

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Cysteine proteases are a large group of enzymes divided into several families and there is one unique group of papain-type Cysteine EndoPeptidases (CysEPs) containing a C-terminal KDEL endoplasmic reticulum (ER) retention signal (KDEL-CysEPs or CEPs) for which no homologous genes have been found in mammals or yeast. Ricinus CEP (RcCysEP) is able to cut within Ser-(Hyp)$_{3\text{-}5}$ repeats, *O*-glycosylated Hyp and prolines at ±1/±2 positions relative to the cleavage site. These Ser-(Hyp)$_{3\text{-}5}$ repeats carrying *O*-glycosylated modifications are commonly found in structural *O*-glycoproteins Extensins (EXTs). EXT Tyr-mediated crosslinking is catalyzed by apoplastic peroxidases and allow them to form a dendritic glycoprotein network in the cell wall affecting *de novo* cell wall formation in polar cell expansion processes. Since CEPs are able to cleave *O*-glycosylated EXTs resulting in weakening agents of cell walls, thus supporting a putative key role of CEPs in cell elongation. There are 3 *Arabidopsis thaliana* CEPs named AtCEP1, AtCEP2, and AtCEP3. These AtCEPs are highly similar in their protein sequence to RcCysEP. Previously, we have addressed a key role of at least six EXTs (e.g. EXT6,7,10–13) co-regulated at transcriptional level in polar-cell expansion process specifically in root hairs. In this work, we have characterized AtCEP1 and AtCEP2 expression in root hair cells as well as performed a mutant analysis of *cep1* and *cep2*. Based on our results, we speculate that AtCEPs could be involved in polar-growth regulation linked to *O*-glycosylated EXT-processing during its maturation in the secretory pathway in growing root hair cells.

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LQ174NQ
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Maria Camila Rodriguez Gallo

Quantitative proteome and PTMome analysis of Arabidopsis thaliana root responses to persistent osmotic and salinity stress.

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Studies investigating plant responses to osmotic and/or salt stress have largely focused on short-term systemic responses, leaving our understanding of intermediate to longer-term adaptation (24 h - days), less understood. In addition to protein abundance and phosphorylation changes, evidence suggests reversible protein acetylation may also be important for abiotic stress responses. Therefore, to characterize protein-level effects of osmotic and salt stress, we undertook a label-free proteomic analysis of *Arabidopsis thaliana* roots exposed to 300 mM Mannitol and 150 mM NaCl for 24 h. We assessed protein phosphorylation, lysine acetylation and changes in abundance, detecting significant changes in the status of 302, 46 and 118 proteins, respectively. Comparison with available transcriptome data from analogous treatments, indicate that transcriptome- and proteome-level changes occur in parallel, while PTM changes do not. Furthermore, significant changes in abundance, phosphorylation and lysine acetylation involve different proteins from the same networks, indicating a concerted, multifaceted regulatory approach to prolonged osmotic and salt stress. Collectively, our findings indicate dynamic protein-level changes continue to occur in plant roots 24 h from the onset of osmotic and salt stress and that these changes differ across multiple levels of the proteome.

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Area: Biochemistry and Metabolism
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Enviado por: Marianela Rodríguez

Dynamics of proline accumulation under salt stress is affected by the conserved kinase SnRK1 in Aarbidopsis thaliana

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Most abiotic stresses induce metabolic alterations and entail a great energy cost, restricting plant growth. Balancing energy requirements with supplies is a major challenge where the kinase SnRK1 plays a central role to maintain energy homeostasis. Under stress conditions, proline accumulation is a typical response in plants, and it is due to the regulation of the genes that encode the biosynthesis (P5CS1, P5CR, OAT) and catabolism (ProDH, p5CDH) enzymes. Considering that the catabolism of proline generates energy and that SnRK1 is involved in plant energy homeostasis, we hypothesized that SnRK1 will be crucial in this process. Thus, we analyzed the spatio-temporal accumulation of proline under salt stress in Arabidopsis plants with altered expression of the catalytic subunit of SnRK1 (SnRK1.1ox: overexpressor, *snrk1.1:* mutant) and wild-type. Our results showed a delayed accumulation of proline under NaCl 100 mM in the SnRK1.1ox with respect to the wild-type in root and shoot, meanwhile, the *snrk1.1* showed a slight rise in the proline content in roots with respect to control. Regarding transcriptional regulation, main differences were observed at catabolism level, since shoot of SnRK1.1ox plants subjected to salt stress for 3h up-regulate proDH1 and p5CDH genes while col-0 and *snrk1.1* did not modify the proDH1 expression and had a minor increase of p5CDH transcript levels. All data suggest that SnRK1 is involved in the dynamics of proline accumulation under salt stress, possibly through the increase of the catabolism at short-term stress and later in the metabolite accumulation.

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358
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Enviado por: Roxana A. Roeschlin

Harvest time and cultivar effects on fiber quality of cotton on different environmental conditions

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Cotton (*Gossypium hirsutum* L.) fiber quality can affect textile industry and impact income of the farmers. The evaluation of the factors that play important role to optimize fiber quality parameters are necessary. Several studies have revealed that environmental factors could affect fiber quality parameters. Determining the appropriate time-lapse for harvesting is one of the main agronomic practices that influence the fiber quality of cotton. The main objective of this study was to determine the effects of environmental conditions on the parameters of fiber quality at different harvesting times. Four cotton cultivars were cultivated as follows: DP402 (early maturity), Guazuncho2000 (mid-maturity), NuOpal (mid-to late maturity) and DP1238 (late maturity) at the Instituto Nacional de Tecnología Agropecuaria (INTA) Reconquista, for two seasons 2016/17 and 2020/21. Seven consecutive harvest times were performed, beginning with the optimal date and finishing 90 days later. Bolls were manually collected, the ginned fibers were conditioned and fiber properties including micronaire, upper half mean fiber length, uniformity index, short fiber index, strength, elongation-to-break, trash and color were measured by a High Volume Instrument. Significant differences were observed in strength and color fiber quality parameters between the harvest times evaluated only during the first season, regardless the cultivar. These results could be associated with the weather conditions, i.e. effective rainfall in the first season was higher than during the second one. Therefore, this study provides information regarding the main weather factors affecting the commercial fiber quality of cotton as harvesting time is delayed.

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359
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Area: Biotic Interactions
Tipo de presentación: video presentacion
Enviado por: Federico Ariel Roig Puscama

Cation composition of contrasting soils in depth and their allocation in leaf, berry, and wine of Vitis vinifera L. cv. malbec

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The soil is one of the main factors that influence the cation composition in grapevine tissues and their derived wines, characterizing its origin of cultivation. In the wine-growing region of Mendoza, Argentina, a great heterogeneity of soils in terms of texture, depth, holding water capacity and chemical components is observed. Twelve cations were determined by Inductively Coupled Plasma Mass Spectrometer (ICP-MS) in a parcel with two contrasting soil depths and *Vitis vinifera* L. cv. Malbec. Principal Component Analysis were applied to evaluate the relationship in the cation composition of the different samples (soil, leaf, berry and wine). Although deep soils have a higher cation exchange capacity, no differences in the total content of cations between the soil types were observed, but deep soils presented higher content of Mn and K, while short soils increased in Ca. The fermentation process modified the cation content between the berry and the wine in most of the elements analyzed. Mn was the only element that differed, presenting higher amounts in the leaf, berry and wine from deep soils, so it could be suggested as a marker element for wines from this type of soil. These results indicate the importance of the soil in the concept of identity and uniqueness of wines, a concept known as terroir.

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360
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Enviado por: Bruno Rojas

Phosphorylation of Arabidopsis thaliana phosphoenolpyruvate carboxykinases

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ATP-dependent phospho*enol*pyruvate carboxykinase (PEPCK, EC 4.1.1.49) catalyzes the reversible decarboxylation of oxaloacetate to phospho*enol*pyruvate. In plants, PEPCK is part of the CO_2-concentrating mechanism operating in C_4 and CAM photosynthesis, participates in biotic and abiotic stress responses, is involved in nitrogen, and amino acid metabolism, and plays a key role in gluconeogenesis. *A. thaliana* has two genes coding for PEPCKs: *AthPEPCK1* (At4g37870) and *AthPEPCK2* (At5g65690). We showed that PEPCKs are regulated allosterically by metabolites and signaling dipeptides. Also, the cleavage of *Ath*PEPCK1 by *A. thaliana* METACASPASE9 alters its response to allosteric effectors. Although previous work showed that plant PEPCKs were phosphorylated, no detailed study explored the possible effects of phosphorylation on *Ath*PEPCKs activity. To identify the target residues, we surveyed phosphoproteomic databases identifying that both *Ath*PEPCK1 and *Ath*PEPCK2 are phosphorylated on multiple N-terminal Ser, Thr, and Tyr residues. We constructed phosphomimetic mutants of *Ath*PEPCK1 on Ser-62, Thr-65, and Thr-66 residues. In comparison with the WT enzyme, S62D and T66D proteins had increased activity in both reaction directions. Even though shikimate, 3-PGA, and Glc6P inhibited the WT enzyme, none of the phosphomimetic mutants were sensitive to these metabolites. We found that *Ath*PEPCK1 was phosphorylated in germinating seedlings 36 hours post imbibition. Our work represents a starting point to study in detail the phosphorylation of *Ath*PEPCKs, the crosstalk of phosphorylation with other posttranslational modifications, and the broader regulation of gluconeogenesis.

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361
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Tipo de presentación: Poster en formato PDF
Enviado por: Facundo Roldan

Cytochrome c and the ABA signaling pathway interact to regulate root cell elongation in Arabidopsis

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Cytochrome c (CYTc) is a soluble protein responsible for the transport of electrons between complexes III and IV of the inner mitochondrial membrane. It has been shown that plants with reduced CYTc levels show low growth rate and late flowering. These phenotypes are due to an altered cellular energy status which impacts on different hormonal pathways to fine-tune plant growth. In this work, we studied the role of CYTc in Arabidopsis root growth. Mutants in *cytc-1*, one of the genes that encode CYTc, showed a decreased root growth rate, with shorter mature elongated cells and reduced number of meristematic cells. Abscisic acid (ABA) is a known player in root cell elongation, with either stimulatory or inhibitory roles depending on the concentration. Roots of *cytc-1* mutants were more sensitive than the wild-type to treatment with stimulatory amounts of ABA, which largely reverted the elongation deficiency of these mutants. In addition, the activity of a fluorescent reporter of the ABA signaling pathway was increased in a *cytc-1* mutant background. These findings suggests that CYTc deficiency affects ABA responses to regulate root cell elongation.

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GR831SG
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Cecilia Soledad Roldán

Photosynthetic response of Aristotelia chilensis clones obtained from trees exposed to contrasting radiation environments in the Andean-Patagonian forests of Argentina

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Maqui (*Aristotelia chilensis*) is a native berry of the Andean-Patagonian forests, with one of the highest antioxidant levels currently known for this region and great interest for domestication purposes. The objective of our study was to characterize the photosynthetic response of 6 maqui clones obtained from trees at two contrasting radiation environments (RE) of two natural forest (coihue forest: shady area and cypress forest: sunny area) after growing 1,5 years in a common garden at full sunlight. We hypothesize that clones from both RE will have high and equal values of maximum photosynthesis when grown under high light conditions. Curves of net photosynthesis *vs.* photosynthetically active radiation (PAR) were performed with an IRGA (LiCor-6400). Three mathematical models (nonrectangular hyperbolas) were used to evaluate the maximum photosynthetic rate (P_{max}), dark respiration rate (R_D), and quantum yield ($\Phi_{(I0)}$). Also, we measured specific leaf area (SLA) on full sun-exposed leaves of both groups of clones. P_{max} was significantly different and the clones from sunny environments showed higher values than those from shady environments. R_D and $\Phi_{(I0)}$ were similar between clones of different RE. Clones from shady environments have higher SLA than clones from sunny environments, in correspondence with their parental environment. Under high radiation conditions, clones from shady environments maintain their leaf morphology with high SLA, but make partial physiological adjustments, with lower photosynthetic rate and the same R_D than clones from sunny environments. These results showed more inefficient carbon assimilation and, therefore, lower growth potential for shady clones in full sun conditions.

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363
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Area: Epigenetics, Chromatin, non-coding RNAs, RNA biology
Tipo de presentación: video presentacion
Enviado por: Andres Romanowski

Global transcriptome analysis reveals circadian control of splicing events in Arabidopsis thaliana

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The circadian clock of *Arabidopsis thaliana* controls many physiological and molecular processes, allowing plants to anticipate daily changes in their environment. However, developing a detailed understanding of how oscillations in mRNA levels are connected to oscillations in co/post-transcriptional processes, such as splicing, has remained a challenge. Here we applied a combined approach using deep transcriptome sequencing and bioinformatics tools to identify novel circadian-regulated genes and splicing events. Using a stringent approach, we identified 300 intron retention, eight exon skipping, 79 alternative 3′ splice site usage, 48 alternative 5′ splice site usage, and 350 multiple (more than one event type) annotated events under circadian regulation. We also found seven and 721 novel alternative exonic and intronic events. Depletion of the circadian-regulated splicing factor AtSPF30 homologue resulted in the disruption of a subset of clock-controlled splicing events. Altogether, our global circadian RNA-seq coupled with an *in silico*, event-centred, splicing analysis tool offers a new approach for studying the interplay between the circadian clock and the splicing machinery at a global scale. The identification of many circadian-regulated splicing events broadens our current understanding of the level of control that the circadian clock has over this co/post-transcriptional regulatory layer.

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364
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Enviado por: Andres Romanowski

Phytochrome regulates cellular response plasticity and the basic molecular machinery of leaf development

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Plants are plastic organisms that optimize growth in response to a changing environment. This adaptive capability is regulated by external cues, including light, which provides vital information about the habitat. Phytochrome photoreceptors detect far-red light, indicative of nearby vegetation, and elicit the adaptive shade-avoidance syndrome (SAS), which is critical for plant survival. Plants exhibiting SAS are typically more elongated, with distinctive, small, narrow leaf blades. By applying SAS-inducing end-of-day far-red (EoD FR) treatments at different times during Arabidopsis (*Arabidopsis thaliana*) leaf 3 development, we have shown that SAS restricts leaf blade size through two distinct cellular strategies. Early SAS induction limits cell division, while later exposure limits cell expansion. This flexible strategy enables phytochromes to maintain control of leaf size through the proliferative and expansion phases of leaf growth. mRNAseq time course data, accessible through a community resource, coupled to a bioinformatics pipeline, identified pathways that underlie these dramatic changes in leaf growth. Phytochrome regulates a suite of major development pathways that control cell division, expansion, and cell fate. Further, phytochromes control cell proliferation through synchronous regulation of the cell cycle, DNA replication, DNA repair, and cytokinesis, and play an important role in sustaining ribosome biogenesis and translation throughout leaf development.

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365
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Enviado por: Francisco Romei

Characterization of HHO5, a transcription factor involved in nitrogen response in both A. thaliana and rice.

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Nitrogen deficiencies and the use of fertilizers is a major issue for crops production having both economic and environmental consequences.

In a previous work, we have demonstrated that HHO5 gene is expressed in both *A. thaliana* and *O. sativa* when the plant is supplied with a nitrogen source and that plays an important role in the nitrogen response regulatory network with a systems biology perspective (Obertello et al., 2015).

Our goal is to characterize HHO5 and to understand its role in nitrogen response pathway in both species. . Our *in silico* analysis of HHO5 endogen promoter compared with data of genes expressed under N supply conditions in both species revealed possible associations of HHO5 and regulatory pathways other than nitrogen use. We found sites targeted by known TFs associated with stress response, such as ABI5 and OsWRKY11 with two and three target sites respectively in OsHHO5 promoter and AtWRKY28 with two sites in AtHHO5 promoter. Based on that analysis, we selected different length of endogenous pAtHHO5 promoters in order to study its regulation and expression pattern in a N context. We generated several transgenic lines in *A. thaliana* using YFP and GUS as reporters genes. Also, in order to analyze HHO5 localization and its effects in N use efficiency, we generated *O. sativa* transgenic 35Sp::OsHHO5-GFP overexpressing lines.

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366
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Area: Biotic Interactions
Tipo de presentación: Poster en formato PDF
Enviado por: Antònia Romero-Munar

Benefits on the ex vitro plant performance of the early arbuscular mycorrhiza symbiosis establishment in rooting process of Prunus rootstocks

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In vitro is a mainstream and successful plant production method. However, during plant propagation, the controlled and aseptic conditions do not provide the plantlets with beneficial microbiota to enhance their development and responses to cope with soil stress, crucial when those plantlets are established as a crop. In natural conditions, seedlings are directly exposed to soil microbiota, potential disease promotors, plant-promoting growth bacteria, and potential symbionts. Arbuscular mycorrhiza (AM) symbiosis was described as the mother of the symbiosis, being the most widespread symbiosis in terrestrial plants. Nonetheless, at tree level, arbuscular mycorrhizal colonization showed low levels and frequently the symbiosis is unsuccessfully established. The objective of the present work was to perform the symbiosis establishment of two AM fungi species, *Clareidoglomus clareidum* (obtained from Chilean soils) and *Rhizophagus intraradices* (widespread fungus in plant AM symbiosis) during the *ex vitro* rooting process, just after finishing the *in vitro* shoot development. Plant survival and biomass production of symbiotic plantlets with each AM fungus were compared with plantlets rooted without symbiosis. Plantlets used were 'Adara' and 'Maxma 14' rootstocks, which are highly produced under *in vitro* process. Survival during the rooting process of non-symbiotic plantlets was 100% in both rootstocks, while symbiotic 'Adara' plantlets of *C. clareidum* presented 20% of losses and 100% survival with *R. intraradices* symbiosis. 'Maxma 14' showed more survival with *C. clareidum*, but the differences with *R. intraradices* were not significant. Regarding to plant fitness, both symbiont rootstocks were significantly higher in total biomass, increasing root and shoot development.

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367
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Enviado por: Pablo Federico Roncallo

Effect of major genes (Rht-B1, Ppd-A1 and Vrn-A1) and loci identified by association mapping on grain yield and morfo-phenological traits in durum wheat

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Grain yield is affected by developmental genes involved in photoperiod sensitivity (*Ppd*), vernalization (*Vrn*) and plant height (*Rht*). However, additional unknown genes are also affecting wheat yield and morpho-phenological traits. The objective of this study was to contribute of deciphering the genetic bases of grain yield and morpho-phenological traits in durum wheat. A collection including a total of 197 durum wheat genotypes was evaluated under field conditions between 2011 and 2019 in Argentina and Mexico, including replicated (9) and non-replicated trials (7), for yield (7), plant height (8), peduncle length (5), heading date (14) and flowering time (1). The alleles at *Rht-B1*, *Ppd-A1* and *Vrn-A1* genes were evaluated using SNP markers (KASP^{TM}). The effect of the *Ppd-A1*/*Vrn-A1* alleles combination on heading date was classified as *Ppd-A1a* (GS-100) > *Ppd-A1a* (GS-105) > *Ppd-A1b*/*Vrn-A1c/a*> *Ppd-A1b*/*Vrn-A1b* across 14 trials. The GS105 allele at *Ppd-A1* resulted in increases in grain yield in five environments whereas the *Rht-B1* gene showed a strong effect on plant height and peduncle length together with loci detected by marker-trait associations (MTA) on 4A, 6A, 7B and 2B chromosomes. For grain yield, MTA were detected on 4A, 7B, 5A, 6B, 3B and 7B. In addition, loci associated with heading date were significant at 5A, 2B, 1A, 3A and 3B. The SNP AX-94494720 on 4AL was significantly associated with plant height in five environments and also with grain yield in three environments. Further exploitation of new loci for morpho-phenological traits should be considered in grain yield improvement.

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368
MQ735FP
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Deborah Rondanini

Photothermal quotient captures adequately the effects of heat and shade stresses on canola seed yield

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Shading and heat stress during critical reproductive period affect negatively yield in canola (*Brassica napus* L.), however, the impact of combined effect of both stresses has not yet studied. Although photothermal quotient (radiation:temperature ratio) is commonly associated with seed yield, its utility under combined stress conditions is unknown. This work was aimed to (i) evaluate the effects of shading and heat stress, alone and combined, on seed yield and quality, (ii) quantify the resulting effect (additive, synergistic, antagonistic) of combined stresses, and (iii) examine the utility of the photothermal quotient to predict seed yield in stressed crops. Two experiments were carried out under field conditions in Buenos Aires (34°35′S, 58°29′W) applying to a canola hybrid a high daytime temperature stress (HT, 25-30°C average from 10:00 to 15:00), a shading stress (SH, -80% irradiance), and combined stresses (SH+HT), with an unstressed Control (C, 20°C and 100% irradiance). Exp 1 was longer (37 d) and less hot than Exp2, which was short (10 d) and heated more intensely. Treatments overlapped the critical periods of 100-500 ºCd and 200-400 ºCd after flowering defined in the literature. Long and short duration SH and HT strongly affected seed yield (reduction from -40 to -90%). Combined SH+HT exhibited additive effects on seed yield and oil concentration for long duration stresses. Photothermal quotient (accumulated between 100-500 °Cd) captured adequately ($p<0.001$; $R^2= 0.87$) the effects of stresses on seed yield. We conclude that the photothermal quotient summarizes the additive effects of combined post-flowering abiotic stresses on canola productivity.

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369
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Area: Biochemistry and Metabolism
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Enviado por: Mariana Daniela Rosa

Possible mechanisms of Cr(VI) reduction in Salvinia minima. Involvement of an h-type thioredoxin.

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Cr(VI) is extremely toxic to plant cells and has been recognized to possess a high redox potential. Tolerant plant species have shown the ability to reduce Cr(VI) but the operating mechanism involved in this process are not elucidated. The aim of this study was to investigate the possible involvement of thiolic and phenolic compounds, and thioredoxin expression during Cr(VI) reduction in *S. minima*. In addition, a probable enzymatic reduction of Cr(VI) was investigated. Plants were exposed to 20 mg L^{-1} Cr(VI) during 7 days under controlled conditions. The amount of metal accumulated in lacinias and fronds indicated that a low percentage of absorbed Cr(VI) was mobilized from lacinias to fronds. X-ray absorption near-edge structure (XANES) analysis revealed that Cr(III) was the only chromium species occurring in *S. minima* plants. The expression of an *h*-type thioredoxin was demonstrated for the first time in Cr-exposed lacinias. Thiols and phenolics of lacinias and fronds were increased significantly by Cr(VI) treatment, but accumulation patterns were different indicating probably different roles in Cr(VI) detoxification. We suggest that operating mechanisms would be related to the amount of Cr absorbed and the organ considered. Thus, in lacinias, where higher Cr accumulation occurs, the most predominant mechanisms could be the metal complexation with insoluble phenolics and thiols bound protein, with a lower participation of soluble compounds (e.g. soluble phenolics, non-protein thiols). While in fronds, with low Cr accumulation, the reduction mechanism would be more related to soluble phenolics, non-protein thiols, and an unknown enzyme able to reduce Cr(VI).

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370
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Area: Epigenetics, Chromatin, non-coding RNAs, RNA biology
Tipo de presentación: Poster en formato PDF
Enviado por: Santiago Rosatti

Integration of multiple regulatory pathways on the expression of microRNA miR398

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MicroRNAs (miRNAs) are small RNAs of 20-22 nucleotides in length, essential for post-transcriptional gene regulation. miR398 is highly conserved in plants and regulates oxidative stress response genes, as opposed to most other miRNAs, which are involved in developmental processes. In *Arabidopsis thaliana*, many factors modulate *MIR398* expression, such as sucrose, oxidative stress, and low copper availability. Two of the three *MIR398* family members have overlapping natural antisense genes that regulate their expression. Nevertheless, little is known about how these multiple regulatory mechanisms integrate. Here, we first assessed the accumulation of miR398 in a set of mutants with affected RNA metabolism. We found that miR398 strongly decreased in *fiery1*, resembling small RNA processing mutants, and especially when plants were grown under copper deficiency, which normally activates MIR398 expression. *Fiery1* mutants accumulate excess 3'-phosphoadenosine 5'-phosphate, a metabolite that is normally generated under stress (like high light or drought) and acts as a retrograde inhibitor of 5'-3' exoribonucleases involved in RNA catabolism. On the other hand, we show that miR398 levels increase when their natural antisense genes are mutated, as well as in mutants with altered double-stranded RNA stabilization. We also tested the expression of miR398 in these mutants subjected to different environmental conditions. Altogether, these results provide new insights into the regulatory mechanisms controlling miR398 expression and function.

371
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Area: Biotic Interactions
Tipo de presentación: video presentacion
Enviado por: Franco Rossi

PHYSIOLOGICAL AND TRANSCRIPTOMIC CHANGES IN Brassica napus COTYLEDONS TREATED WITH SIRODESMIN PL PHYTOTOXIN

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Brassica napus (colza, canola) is the second-largest oilseed crop produced worldwide. Hemibiotrophic fungus *Leptosphaeria maculans,* is a devastating pathogen that causes blackleg disease in this plant species. Yield reduction and important economical losses are associated to infected plants because of a restriction in water and nutrient transport through the stem. It has been demonstrated that Sirodesmin PL is the major component of phytotoxic extracts produced by *L. maculans* and mutant isolates, unable to produce Sirodesmin PL, are less virulent on stems of *B. napus*. Nevertheless, the toxicity-mediating mechanisms are yet far from being understood. Here, we present results from global transcriptomic and physiological studies after treatment of *B. napus* cotyledons with Sirodesmin PL. Gene Ontology term enrichment of differentially expressed genes (DEGs) indicated that this toxin induced genes associated to different plant defense responses such as those involved in hormonal pathways, ROS accumulation and callose deposition. We also found that Sirodesmin PL suppressed genes associated to photosynthesis. In agreement with this, we corroborated that the whole photosynthetic activity was negatively affected by the treatment. Parameters associated with chlorophyll fluorescence and number of chloroplasts per cell were significantly lower in the spongy and palisade parenchyma of leaves treated with Sirodesmin PL. This study makes a significant contribution to understanding the molecular responses of *B. napus* to Sirodesmin PL, which could promote the development of effective strategies in *L. maculans*-resistance breeding programs.

372
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Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Verónica Eugenia Ruiz

SOLAR RADIATION AS A PREHARVEST FACTOR AFFECTING THE TOMATO SUSCEPTIBILITY TO POSTHARVEST CHILLING INJURY

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Tomato tolerance (*Solanum lycopersicum* L.) to low temperatures decreases in sunshine fruit. Considering tomato is cultivated under different cultivation system modifying light conditions, and its potential impact on fruit postharvest life, the aim of this work was to study the relationship between solar radiation and the fruit susceptibility to postharvest chilling injury. For this, two preharvest treatments were applied: permanent shaded plants (Sh) and direct sunligth exposed plants (Ex) as controls. The accumulated daily solar radiation, the air temperature and the vapor pressure deficit were determined, as well as the fruit temperature. After harvesting, fruit were stored at 10 and 4 ºC during ten days. Then, several determinations were carried out: calcium content, postharvest parameters, ions leakeage and thiobarbituric acid reactive species content, chilling injury index (CII) and morphological and anatomical description of epicarp pits. A randomized design with three replications was applied. An ANOVA with a comparison of means by Tukey test was performed ($p \leq 0.01$). The results showed that Ex fruit had higher CII values than the Sh fruit, as well as fruit stored at 4 ºC presented a more marked damage than those under 10 ºC. The membrane stability and the rot incidence presented a close correlation with the CII. The lower calcium content in the Ex fruit could be one of the causes of their response to chilling. Accumulated temperature at the field resulted critical factor affecting postharvest chilling injury susceptibility. These evidences could help making decisions for crop management, according to the market target.

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373
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Tipo de presentación: video presentacion
Enviado por: Yve V S Magedans

Triterpenoid saponin biosynthesis and elicitation strategies in cell suspension cultures of Quillaja brasiliensis

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Quillaja brasiliensis (A. St.-Hil. & Tul.) Mart. is an evergreen tree of southern Brazil and neighboring countries. *Quillaja* spp. are known to produce triterpenoid saponins that have application in different industrial sectors. Recently, *Quillaja saponaria* saponins were added to the adjuvant system of Novavax's vaccine formulation against the Sars-Cov-2, an immunization product that has shown good efficacy and safety. Sustainable strategies to obtain high-quality plant material for industrial applications are needed. Our goal was to establish cell suspension cultures of *Quillaja brasiliensis* and modulate their saponin metabolism through different elicitation treatments. Cells were grown in Murashige & Skoog media for 21 days, and biomass parameters were evaluated. Saponin profile was estimated by thin-layer chromatography, and total saponin content was quantified by a colorimetric assay. HPLC profile evaluation is ongoing. Elicitation treatments were applied at the late log phase of the cell cycle, and total saponin content was quantified up to 10 days after application. Cell cultures of *Q. brasiliensis* synthesize triterpenoid saponins with a profile comparable to that of leaf aqueous extract, the main source in this species. Jasmonic acid stimulated total saponin content one and two days after treatment application with minimal effects on growth. Initial tests show that other elicitor treatments (both chemical and physical) can also promote saponin yield. Our work suggests cell cultures of *Quillaja brasiliensis* are a potential source of saponins, and that their metabolism can be significantly modulated by stimuli related to environmental factors.

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374
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Enviado por: Bruna Alves da Silva Bruna Alves

Biostimulant action in the attenuation salt stress in cowpea

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Soil salinization is one of the main causes of reduced crop yields in the field, since excess salts, in soil or irrigation water, trigger a series of events that promote imbalances in plant metabolism.Therefore, the development of technologies that aim to reduce the harmful effects of salinity are alternatives to minimize losses.Therefore, the objective was to evaluate the use of a biostimulant based on fulvic acids and seaweed extract (Ascophyllum nodosum (L.)) as an attenuating agent for salt stress in cowpea.The experiment was carried out in a greenhouse, in a completely randomized experimental design (DIC) in a 2x4+1 factorial scheme, with two application times (before and after the imposition of stress) and four doses (0; 0.1; 0, 25 and 0.5 kg ha-1), applied via foliar spray, totaling eight treatments irrigated with saline solution at 6.0 dS m-1, with five repetitions and an additional control (without salt stress and without biostimulant).Photosynthetic pigments, membrane damage and gas exchange were analyzed. The dose of 0.25 kg ha-1 showed better results with significant increases for chlorophyll a and chlorophyll b, photosynthesis and transpiration when applied before the imposition of stress. As for conductance, the mean of the doses before stress and control were statistically equal. Membrane damage was greater in the treatment without application of the biostimulant. In general, the use of the biostimulant reduced the harmful effects of salinity, being recommended for cowpea at a dose of 0.25 kg ha-1 applied before stress.

Keywords: Vigna unguiculata (L.) Walp.; FH ATTIVUS; Salinity, Anti-stress effect.
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375
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Role of SlTPD1 in the regulation of redox homeostasis during anther development in tomato

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Tomato is an important crop and a model species for fleshy fruit plants. Fruit set starts after pollination and fertilization, but increasing unfavorable environmental conditions reduce pollen viability and fruit and seed production. Thus, studying the genes controlling pollen development can give insight into this process and provide biotechnological tools to increase crop production. We used information from *Arabidopsis*(Yang et al., 2003), to identify the tomato *TAPETUM DETERMINANT 1* (*Solanum lycopesicum TPD1, SlTPD1*) homolog, which encodes a small protein ligand necessary for the correct development of tapetum. Using *in situ* hybridization, we found that *SlTPD1* transcript was present in the L2 cells of anther primordia and expression continues until later stages in the tapetum and pollen grains. Then, several mutant lines were produced using the CRISPR/Cas9 technology in the commercial tomato cultivar Moneymaker. Histological sections of mutant anthers revealed the absence of tapetum and an over-proliferation of microsporocyte cells that, at late stages, degenerated and collapsed inside the anther locules. In consequence, mutant plants were male sterile. RNA-Seq analysis conducted in wild-type and mutant anthers from an early stage revealed differential expression of several reactive oxygen species (ROS)-related genes, including transcription factors involved in tapetum development. Interestingly, the expression of several of these genes was significantly downregulated in *Sl-tpd1* mutants. Furthermore, the formation of ROS determined by DAB staining is lower in the mutant than in wild-type anthers. We conclude that *SlTPD1* is required for tapetum differentiation and for the regulation of redox homeostasis during anther development in tomato.

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ROLE OF SlTPD1 IN THE REGULATION OF REDOX HOMEOSTASIS DURING ANTHER DEVELOPMENT IN TOMATO

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Tomato is an important crop and a model species for fleshy fruit plants. Fruit set starts after pollination and fertilization, but increasing unfavorable environmental conditions reduce pollen viability and fruit and seed production. Thus, studying the genes controlling pollen development can give insight into this process and provide biotechnological tools to increase crop production. We used information from *Arabidopsis* (Yang et al., 2003), to identify the tomato *TAPETUM DETERMINANT 1* (*Solanum lycopesicum TPD1, SlTPD1*) homolog, which encodes a small protein ligand necessary for the correct development of tapetum. Using *in situ* hybridization, we found that *SlTPD1* transcript was present in the L2 cells of anther primordia and expression continues until later stages in the tapetum and pollen grains. Then, several mutant lines were produced using the CRISPR/Cas9 technology in the commercial tomato cultivar Moneymaker. Histological sections of mutant anthers revealed the absence of tapetum and an over-proliferation of microsporocyte cells that, at late stages, degenerated and collapsed inside the anther locules. In consequence, mutant plants were male sterile. RNA-Seq analysis conducted in wild-type and mutant anthers from an early stage revealed differential expression of several reactive oxygen species (ROS)-related genes, including transcription factors involved in tapetum development. Interestingly, the expression of several of these genes was significantly downregulated in *Sl-tpd1* mutants. Furthermore, the formation of ROS determined by DAB staining is lower in the mutant than in wild-type anthers. We conclude that *SlTPD1* is required for tapetum differentiation and for the regulation of redox homeostasis during anther development in tomato.

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377
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Enviado por: Lucila Salvatore

Role of DOF 1.5 transcription factor in shade and temperature response

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We found high similarities when we compared photomorphogenesis and thermomorphogenesis responses, in particular shade and high temperature responses. In both cases, photoreceptor phyB and cry1 are at least in part responsible for the perception. However much less is known about the signalling mechanisms involved. In a screening based on pools of the T-DNA activation tagging lines, we selected a mutant line that shows long hypocotyls in light. That transgenic line has elevated levels of DOF 1.5 transcription factor. On the other hand, analysing a dataset from an RNAseq carried out in our lab of Arabidopsis seedlings exposed to light or shade, in combination with two temperatures (20 and 28°C), we found an increased expression of *DOF1.5* in response to shade and high temperature. Taking into account this background we decided to study the role of DOF 1.5 in light and temperature signalling responses. We analysed the hypocotyl growth rate of an overexpressing line and a loss of function mutant of DOF 1.5 in different combinations of white light, shade and temperature (15, 20 and 28°C). The loss of function mutant showed a reduced growth rate in shade and high temperature response in comparison with WT. Whereas the overexpressing line showed an exaggerated growth response in these conditions. This data suggests that DOF1.5 transcription factor is involved in the convergence between light and temperature response.

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378
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Osmotic dehydration of Elegant Lady and Gold Prince peach slices in sucrose solution

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Peach is a natural source of bioactive compounds but is perishable. Dehydration of fresh fruit is other option for the consumers and industry. Osmotic dehydration previously applied to the conventional dryness is a promising alternative to preserve fruit quality and reduce processing costs. In this work, bioactive compounds and antioxidant capacity were analyzed in slices of two commercial peach cultivars Gold Prince (GP) and Elegant Lady (EL) subjected to sucrose dehydration. Treatment (OD) consisted of 3 h incubation in a 47°Brix sucrose solution containing 2%(w/v) $CaCl_2$ at 40°C under stirring. OD decreased the water content of fresh slices from 87±0.5 to 61±0.8. Samples were further dried at 58°C during 5 hs (OD+D). Treated slices were compared with those exclusively oven dried at 58°C. OD and OD+D slices displayed a remaining water content of 21±8%, with similar values within each cultivar. Based on either fresh or dry weight basis, there were not differences between OD+D and D samples in the content of total carotenoids, total proteins and antioxidant capacity measured by ABTS method for EL and GP, and in total phenolic content of GP. In contrast, total phenolics were higher in sucrose dehydrated samples than in D in EL fruits. Nevertheless, the content of ascorbic acid, flavonoids and antioxidant capacity measured by the DPPH method were lower in OD+D than in D slices of EL and GP. Essentially, the same behavior was observed in both cultivars. Benefits and cons of each treatment are discussed and results are compared to fresh fruit.

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379
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Enviado por: Diego Salve

Could plant density be increased in Andean maize grown at high altitudes?

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Although plant density is a critical management variable affecting maize yield, little is known about optimal plant density for Andean maize grown at high altitude environments with larger irradiance availability. Field trials were conducted in Posta de Hornillos, Maimará, Argentina (23º39’S, 65º25’W, 2300 m.a.s.l.) in 2019-20 on a sandy clay loam soil without water or nutrients limitations. Two maize lines, Amarillo de ocho ("A", planophile) and Capia blanco (“B”, erectophile), were grown at two plant densities: 5.71 –conventional for this area- and 8.57 pl m^{-2}.

At the beginning of the critical period, leaf area index increased at high density ($P<0.06$) but remained below critical values (1.8 *vs*. 2.1 at 5.71 and 8.57 pl m^{-2}) and was generally higher in genotype A (2.2 *vs.* 1.7 in B, $P<0.01$). Consequently, the light interception was higher at high density (58% vs 75% in 8.57 pl m^{-2}, $P<0.01$) but without reaching critical values.

No density effects were detected for yield or yield components. Kernel number per unit area was 18% higher in genotype A ($P<0.05$), but this was compensated for by 27% higher individual grain weight in genotype B ($P<0.05$), resulting in similar yields (6128 - 6676 kg ha^{-1}) between genotypes. Kernel number per unit area was highly negatively correlated with individual grain weight across treatments ($r^2=-0.9$). Our results suggest a low source-sink balance during the reproductive period that impairs KNP advantages to be translated into higher yields.

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Area: Abiotic Stress
Tipo de presentación: video presentacion
Enviado por: Muhammad Sameeullah

Transplastomic expression of 3β-hydroxysteroid dehydrogenase and progesterone 5β-reductase genes confer enhanced salt tolerance in tobacco (Nicotiana tabacum L.)

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Short chain dehydrogenase/reductase (SDR) gene family is widely distributed in all kingdoms of life. However, their role in plant stress, especially in salinity stress management, remains elusive. In the present study, the stable integration of *3β-HSD*, *P5βR1* and *P5βR2* genes in plastomes, copy number and transgene expression at transcript and protein level in transplastomic plants were confirmed by PCR, end-to-end PCR, qRT-PCR and Western blot analysis, respectively. Transplastomic plants exhibited high growth and enhanced biomass than wild type (WT) under control and salt stress. Transgenic plants showed enhanced growth in terms of biomass and chlorophyll content compared to the WT under salt stress. Under 300 mM salt stress, transplastomic lines remained much greener without negative impact on shoot or root growth compared to the WT. Salt tolerant phenotype in transplastomic lines was supported by enhanced synthesis of metabolites (sucrose, glutamate, glutamine and proline) under 300 mM NaCl stress. Further, lower Na^+/K^+ ratio in transplastomic lines than WT also supported the salt tolerance. The possible mechanisms could involve in upregulation of nitrogen assimilation, osmolytes as well as lower Na^+/K^+. These results suggest that the *3β-HSD*, *P5βR1* and *P5βR2* could be involved in growth and development under salt stress.

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381
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Area: Epigenetics, Chromatin, non-coding RNAs, RNA biology
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Enviado por: Diego H. Sanchez

Dual role of specific non-coding tandem-repeats integrating epigenetic silencing with stress response

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Satellites are non-coding tandemly repeated sequences very ubiquitous in genomes, yet knowledge about their biological relevance is still scarce. In plants, few described case examples point to roles in gene regulation and heterochromatin biology; however, a direct link to plant stress responses is yet to be uncovered. We present data demonstrating that particular tandem-repeats may display a central function in the intersection between epigenetic silencing and environmental gene expression. *Arabidopsis thaliana*'s imprinted *SDC* locus bears within its promoter a tandem-repeated area recognized as a transcriptional-gene-silencing target, which largely mediates epigenetic suppression and imprinting. Here we demonstrate that this area, possibly acting as *cis*-element/enhancer, is necessary and sufficient for *SDC* heat transcriptional induction in vegetative tissues with characteristic anatomical pattern. These results indicate that a non-coding tandem-repeat may actually exhibit *bona fide* dual roles, not only as a silencer at normal temperatures but also directly mediating expression-triggering upon stress. This implies a rather unusual form of abiotic transcriptional control, but we provide initial evidence suggesting that such type of regulatory influence might also be operative in some few protein-coding genes other than *SDC*. The observations thus emphasize the importance of satellites for plant environmental epigenetics.

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382
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Enviado por: Carlos Sanchez-Gomez

CHARACTERIZATION OF RIPE FRUIT EPIDERMIS-SPECIFIC TRANSCRIPTION FACTORS IN STRAWBERRY

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The epidermis is the external cell layer in direct contact with the environment, and it plays essential biological roles. Transcriptome analysis (RNA-seq) of *Fragaria vesca* fruit receptacles at four ripening stages and of different tissue types of receptacles (pith, vascular bundles, cortex and epidermis) at two ripening stages (green and red) allowed us to infer tissue- and stage-specific Gene Regulatory Networks (GRN). Due to the potential role of the epidermis in defense and in the differential anthocyanin accumulation pattern that shows *F. vesca* fruits at the ripe stage, we have focused on the GRN of the epidermis of red receptacles. In this study, we aim at the functional characterization of two transcription factors (TFs) that constituted the main hubs: a MYB-like gene, and a member of the NAC family of TFs. MapMan analysis of the GRN showed that wax and flavonoid biosynthesis were significantly overrepresented functions. Using the Luciferase/Renilla system, the interaction of the MYB and NAC TFs with their wax-related putative targets was validated. To experimentally validate the target genes of these two TFs, their binding sites were mapped genome-wise using DAP-seq analyses. Consistently, MYB bound to genes involved in cuticle formation and flavonoid biosynthesis, while genes involved in solute transport were enriched among NAC targets. Finally, protein interaction assays showed that MYB physically interacts with two members of the bHLH family specifically expressed in the red epidermis, leading to the subcellular relocalization of one of them from the cytoplasm to the nucleus.

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383
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Area: Biotic Interactions
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Enviado por: Gemma Sans Coll

CHARACTERIZATION OF THE TRANSLATIONAL LANDSCAPE OF THE PLANT-VIRUS INTERACTION

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Viral diseases are a main limiting factor for agronomic production. Viruses require the host’s cellular machinery to be able to infect, which implies complex interactions between it and the plant. Knowledge of the regulation of these interactions is essential for the design of effective and durable control strategies. Most studies are based on transcriptomics and interactomics, while translatomics analyses have, so far, been scarce despite the importance of the interaction between the virus and host’s translation machinery. This project’s objective is to characterize the translational landscape of the interaction between Tomato yellow leaf curl virus (TYLCV) and tomato plants. We’re using Ribo-Seq to identify the translational changes that occur in response to infection by TYLCV and to characterize the translation of viral genes. We are using two isogenic tomato lines: *ty-5* mutant, tolerant, and Santa Clara, susceptible. Ty-5 contains a recessive mutation located on the Pelota gene, which is involved in the recycling phase of the translational cycle[1]. The study of this mutant will give additional information about the role the translational machinery plays in the viral infection. In addition, using RNA-IP, we’re attempting to uncover the translational machinery associated to viral transcripts so that we can determine whether certain riboproteins or translation factors are preferred over others. We will present the advances we have made regarding these objectives.

[1]Lapidot et al. (2015). PLoS Genet. 11:e1005538

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384
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Enviado por: Jacqueline Santos

Multigenic regulation in the ethylene biosynthesis pathway during coffee flowering

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The ethylene hormone regulates different aspects of the plant life cycle, such as flowering, and acts as a defense signal in response to environmental stresses. Changes induced by water deficit in gene expression of the main enzymes involved in ethylene biosynthesis, 1-aminocyclopropane-1-carboxylic acid synthase (ACS) and oxidase (ACO), are frequently reported in plants. In this study, ACS and ACO family genes were characterized. In silico identification and phylogeny of *Coffea arabica* genes were performed using similarity searches in genomes of plant species from different orders. Leaves, roots, flower buds, and open flowers from plants under well-watered (WW) and water deficit (WD) conditions, were used for gene expression analyses. Tree new genes were identified for the ACS family (CaACS2- like, CaACS3-like, CaACS7-like), but new genes did not identify for the ACO family (CaACO3-like, CaACO4-like, CaACO5-like). Under WD, all ACO genes were suppressed in roots and two ACO genes showed an expression level 6 times lower in leaves when compared to the WW. Despite the contribution of ACS genes, it is may suggest that the regulation of CaACO3-like and CaACO4-like in roots and leaves acts as the control point in the ethylene biosynthesis pathway in coffee during the wet and dry period. Especially in roots, ACO genes have been shown to play an important role in ethylene production during the dry period. These results help to explain the importance of the soil water variation during coffee flowering and, this mechanism may be a regulatory model for flowering in other woody species.

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385
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Area: Plant Hormones
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Drought and re-watering modify ethylene production and sensitivity, and are associated with coffee anthesis

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Coffee flowering requires a period of water deficit followed by rainfall to break flower bud dormancy and promote anthesis. Since drought followed by re-watering can increase shoot ethylene production. In this study, ethylene production changes in roots, leaves, and flower buds were investigated. In addition, ethylene biosynthesis genes, signaling pathways genes and, their relationship to coffee flowering was explored. Two experiments were conducted, in a greenhouse with coffee seedlings and a field, with different genotypes (Coffea arabica and Coffea canephora). Predawn leaf water potential, ethylene concentration, gene expression, and anthesis percentage were measured. The effect of 1-MCP (1-Methylcyclopropene), an ethylene action inhibitor, was also evaluated. Drought decreased foliar and flower bud ethylene production without changing root ethylene production, even though all tissues likely accumulated the ethylene precursor ACC (1-aminocyclopropane-1-carboxylic acid), as ACS gene expression was maintained, while ACO gene expression decreased. The ethylene receptor CaETR4-like was not differentially expressed in leaves under water deficit, but it was downregulated in roots. Re-watering restored shoot ethylene production, which seems important in promoting anthesis. 1-MCP triggered coffee anthesis without re-watering the plants, which hitherto was considered essential to allow flowering. 1-MCP positively regulated foliar and flower bud ethylene biosynthesis genes (CaACS1-like and CaACO1-like), similar to re-watering, and downregulated CaETR4-like. It suggests that changes in ethylene levels and sensitivity are required to promote coffee anthesis. Thus, drought and re-watering-induced changes in ethylene levels and sensitivity allow coffee flowering, while the growth regulator 1-MCP can potentially regulate anthesis time and intensity.

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386
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Enviado por: Gonzalo J. Sartor

Evaluation of different sowing dates in two cotton genotypes on seed cotton yield and fiber quality parameters.

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Production of all agronomic crops, such as cotton (*Gossypium hirsutum* L.), is governed by three primary factors: genotype, environment and cultural practices and their interaction. Based on different crop management practices, we could optimize the use of available environmental resources to improve production. The selection of an optimal sowing date is an important management decision since it could increase lint yield and quality. The aim of this work was to evaluate the combination of two commercial cotton varieties (NuOpal and DP 1238) on different sowing dates. A field experiment was carried out using eight different sowing dates distributed from the beginning of September to the end of December of 2020. Agronomic traits such as lint yield and quality and phenological development parameters were evaluated. The results showed significant differences in lint yield between sowing dates and varieties without interactions between them. The intermediate sowing dates of October 30 and November 11 presented 50% higher seed cotton yields in comparison with others sowing dates. The lint percentage was higher in early sowing dates (first and second). Lint quality parameters showed significant differences between sowing dates and cultivar. The eighth sowing date showed the greatest lint length, micronaire, uniformity index and strength. On the other hand, late sowing dates exhibited shorter cycle than early sowing dates due to the effect of higher temperatures that could accelerated the development in both cultivars. The correct election of sowing date is one of the main agronomic practices that influence the lint yield and quality of cotton.

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387
CM896PJ
Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Gonzalo Scarpin

Effect of row spacing and nitrogen fertilization on radiation use efficiency of two cotton cultivars

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Radiation use efficiency (RUE) is one of the variables that influence on the dry matter accumulation of plants, including crops such as cotton (*Gossypium hirsutum* L.). Several researchers have shown that RUE may change with different management practices. However, no reports are available demonstrating the effect of row spacing and nitrogen fertilization on the RUE of cotton in Argentina. Thus, the aim of this study was to evaluate the effect of these two management variables on the RUE of two cotton cultivars (Nuopal and DP 1238). A field study was conducted at the National Institute of Agricultural Technology (INTA) Reconquista (Santa Fe province) in 2019/2020. The experiment included the evaluation of two row spacings: conventional (C) and narrow row (NR) and a nitrogen fertilization with 100 $kg.ha^{-1}$ of urea (N100), in comparison with the unfertilized control (N0). The results showed that C and N100 presented highest RUE without differences between cultivars. Average RUE values for C-N100, C-N0, NR-N100 and NR-N0 were 1.55, 1.42, 1.22 and 1.08 $g.MJ^{-1}$, respectively. The higher RUE in C could be due to light distribution and shading effects, whereas the higher RUE in N100 could be due to an increase in dry matter accumulation. The results of this study may contribute to adjusting management practices with eco-physiological bases and to providing local data for crop modeling.

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388
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Area: Biotechnology, Research Tools, Resources
Tipo de presentación: Poster en formato PDF
Enviado por: Juan Pablo Selva

Characterization of EcROS1-like, a putative gene indirectly involved in apomixis in Eragrostis curvula

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Eragrostis curvula is a forage grass naturalized in semi-arid regions of Argentina that reproduces by diplosporous apomixis, having mainly facultative genotypes that retain certain percentage of sexual pistils that increase under drought and other stressful situations, indicating that some regulators activated by stress could be affecting the apomixis/sexual switch. Our previous results showed increases in the percentage of sexual embryo sacs when facultative plants were exposed to drought and other abiotic stresses. Interestingly, the EcROS1-like gene was found differentially expressed between apomictic plants growing under normal and water stress conditions, being up-regulated in stressed plants. Repressor of Silencing 1 (*ROS1*) is involved in DNA de-methylation on certain genes and, based on the hypothesis that sexual pathways are repressed but intact in facultative apomictic plants, it could explain the increases in sexual embryo sacs observed under stress situations. The objective of this work was to assess the genomic structure of the gen *EcROS1*-like and find out allelic differences in full apomictic, facultative and sexual genotypes. Genomic and transcriptomic sequences were used as templates to perform cloning validations and compare the structure between genotypes with contrasting reproductive modes. The genomic structure shows that EcROS1-like is composed by a total of 10759bp including UTRs, 20 introns and 21 exons. Five different isoforms were found in the facultative cultivar DW and four in the obligate and sexual genotypes. These results will be useful to understand the role of this gene and its alleles and its association with the reproductive mode of *Eragrostis curvula*.

389
RM935DJ
Area: Biotic Interactions
Tipo de presentación: video presentacion
Enviado por: PALOMA SERRA

ROLE OF FLAVONES BIOSYNTHESIS AND SALICYLIC ACID METABOLISM IN BIOTIC STRESS RESPONSES.

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Two different types of flavone synthases (FNS I and FNSII) catalyze the biosynthesis of the main flavone, apigenin. In *Arabidopsis thaliana*, *Downey Mildew Resistant 6* (*DMR6*) encodes an FNS I type enzyme. *dmr6* mutant plants show increased resistance against *Pseudomonas syringae* pathogen, which is associated to an accumulation of salicylic acid (SA). When we complemented *dmr6* plants with FNS I and II from maize, there was a restoration of susceptibility to the pathogen infection. Thus, the aim of this work is to study the possible interconnection between flavones synthesis and SA metabolism. We analyzed the susceptibility against *P. syringae* infection in Arabidopsis wild type, transgenic and mutant plants in the *SALICYLIC ACID 3-HIDROXYLASE* (*S3H*) gene. S3H catalyzes the conversion of SA to 2,3-dihydrobenzoic acid. Therefore, *s3h* mutants accumulate SA, which results in enhanced resistance to pathogen infection. Transgenic plants used in this experiment express FNS I and II enzymes from maize in a mutant *s3h* background. These lines exhibited restoration of susceptibility to Pseudomonas infection. We also quantified the SA and apigenin levels in transgenic lines post-infection, showing that restoration of susceptibility is a consequence of a decrease in SA levels and apigenin accumulation. In order to analyze if other flavonoids were involved in the response of plants to biotic stress, infection experiments were performed using plants with mutations in genes of the flavonoids biosynthetic pathway. In addition, we analyzed the possible regulatory effect of flavonoids on the expression of genes associated with SA metabolism using RT-qPCR.

390
RH522HF
Area: Epigenetics, Chromatin, non-coding RNAs, RNA biology
Tipo de presentación: Poster en formato PDF
Enviado por: Lucas Servi

Impact of alternative splicing on Arabidopsis thaliana. Splicing factors and the role of non-coding isoforms.

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Light signals induce a massive reprogramming of gene expression in plants. Alternative splicing (AS) produces multiple mRNAs (variants or isoforms) from a single gene through the variable, and regulated, choice of different splicing sites. In addition to generating several isoforms that can be translated into different proteins, this process can also give rise to variants without coding capacity, allowing a fine control of protein levels. The non-coding AS-derived isoforms could be also acting as long non-coding RNAs (lncRNAs). These regulatory RNAs can control chromatin status, modulate the abundance of other RNAs, and affect translation. Light regulates the AS in *A. thaliana*, including the gene At-RS31. Changes in the splicing patterns of this gene modulate the amount of protein generated (splicing factor), since only one isoform is translatable, mRNA1. Although the overexpression of mRNA1 generates deleterious phenotypes, by overexpressing all the variants (genomic construction), the resulting plants present normal phenotypes. We previously demonstrated that the other predominant isoform of At-RS31, mRNA3, is retained in the nucleus. These findings invited us to hypothesize that this transcript could be fulfilling a nuclear regulatory function, being a lncRNA generated by AS. This reasoning led to the bioinformatics search for other potential transcripts showing similar characteristics. For this, the differential expression of the isoforms of *A. thaliana* was analyzed in multiple RNAseq (from public repositories) linked to RNA translation, degradation, and localization. As a result of this analysis, we found numerous novel candidates, which resemble the At-RS31 mRNA3 and could function as lncRNAs in Arabidopsis.

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391
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Area: Developmental Biology
Tipo de presentación: Poster en formato PDF
Enviado por: Nicolás Setzes

A mitochondrial ADX-ADXR-P450 shuttle is essential for HOMOCASTASTERONE SYNTHESIS in gametophytes of A. thaliana.

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Gametophytes are haploid structures where gametes are specified, which make them essential for plant reproduction. We have identified and studied Arabidopsis mutants with an insertion in a nuclear gene encoding for a mitochondrial adrenodoxin reductase (ADXR) that display female gametophyte development defects and aberrant embryogenesis. In mammals and insects adrenodoxin (ADX) mediates the electron transfer from NADPH towards a cytochrome P450 (P450) in a reaction catalyzed by adrenodoxin reductase (ADXR) that constitutes the first step in steroid hormones synthesis. Through Y2H studies and bimolecular fluorescence complementation assays, we have established that three Arabidopsis P450s (CYP711A1, CYP90A1, CYP75B1) interact with ADX1. We demonstrated that these P450s have mitochondrial localization by co-localization experiments in *N. benthamiana* and in stable transformants of Arabidopsis. However, *knockout* mutant lines for these P450s do not show gametophytic defects. Since this could be due to functional redundancy, we obtained double and triple mutants. We found that although double hemizygous mutants didn't show any defects, the *cyp711a1, CYP90A1/cyp90a1, cyp75b1* triple mutant showed a percentage of aborted seeds that suggested a gametophytic defect. The analysis of embryo sacs under DIC microscopy showed developmental defects similar to those found in *ADXR* mutants. Moreover, these defects in both the triple mutant and the *ADXR* mutant were partially rescued by the addition of the steroid hormone homocastasterone (HCS). As an active brassinosteroid in plants, HCS takes part in the regulation of plant development and may be of key importance for both the female gametophyte and embryo development.

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392
BR792NN
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: María Luján Sheridan

E2Fb and E2Fa transcription factors independently regulate UV-B responses in Arabidopsis

E2Fb and E2Fa transcription factors independently regulate UV-B responses in Arabidopsis

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UV-B radiation affects plant growth inhibiting cell proliferation. This inhibition is in part controlled by the activity of transcription factors of the E2F family. In particular, the participation of E2Fc and E2Fe in responses to UV-B in Arabidopsis plants was previously reported. However, the contribution of E2Fa and E2Fb in these processes has not been yet investigated. Thus, in this work, we provide evidence that, in Arabidopsis, both E2Fa and E2Fb control leaf size under UV-B conditions without participating in DNA damage repair. On the contrary, in seedlings exposed to UV-B, E2Fa but not E2Fb regulates primary root elongation, cell proliferation and programmed cell death in the meristematic zone. Using *e2fa* mutants that overexpress *E2Fb*, we here demonstrate that the role of E2Fa in the roots cannot be replaced by E2Fb. Finally, the results presented show that E2Fa and E2Fb differentially regulate the expression of genes that activate the DNA damage response, both under conditions without UV-B and after exposure. Together, we here show that both E2Fa and E2Fb have different and non-redundant roles in developmental and DNA damage responses in Arabidopsis plants exposed to UV-B radiation.

393
FJ689HN
Area: Abiotic Stress
Tipo de presentación: video presentacion
Enviado por: Bruna Evelyn Paschoal Silva Bruna

Effects of elevated carbon dioxide on photosynthetic parameters and on pseudo-cereal carbohydrate metabolism

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Climate change caused by increased emissions of greenhouse gases like carbon dioxide (CO_2) will impact many activities around the world and these effects on agricultural production could be large. Thus, the objective of this research was to evaluate the gas exchange and carbohydrates metabolism in plants of *Chenopodium quinoa* and *Amaranthus cruentus* subjected to an increase in CO_2. Seeds of BRS Piabiru and BRS Alegria cultivar were used, cultivated in open-top chambers with 400 and 700 ppm of CO_2. At the end of the vegetative stage, we evaluated the gas exchange, and the plants were collected, and the total amount of soluble sugars, starch, sucrose, water-soluble polysaccharides, and total amino acids was quantified. It was possible to observe significant changes of photosynthetic parameters and an increase of total soluble sugars, starch, sucrose for both species when in 700 ppm of CO_2. However, for water-soluble polysaccharides and total amino acids content, there was no significant change. Therefore, we can conclude that the accumulation of assimilates in 700 ppm was larger because, possibly, there has occurred a positive regulation of metabolic parameters like photosynthesis maintaining homeostasis.

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394
RD624KH
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Antonia Almeida da Silva Antonia

Photosynthetic metabolism of sugarcane plants exposed to high concentration of CO2 in the air and to drought

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In theory, C4 plants do not respond to increased concentrations of atmospheric CO_2 [CO_2], due to their concentration mechanism. However, sugarcane plants (Saccharum spp.) may respond to this increase, suggesting that there is inefficiency in the concentration mechanism. Thus, the objective was to identify the key processes involved with this inefficiency in sugarcane plants. The study was conducted in open top chambers using two sugarcane varieties (RB867515 and RB855536) grown in environments with two [CO_2] (380 and 680 ppm) and exposed to water restriction. Biomass accumulation, A/Ci and A/Q curves under high (21%) and low O_2 concentration (2%) were analyzed. Both varieties, when subjected to water deficit, showed less accumulation of biomass, and the high [CO_2] favored the increase between the different tissues. This concentration led to decreases in the PEPcase enzyme carboxylation rate, while that of Rubisco was maintained. There was an increase in the quantum efficiency of carboxylation under high CO_2 without influencing photosynthesis, indicating a decrease in CO_2 leakage under these conditions. During measurements with 2% O_2 and 380 ppm CO_2, there was an increase in Rubisco activity, suggesting a limitation in photosynthesis by photorespiration. Thus, it is concluded that under the current condition of CO_2 the photosynthetic process of sugarcane plants can be limited by the higher carboxylation velocity of PEPCase in relation to Rubisco, which leads to CO_2 leakage, resulting in lower quantum efficiency of carboxylation.

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395
SS279GJ
Area: Abiotic Stress
Tipo de presentación: video presentacion
Enviado por: Mariana Silva Artur

Fine drying: Plant preparation for the dry state

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Resurrection plants and orthodox seeds survive after losing almost all water from their cells. This astonishing desiccation tolerance (DT) ability allows these organisms to remain alive in the dry state for long time. For that, their cells are protected by compounds such as Late Embryogenesis Abundant (LEA) proteins. We found that *LEAs* are conserved within clusters of desiccation-associated genes in the resurrection plant *Xerophyta viscosa* and show sequence conservation in land plants. Furthermore, we found that the protective ability of *X. viscosa* LEAs correlates with their intrinsically disordered sequence and ability to undergo disorder-to-order transitions under stresses. Despite their undeniable importance, little is still known about how these proteins are regulated in seeds. Most *LEA* genes are expressed during seed maturation, but the proteins accumulate only when the seeds are drying. **Our current work focus on elucidating how LEA gene expression, mRNA translation and protein accumulation are regulated during seed development**. By exploring the transcriptome and translatome of developing and dried seeds of the model plant *Arabidopsis thaliana* we will identify what regulatory pathways are controlled by drying. We will then test the role of drying on regulating LEAs in seeds and vegetative tissues. Finally, we will study what are the mechanisms involved in *LEAs* mRNA translation and protein accumulation. Our preliminary results point toward the presence of translation-related sequence features involved with LEAs accumulation in dry cells. This pioneering research on the regulation of DT is also of great relevance for plant conservation, agriculture and food security.

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396
RR374TS
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Rafael Freitas

Do changes in light supply during growth affect stomatal time response to light?

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Stomata are small epidermal pores responsible for strict control of the amount of CO_2 that diffuses into the leaf, while controlling the concentration of water vapor lost to the atmosphere. The stomatal activity is sensitive to variations in surrounding environment and its optimization is linked to an efficient hydraulic conduit system. Here we investigated leaf hydraulic and morphoanatomical changes associated with light availability in *Podocarpus macrophyllus*, *Eucalyptus urophylla* and *Capsicum chinense* plants, aiming at understanding whether these changes would translate into alterations in stomatal kinetics. Plants were grown under full sunlight or intense shade (10% of direct solar radiation). Shading reduced leaf hydraulic conductance and stomatal density, but not stomatal length for the three woody species. However, both stomatal opening time (time required for stomatal conductance to increase by 90% after a step increase in light intensity) and stomatal closing time (time required for stomatal conductance to decrease by 90% after a step decrease in light intensity) were mostly unaffected by the light condition during growth. Our findings demonstrate that the stomatal response time to dynamic changes in light is likely genetically regulated and thus essentially unaffected by growth light conditions.

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397
GB224PM
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Lucio Simonelli

“Effects of UV-B radiation on primary root elongation of different Arabidopsis thaliana ecotypes”

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Because of their sessile condition, plants are continuously exposed to solar radiation. One component of the solar spectrum is UV-B radiation (280-315 nm). Besides acting as a photomorphogenic signal, UV-B radiation at high intensities can damage the DNA, lipids and proteins. In addition, it can inhibit plant growth and elongation of primary root elongation. In particular, inhibition of primary root elongation after UV-B exposure occurs after exposure to UV-B intensities that produce DNA damage in Arabidopsis; however, the molecular pathway that regulates this process has not been investigated.

In this work, we studied the responses of primary roots upon exposure to UV-B using five different *A. thaliana* ecotypes (Col-0, Col-3, Col-4, WS and LER). Previously, the inhibition of Arabidopsis primary root elongation after UV-B irradiation was correlated to a decrease in the length and in the number of cells of the meristematic zone of the primary roots in Col-0. The primary roots of all ecotypes were significantly shortened by UV-B, with Col-3 showing a more significant inhibition than the other ecotypes. This higher inhibition correlated with a higher decrease in the meristematic zone size, having less cells after the treatment. Interestingly, both Col-3 and Col-4 had a lower number of dead cells after a UV-B treatment than the other ecotypes, which are produced after irradiation. Our results show that primary roots from different Arabidopsis ecotypes respond differently to a similar UV-B exposure, suggesting that natural variation exist in this response.

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HC918HD
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: João Antonio Batista de Siqueira

"A long and stressful day": the photoperiod significance for aluminium tolerance in plants

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Aluminium (Al) is a limiting factor for crop productivity in acidic soils (pH ≤ 5.5), imposes drastic constraints for food safety in many developing countries. The major mechanisms that allow plants to cope with Al stress reflects from manipulations of organic acids metabolism and DNA-checkpoints. Nevertheless, when assumed individually both approaches have been demonstrated to be insufficient to overcome Al toxicity. Furthermore, acid soils distribution on Earth cannot adequately explain the differential Al tolerance across the plant kingdom. On analysing the centre of origin of most cultivated plants, we hypothesised that day-length may be a pivotal agent modulating Al tolerance across distinct plant species. We observed that with increasing distance from the Equator, Al tolerance decreases, suggesting a relationship with the photoperiod. Long-day (LD) species are generally more Al-sensitive than short-day (SD) species, whereas genetic conversion of tomato for SD growth habit boosts their Al tolerance. Reduced Al tolerance correlates with DNA-checkpoints activation under LD. DNA-checkpoint-related genes are under positive selection in Arabidopsis accessions from regions with shorter days, suggesting photoperiod may act as a selective barrier for Al tolerance. Our findings revealed that diel regulation and genetic diversity affect Al tolerance, suggesting that day-length orchestrates Al tolerance. Altogether, photoperiodic control of Al tolerance might contribute to solve the historical obstacle that imposes barriers for developing countries to reach a more sustainable agriculture.

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399
JS764NN
Area: Biochemistry and Metabolism
Tipo de presentación: Poster en formato PDF
Enviado por: Paulo Souza

The NADPH-dependent thioredoxin reductase (NTR) system is important, but not essential for plant growth

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Thioredoxin (Trx) is a family of ubiquitous proteins capable to reduce target proteins, which alters their activities and thus regulate the metabolic fluxes through different metabolic pathways, such as photosynthesis and (photo)respiration. To gain catalytic power, Trxs must fiberst reduced. In the chloroplast, there are two enzymes responsible for reducing Trx, namely ferredoxin thioredoxin reductase (FTR) and NADPH-dependent thioredoxin reductase C (NTRC). In mitochondria and cytosol, the enzymes capable of reducing Trxs are NTRA and NTRB. Whilst the *ntrc* mutant and the double *ntra ntrb* mutant have been characterized, information regarding the characterization of the triple *ntra ntrb ntrc* mutant is missing. Here, aiming to fulfill this gap, we characterized Arabidopsis mutant plants knockout for all NTR proteins. Intriguingly, plants lacking NTR proteins remains viable, which contrast with the essentiality of NTR proteins in animal cells. Multivariate analysis of the metabolite profiling of leaves harvested at the end of day(ED) and at the end of night(EN) indicates the metabolite profile of the triple mutant is highly similar to the *ntrc* mutant at ED and to the *double* mutant at EN. These results suggest the lack of NTR proteins is likely compensated by additional redox systems at different cell location. Indeed, no difference in in the content of pyridines between WT and the triple mutant was observed. Our study highlights the complexity of the plant redox system, in which the lack of the NTR system substantially reduce plant growth, but the viability of the plant is still maintained by compensatory systems.

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400
DB544FS
Area: Biochemistry and Metabolism
Tipo de presentación: Poster en formato PDF
Enviado por: Bruna Regina Souza Alves Alves

Oxidative stress in pinto beans plants submitted to heavy metals

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Brazil is the world’s third-largest producer of beans (Phaseolus vulgaris L.), producing around 3.104 million tons per year with Minas Gerais being the main producer in the country. However, after November of 2015, the state suffered one of the largest environmental disasters in Brazil’s history, leading to extensive contamination of the environment by heavy metals, including iron (Fe_2O_3) and zinc (ZnO). Thus, the objective of this research was to evaluate biochemical changes, induced by different concentrations of iron and zinc in pinto bean plants. Seeds of the BRS Madreperola cultivar were used, cultivated in a substrate (Plantmax®). Upon reaching growth stage V2, they were transferred and acclimatized into a hydroponic system of floating root and continuous flow in a nutrient solution, half strength of Hoagland and Arnon (1938), containing different concentrations of Fe_2O_3 (0.0; 5.0; 10.0 and 20.0 mg L-1) and ZnO (0.0; 5.0; 7.5; and 10.0 mg L-1), and remaining on it for more seven days. After this period, the biochemical analysis occurred, being Antioxidant Enzyme Activity, Lipid Peroxidation, and Peroxide Content. It was possible to observe a significant increase in activity of Superoxide Dismutase, Ascorbate Peroxidase, Catalase, and the Malondialdehyde content, but for Hydrogen Peroxide content, there was no significant change. Therefore, we can conclude that iron and zinc metals are harmful to the antioxidant system causing oxidative damage and possible deleterious consequences for the pinto beans plants at the vegetative stage.

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401
PL969DQ
Area: Other
Tipo de presentación: video presentacion
Enviado por: Fiorella Spies

The interacting transcription factors PHL1 and AtHB23 stimulate carbohydrate transport from source to sink tissues

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Carbohydrates are produced in green tissues through photosynthesis and then transported to sink tissues. Carbon partitioning is a strategic process, fine regulated, involving specific sucrose transporters in each connecting tissue. Here we report that a screening of an Arabidopsis transcription factor (TF) library using the homeodomain-leucine zipper I member AtHB23 as bait, allowed identifying the TF AtPHL1 interacting with the former. An independent Y2H assay, and *in planta* by BiFC, confirmed such interaction. AtHB23 and AtPHL1 coexpressed in the pedicel-silique nodes and the funiculus. Mutant plants (*phl1* and *amiR23*) showed a marked reduction of lipid content in seeds, although lipid composition did not change compared to the wild type. While protein and carbohydrate contents were not significantly different between mutants and control mature seeds, we observed a reduced carbohydrate contents in mutant plants' young siliques. Moreover, using a CFDA probe, we revealed an impaired transport to the seeds, and the gene encoding the carbohydrate transporter *SWEET11*, usually expressed in connecting tissues, was repressed in the *amiR23* and *phl1* mutant plants. Altogether, the results indicated that AtHB23 and AtPHL1 act together, promoting sucrose transport, and the lack of any of them provoked a reduction in seeds lipid content.

420
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Enviado por: Cássia F. Stafen

A survey of public datasets for the identification of shoot light-responsive genes in Arabidopsis thaliana

A survey of public datasets for the identification of shoot light-responsive genes in Arabidopsis thaliana

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Light is essential for photosynthesis and directly influences plant growth and development. Arabidopsis seedlings grown under light, display a photomorphogenic development pattern, showing short hypocotyl and long roots. The early transcriptional responses to light that stimulate the communication between shoots and roots are still unknown. Aiming to elucidate how early photomorphogenic signaling in shoots might affect root growth we performed a survey comparing commonly regulated genes in public datasets of transcriptomic studies from etiolated seedlings exposed to short light treatments. Comparing datasets derived from short light exposures (30 to 60 minutes) to longer exposures (4 to 6 hours), we demonstrate that light strongly affects the gene expression of the shoot, triggering signaling and redox responses. We identified that the regulation of transcription of the early light response is centered on the ABA-Insensitive5 (ABI5) transcription factor along with ABA-responsive bZIP factors (ABFs). We observed that some abf mutants display a higher chlorophyll content with increasing light exposure, when compared to the wild type. Promoter reporter lines exposed to light increase their expression in roots, suggesting a role as positive photomorphogenic regulators. We propose that early light responsive gene expression in shoots repurposes dark-expressed ABA-responsive bZIP transcription factors to activate photomorphogenic responses.

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421
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Area: Developmental Biology
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Enviado por: Carlos Guillermo Bartoli

Ethylene regulates H2O2 production during tomato fruit ripening

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Previous works demonstrated the participation of H_2O_2 during tomato fruit ripening. A peak in H_2O_2 production is observed at green-red transition stages in wild type tomatoes. Fruits of ascorbic acid deficient plants with increased concentration of other antioxidants do not present the peak of this oxidant and show a delayed senescence. A combined high irradiance and temperature treatment accelerates ripening what is accompanied by an increase in the H_2O_2 production in fruits of wild type and ascorbic acid deficient plants. To further characterize the function of H_2O_2 during tomato ripening its association with ethylene signaling was studied. The experiments were conducted with wild type and ascorbic acid deficient Micro-Tom plants grown under greenhouse conditions. Treatment with 1-aminocyclopropane-1-carboxylic acid (ACC, an ethylene precursor) accelerated the progress of fruit ripening in all genotypes and treatment with 1-methylcyclopropene (1-MCP, an ethylene inhibitor) provoked the opposite effect. H_2O_2 peroxide production was largely increased or decreased in all genotypes after ACC or 1-MCP treatments, respectively. However, lipid peroxidation, ascorbic acid and glutathione contents were not altered by these treatments.

These results suggest the participation of H_2O_2 downstream of ethylene in the signaling pathway regulating the development of fruit ripening. The analysis of the expression of genes involved in ethylene signaling and synthesis and other specifically induced by H_2O_2 that is now in progress will give more insights in the hormone-redox interaction.

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422
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Area: Biotic Interactions
Tipo de presentación: video presentacion
Enviado por: Daniela Sueldo

Extracellular ATP induces photo bleaching and cell death in Arabidopsis

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Plant cell death involves tightly controlled signalling cascades that can be genetically or chemically modulated. Environmental stress can lead to cell death, and accurate control is key to minimise tissue damage whilst conferring adaption. Despite having a significant impact on crop performance, the mechanisms that plants use to control cell death propagation are largely unknown. We hypothesise that cell-cell communication, mediated by molecules acting as ‘death’ or ‘life’ signals, is instrumental for the control of plant cell death spatiotemporal propagation. Purine nucleotides (ATP, UTP and derivatives) are well described signalling molecules in animals, where they mediate cell death upon injury and during immune responses. In plants, extracellular ATP (eATP) has been identified as a key signalling molecule involved in several physiological processes such as stomatal closure, pollen tube growth, and response to environmental stress. Cell damage (i.e., upon biotic stress) is considered a source of plant eATP and changes in eATP concentration in the apoplast lead to cell death, suggesting eATP can act as a death signal. However, the adaptive role of eATP-cell death and its relation to other types of stress-triggered cell death pathways is poorly understood. At this conference, we will discuss the effect of ATP and derivatives on the viability of Arabidopsis seedlings and the induction of cell death programs. Furthermore, we will present preliminary data aimed at the establishment of new model species to study eATP physiology in plants.

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423
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Area: Epigenetics, Chromatin, non-coding RNAs, RNA biology
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Enviado por: Vivek Hari Sundar G

Rice RNA polymerase IV modulates small RNAs and epigenetic fates

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Aspects of epigenetic regulation in plants are peculiar and remarkable in innumerable ways. One such novelty is the evolution of additional DNA dependent RNA polymerases in land plants. These novel polymerases generate a large pool of non-coding RNAs that establish DNA methylation *de novo* and hence the epigenome. RdDM directs epigenetic regulation of several genomic loci aiding in transposon inactivation, imprinting, growth and development, postzygotic hybrid barriers and also in genome stability.

We probe the implications of this machinery in rice, a plant with complex genome architecture rich in repeats and transposons. Loss of function of RdDM resulted in transgressive reproductive defects in rice unlike the model plant *Arabidopsis*. Small RNA profiles, genome-wide DNA methylation status and tissue specific transcriptomes revealed perturbation to a great extent upon loss of RdDM. We also evidence transposon proliferation in the mutants. Taken together, these analyses reveal the strong multifaceted influence of the machinery on several epigenetic layers unlike observed in the plants with less complicated genomes.

424
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Area: Biotic Interactions
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Enviado por: Juan Manuel Sánchez

YIELD COMPONENTS INTERACTIONS IN SOYBEAN SIBLING LINES WITH VARIABILITY IN THE NUMBER OF SEEDS PER POD AND SEED WEIGHT

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Soybean yield is a complex quantitative trait controlled by genetic and environmental factors. The main soybean yield components are seed number (SN) and seed weight (SW). SN is the result of pod number (PN) and the number of seed per pod (SPP). The relations between these yield components at canopy level are incompletely understood. In this study, we assessed the association between the yield components PN, SPP and SW, using sibling lines with variability in SPP and SW. A field experiment was conducted at the Faculty of Agricultural Sciences, National University of Rosario, during 2019/20 growing season. A total of 29 lines plus a commercial variety were sown at two densities: 12 and 24 plants.m^{-2}, respectively. The experimental design was a randomized block with three replications. Data was subjected to principal components analysis and Pearson's correlation. For both densities, yield was positively associated with PN (r=0.5; p<0.01) and SPP (r=0.6; p<0.01) but negatively associated with SW (r=-0.4; p<0.05). The SPP showed a positive correlation with SN (r=0.5; p<0.05) but low and non-significant correlation with PN (r=-0.2; ns) and SW (r=-0.3; ns). Conversely, strong negative correlation was found between SW and PN (r=-0.7; p<0.001). The results confirmed the hypothesis that the increase in SPP will have a positive impact on SN without negative effect on PN and SW. Thus, the incorporation of the high SPP trait becomes a useful strategy to enhance soybean yield potential.

425
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Area: Developmental Biology
Tipo de presentación: Poster en formato PDF
Enviado por: Victoria Sánchez-Vera

Autophagy is required for strawberry fruit ripening

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Autophagy is a catabolic and recycling pathway to maintain cellular homeostasis under normal growth and stress conditions. During macroautophagy, hereafter referred as autophagy, cellular content is engulfed by a double-membrane vesicle called autophagosome. This vesicle fuses its outer membrane with the tonoplast and releases the contents into the vacuole for degradation. During certain developmental processes, autophagy is enhanced by induction of several autophagy-related genes (*ATG* genes). Fruit ripening is a developmental process that involves changes in cell size, color, metabolic conversion of molecules, events in which autophagy-related processes could be having a yet unknown role. Strawberry is an important berry crop, representative of non-climacteric fruit. We have analyzed the occurrence of autophagy in developing and ripening fruits of the cultivated strawberry. At the cellular level, we confirmed the presence of autophagy related structures at different stages of the strawberry ripening using electron microscopy analyses. At the molecular level, our data show that most *ATG* genes are conserved in the genome of the cultivated strawberry *Fragaria x ananassa* and they are differentially expressed along the ripening of the fruit receptacle. Protein expression and ATG8-lipidation analyses indicated the occurrence of two autophagic waves during ripening. Finally, blocking autophagy either biochemically or genetically dramatically affects strawberry ripening. Our data support that autophagy is an active and essential process with different implication during strawberry fruit ripening.

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426
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Enviado por: Moab Andrade

Plant hydraulic efficiency limits photosynthesis in the auxin perception mutant diageotropica

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Auxins are known to regulate leaf morphology, anatomy, and xylem development in plants, however, the functional effects of this hormone on water transport efficiency and photosynthetic capacity are yet to be determined. Here we utilized tomato plants of *diageotropica* mutant (*dgt*) and its wild type (WT) to explore whether a decreased auxin perception affects plant hydraulic conductance and leaf gas exchange. The xylem conduits of *dgt* plants showed a reduced hydraulic weighted vessel diameter (D_h) (43%) and conduit number (25%) in petioles as well in stems (24 and 58%, respectively), resulting in lower theoretical hydraulic conductivity (K_t); on the other hand, no change in root D_h and K_t were observed. Interestingly, the measured stem and leaf hydraulic conductances of *dgt* plants agreed with the theoretical values and were lower by 81 and 21%, respectively; however, despite presenting similar root D_h and K_t when compared with WT plants, the measured root hydraulic conductance of *dgt* plants was 75% lower. The *dgt* mutation increased the density of minor veins (VD) and stomata (SD), which could potentially increase photosynthesis. Nevertheless, the *dgt* plants showed a photosynthetic rate *c.* 25% lower over the wild type, coupled with a stomatal conductance reduction of 52%, resulting in a 55% higher instantaneous water use efficiency. These results suggest that the impairment of the hydraulic efficiency of the *dgt* plants might have counteracted the increases in VD and SD, ultimately limiting the leaf water supply for leaf gas exchange.

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427
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Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Noelia Romina Tabernero

IDENTIFICATION OF BIOMARKERS IN Salvinia minima PLANTS EXPOSED TO CHROME HEXAVALENT

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Water resources contamination of by Cr(VI) is a serious problem due to its persistence, bioaccumulation in tissues and biomagnification along trophic chains. Cr(VI) is used in several industrial processes and reaches water bodies through the uncontrolled discharge of effluents. Effluent treatment is essential to reduce its impact and facilitate the rehabilitation of contaminated environments. Phytoremediation is an economical option to be implemented as part of these treatments. Exposure of plants to heavy metals triggers metabolic and physiological responses, which can be used as biomarkers during pollutants induced stress. Thus, the objective of the present work was to identify metabolites that can be used as early or late alarm signals in the presence of the contaminant. For this, *S. minina* plants were grown in the presence or absence of Cr(VI) during 7 days. The contents of H_2O_2, MDA, soluble phenols (FS) and insoluble (FI), thiolic compounds and sucrose, were determined spectrophotometrically. It was observed that MDA was a relevant parameter as an early marker of chromium stress in fronds. On the other hand, sucrose and FI levels increased late, both in fronds and lacinias, during exposure to chromium. The H_2O_2 content only increased towards the end of the trial, in response to prolonged exposure to the contaminant. These results show the feasibility of using these parameters as markers in future research aimed at characterizing and optimizing the use of *S. minima* in phytoremediation treatments.

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428
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Enviado por: Amalia Chiesa

Effect of autochthonous isolates of Streptomyces spp. on growth, development and plant protection in soybean

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One of the biggest challenges facing the world is to increase food production from agriculture, minimizing the impact on the environment, mainly on the soil. A sustainable and eco-friendly strategy to reduce the intensive use of agrochemicals is its replacement by plant growth-promoting rhizospheric beneficial microorganisms. In this work, seventy-eight actinobacteria belonging mainly to the genus *Streptomyces* were isolated from the rhizosphere of soybean plants from the core productive zone of Argentina. Four strains were selected based on their compatibility with *Bradyrhizobium japonicum*, their ability to produce phytohormones, siderophores and solubilize phosphate and their antagonism to different fungal pathogens, *in vitro*. Then, the impact of adding *Streptomyces* strains on growth and development at different stages of soybean plants and their effect on plant protection, was tested. As results, plant growth and development promotion were evidenced. The percentage of seed germination and seedlings emergence were significantly higher in non-sterile soil compared to the non-treated control and the antifungal treatment ($P<0.05$). Moreover, leaf area, the number of nodes and branches, and dried weight of aerial parts and roots, were greater in treatments with *Streptomyces* strains ($P<0.05$). In addition, their biocontrol capacity was tested against two model infection pathosystems using *Macrophomina phaseolina* and *Diaporthe aspalathi*, showing a marked delay in the symptom's development and a significant decrease in the percentage of dead plants ($P<0.05$). Thus, we demonstrated that the isolated actinobacteria promote growth and development of soybean plants, and also improve the defense status in the tested conditions

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429
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Area: Biotic Interactions
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Enviado por: Mauricio Reynoso

Chromatin accessibility in legumes depicts transcriptional regulatory elements in symbiosis with rhizobia

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Legumes have the unique capacity of establishing symbiosis with soil bacteria known as rhizobia that leads to nitrogen fixation. Technologies developed in the last decade have facilitated inquiring gene regulation at chromatin level by providing simple protocols and low requirements of nuclei. Accessibility to regulatory factors is a decisive factor in the control of transcription. Bibliography examples in *Medicago truncatula* highlight that nodulation genes can harbor regulatory elements located in accessible chromatin regions that are necessary for functional development of nodules. *daphne* mutant in *Medicago* disrupt a region >15kb apart from the *Nodule INception* gene (*NIN*), affecting *NIN*'s expression pattern and hindering the plant's capacity to establish infected nodules. Other examples include the regulation in the first intron of *LBD18* by NIN. Both regions are conserved across legumes. Our aim is to evaluate the extension of this regulation by regions of accessible chromatin in *M. truncatula*, the conservation across nodulating plants, and understand their contribution to the control of symbiosis. Using a combination of INTACT and ATAC, we found that accessible regions largely locate between 2kb/1kb upstream/downstream of genes (~65%), and the rest located between genes (intergenic regions). Genes characterized for legume symbiosis at different stages are enriched in regions of accessible chromatin in roots. A fraction of those genes are also accessible in syntenic chromatin regions in the genome of *Phaseoulus vulgaris*. Lastly, using INTACT to capture nuclei from a specific cell population can dissect more specific regulation during nodule morphogenesis.

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430
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Area: Plant Hormones
Tipo de presentación: Poster en formato PDF
Enviado por: María Cecilia Terrile

Regulation of jasmonate signaling by S-nitrosation of SCFCOI1 complex components

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E3 ubiquitin ligases are enzymes responsible for the last step of the ubiquitination pathway and are implicated in nearly every aspect of plant biology. The SCF complex is the largest multimeric E3 family and is composed of four subunits: CUL1, SKP1 (ASK1 in Arabidopsis), RBX1, and F-box protein. E3 complexes are involved in the modulation of different hormonal pathways. Particularly in the auxin and jasmonate (JA) signaling, the F-box proteins, TIR1 and COI1, are themselves the hormone receptors. Hormone perception stabilizes TIR1 and COI1 interaction with their transcriptional repressor, Aux/IAA and JAZ, respectively, promoting proteasome degradation. Previously, we demonstrated that TIR1 and ASK1 are targets of S-nitrosation, a nitric oxide (NO)-dependent post-translational modification. We hypothesize that S-nitrosation of TIR1 and ASK1 positively regulates SCF^{TIR1} complex assembly increasing Aux/IAA repressor degradation, and consequently, activates the hormonal signaling pathway. Since ASK1 can interchangeably associate with F-box proteins from different SCF complexes, studying SCF assembly regulation is particularly relevant. In this work, we explore the regulation of JA perception by S-nitrosation of SCF^{COI1} complex components. We demonstrated that S-nitrosation of ASK1 enhanced ASK1-COI1 interaction. Overexpression of a non-nitrosable ask1 mutant protein impaired the activation of JA-responsive genes mediated by SCF^{COI1}, illustrating the functional relevance of this post-translational regulation *in planta*. *In silico* analysis also positioned COI1 as a promising S-nitrosation target. NO-mediated regulation of SCF^{COI1} components may represent a key strategy to modulate the precise time and site-dependent activation of the JA transduction pathway to respond to changing environmental scenarios.

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431
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Area: Developmental Biology
Tipo de presentación: Poster en formato PDF
Enviado por: Dilek Tekdal Tekdal

Comparison of Microsporogenesis in Various Genotypes of Phaseolus vulgaris L.Grown Under The Same Conditions in Mersin, Turkey

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The response of four determinate common bean genotypes (Akman, Bitlis117, Göksun, and Karacaşehir) to male development were studied. Plants were grown at 21/16°C, day/night, 16 h photoperiod in a greenhouse in Mersin, Turkey. Effects of genotypes on pollen development, pod, and seed set were assessed by scanning electron microscopy. The species have distinct morphological characteristics concerning pollen size, SEM ornamentation patterns of the exine, and endoaperture style. Therefore, it is crucial to examine pollen dispersion in the pollinated flowers, as it may influence reproductive success. Pollen wall architecture was similar in all genotypes tested. However, in contrast to the morphological difference, reduced pollen viability and different pod and seed amounts were observed.

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432
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Area: Plant Physiology and Ecophysiology
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Enviado por: Cibele Tesser da Costa

Effects of plastic mini-tunnel treatment on cutting productivity, hexose, and starch concentrations in Eucalyptus spp mini-clonal garden

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Adventitious root (AR) development is a key step for plant propagation of elite clones with advantageous characteristics. In the case of *Eucalyptus*, the ability to produce ARs varies according to the species and some clones of interest exhibit hard-to-root phenotype. To improve rooting, environmental modulation strategies can be used. For this purpose, we used plastic mini-tunnels (MTs) on donor plants of the easy-to-root *E. urophylla* x *E. grandis* AEC0144 and the hard-to-root *E. dunnii* 6201 clones over summer and winter (placed daily from 4pm-10am). MT effects on AR development and whole-cutting carbohydrate contents were assessed on cuttings at 0, 7 and 14 days after excision (dae) and compared to control. As expected, AEC0144 showed higher mean cutting productivity (*i.e.*, monthly number of successfully rooted cuttings per donor plant) in both seasons. During summer, MT improved mean cutting productivity of both clones. No effect was observed in winter. Hexose and starch concentrations were estimated by spectrophotometric analysis. During summer, a peak of hexoses was observed 7 dae on control in AEC0144 but not on MT treatment. No other changes were observed in this season. Over winter, AEC0144 starch levels decreased from 0 to 7 dae, as did hexose content, except in the MT condition. Also in winter, AEC0144 showed reduced levels of hexose in relation to 6201 and to summer in both treatments. A similar pattern was also noticed for starch concentrations. These observations indicate that whole-cutting carbohydrate levels are not a major factor involved in MT-induced cutting productivity.

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433
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Area: Abiotic Stress
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Enviado por: Angelica Nunes Tiepo

Plant growth-promoting bacteria influence on the nitrogen metabolism of drought-stressed Cecropia pachystachya Trécul seedlings.

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Drought events increased in the last decades, negatively affecting the establishment of seedlings used in Brazilian Atlantic Forest restoration programs. This abiotic stress is associated with alterations in nitrogen (N) metabolism, such as the activity of N-assimilation enzymes, amino acid metabolism, and protein content. The inoculation with plant growth-promoting bacteria (PGPB) can mitigate the deleterious effects of drought on Neotropical trees. We aimed to observe if the inoculation with *Azospirillum brasilense* (Ab-V5) and *Bacillus velezensis* (ZK) affected parameters related to N metabolism in seedlings of *Cecropia pachystachya* Trécul, increasing their drought tolerance. We evaluated the glutamine synthetase activity (GS), total amino acid, protein, alanine, and trigonelline content in the leaves. Moderate drought reduced the leaf GS activity. However, *B. velezensis* prevented the drought-induced reduction of the GS activity and reduced the protein content. *A. brasilense* induced reduction in the alanine content. Both PGPB increased the total amino acids and the trigonelline content. Protein breakdown and amino acids catabolism are important in stress tolerance since the degradation of amino acids can provide an energetic connection between carbon and nitrogen metabolism, allowing plants to cope with stress conditions. Another tolerance response to drought stress is the destination of the amino acids to alkaloids' synthesis, like trigonelline, which can have a similar role to the osmoprotectant glycine betaine. The inoculation with both PGPB induced responses on N metabolism that suggest an improvement in drought tolerance in the seedlings of *C. pachystachya*.

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434
QH184FQ
Area: Plant Physiology and Ecophysiology
Tipo de presentación: video presentacion
Enviado por: Rocío Tognacca

ATHB2 is a negative regulator of germination in Arabidopsis thaliana seeds.

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The germination timing of seeds is of the utmost adaptive importance for plant populations. Light is one of the best characterized factors promoting seed germination in several species. The germination is also finely regulated by changes in hormones levels, mainly those of gibberellin (GA) and abscisic acid (ABA). Here, we performed physiological, pharmacological, and molecular analyses to uncover the role of ATHB2, an HD-ZIP II transcription factor, in germination of Arabidopsis seeds. Our study demonstrated that ATHB2 is a negative regulator and sustains the expression of transcription factors to block germination promoted by light. Besides, we found that ATHB2 increases ABA sensitivity. Moreover, ABA and auxin content in *athb2-1* mutant is higher than wild-type in dry seeds, but the differences disappeared during the imbibition in darkness and the first hours of exposition to light, respectively. Some ABA and light transcription factors are up-regulated by ATHB2, such as *ABI5*, *ABI3*, *XERICO*, *SOMNUS* and *PIL5/PIF1*. In opposition, *PIN7*, an auxin transport, is down-regulated. The role of ATHB2 as a repressor of germination induced by light affecting the gemination timing, could have differential effects on the establishment of seedlings altering the competitiveness between crops and weeds in the field.

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435
ND169QL
Area: Biochemistry and Metabolism
Tipo de presentación: video presentacion
Enviado por: Tomás Tonetti

Analysis of trehalose 6-phosphate metabolism in Setaria viridis leaves

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Trehalose 6-phosphate (Tre6P) is a signal metabolite linking plant carbon metabolism with growth and development. The Tre6P-sucrose nexus model postulates that Tre6P is a signal and a negative feedback regulator of sucrose levels to maintain intracellular concentrations within an optimal range. Our current understanding of Tre6P metabolism and signalling in plants is based almost entirely on studies performed with *Arabidopsis thaliana*, an eudicot performing C_3 photosynthesis. In this work, we analysed the intercellular distribution of Tre6P metabolism in leaves of *Setaria viridis* (Setaria), a model species for the major C_4 crops. We found 21 putative transcripts coding for Tre6P-related enzymes: 10 Tre6P synthases (TPS), 10 Tre6P phosphatases (TPP), and 1 trehalase (TRE). Phylogenetic analysis showed there is only one Class I TPS isoform (*Sv*TPSI.1, responsible for Tre6P synthesis) and nine Class II TPS isoforms (putatively involved in Tre6P perception and/or signalling). We prepared samples enriched in mesophyll cells (MC) by leaf rolling, and in bundle sheath cells (BSC) by blending and filtering. Analysis of these samples showed that the *Sv*TPSI.1 transcript and protein are mainly located in BSC. Using a different separation method (suitable for the analysis of metabolites) we found that Tre6P is mainly located in BSC. Finally, incubation of isolated BSC strands with 1 mM Tre6P inhibited degradation of transitory starch, which fits the data reported for *A. thaliana*. Our results strongly suggest that Tre6P metabolism occurs in BSC and represent an initial step towards the elucidation of Tre6P signaling in C_4 photosynthesis.

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436
GQ146MJ
Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Taís Torres

Changes in photosynthetic parameters in young seedlings of Zeyheria tuberculosa exposed to excess iron and manganese

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Photosynthesis is a fundamental metabolic process for plants. However, it is susceptible to several biotic and abiotic factors. Thus, this work aimed to evaluate the effects of excess iron and manganese on photosynthetic parameters in young plants of *Zeyheria tuberculosa* (Vell.) Bureau ex Verl. For this, seedlings were exposed for 20 days to the treatments: Control (T1), composed of complete nutrient solution (SNC), according to Bolle-Jones, SNC + Fe 9 ppm (T2), SNC + Mn 18 ppm (T3) and SNC + Fe 9 ppm + Mn 18 ppm (T4). Using a MultispeQ connected to the PhotosynQ platform, initial fluorescence of Chl *a* (F0'), maximum fluorescence (Fm'), photosystem II quantum efficiency (Fv'/Fm'), the flow rate of protons passing through ATP synthase (gH^+), electron transport rate (ETR) and non-photochemical *quenching* (NPQt) were evaluated. The analyses were performed on the last fully expanded leaf on the last day of the experiment, between 08:00 and 10:00 am. The experimental design was entirely randomized, composed of 4 treatments and 6 repetitions. Data were submitted to analysis of variance (ANOVA) and the Tukey test at 5% significance using the R® software. The results showed that at T2, the lowest mean values were obtained for Fm', Fv'/Fm', ETR and gH^+. However, the NPQt estimate was significantly higher at T2. The F0' of Chl *a*, showed no significant differences between treatments. These results demonstrate that excess iron led to a lower photosynthetic efficiency in *Z. tuberculosa* when compared to the other treatments.

Keywords: Ipê-felpudo; Trace Elements; Photosynthesis.
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437
CS929RS
Area: Biochemistry and Metabolism
Tipo de presentación: Poster en formato PDF
Enviado por: Jose Torres

The DNA glycosylase AtMBD4L mediates removal of 5-BrU from DNA in vivo

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The base analog 5-bromouracil (5-BrU) can be incorporated into DNA by living cells during replication. 5-BrU is used in place of thymidine and is inserted opposite to adenine in DNA. However, 5-BrU can also be paired with guanine so if it is not removed, it can result in AT-GC transition mutations during subsequent replication cycles. DNA base modifications can be repaired by the excision repair system (BER). The DNA glycosylases are enzymes that participate in BER recognizing and removing the damaged DNA bases. Methyl-binding domain 4-like (MBD4L) is a monofunctional DNA glycosylase described in Arabidopsis that can efficiently remove uracil and uracil halogenated derivatives *in vitro*. For this reason, we asked if MBD4L is able to remove 5-BrU on DNA *in vivo.* To test this, we treated wild type (WT) and MBD4L mutant (*mbd4l*) plants with different concentrations (0, 100 y 200 uM) of 5-BrU, and analyzed its effects on plant development (root growth), DNA strand breaks (comet assays) and cell viability (propidium iodide staining). Our results suggest that MBD4L is essential to promote growth, DNA repair and cell viability of plants, counteracting the harmful effect of 5-BrU accumulation in DNA.

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438
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Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Pablo Torti

OXR2 PROTEINS FROM ARABIDOPSIS AND SUNFLOWER IMPROVE TOLERANCE TO UV-B DAMAGE IN ARABIDOPSIS

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Oxidation resistance (OXR) proteins are members of a protein family present in Eukaryotic organisms involved in alleviating stress, ageing, inflammatory responses and DNA damage in mammals. We previously demonstrated that increased expression of the OXR2 gene from Arabidopsis (AtOXR2) or their sunflower homologous (HaOXR2) confers tolerance to oxidative stress in Arabidopsis and maize. Here, we show that AtOXR2 transcript levels increased after UV-B exposure. Moreover, the rosette diameter and leaf area of Arabidopsis AtOXR2 and HaOXR2 overexpressor (OE) plants were not affected after repeated plant exposition to UV-B, related to the phenotype observed in Wild-type (WT) plants. We evaluated the effect of UV-B on the primary root development and demonstrated that AtOXR2 and HaOXR2 OE plants were less affected in the root growth parameters compared to WT, showing reduced levels of cell dead per root meristem. Molecular analysis of the AtOXR2 and HaOXR2 OE plants showed a differential expression of enzymes that participate in the DNA damage repair produced by UV-B and enzymes responsible for the ROS homeostasis control after UV-B exposure. These OXR2 OE plants produce lower levels of anthocyanins than WT plants after UV-B challenges. In sum, our results suggest the existence of a protective role performed by the OXR2 proteins against DNA damage in plants, exerting a positive effect, possibly regulating the cellular redox balance.

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SP965SF
Area: Epigenetics, Chromatin, non-coding RNAs, RNA biology
Tipo de presentación: video presentacion
Enviado por: Ileana Tossolini

Co-transcriptional miRNA biogenesis in plants is boosted by R-loop formation between nascent pri-miRNA and the encoding loci

Co-transcriptional miRNA biogenesis in plants is boosted by R-loop formation between nascent pri-miRNA and the encoding loci

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Plant microRNAs (miRNAs) are transcribed by RNA Polymerase II (RNAPII) as capped and polyadenylated primary transcripts (pri-miRNAs). The variable size and structure of pri-miRNAs lead to alternative processing directions either from the hairpin base to the loop (BTL) or from the loop to the base (LTB). Recent studies suggest that at least part of the processing complex is recruited to pri-miRNA loci.

In this work, we observed that pri-miRNA processing takes place totally or partially in a co-transcriptional way. We used sequencing of plant native elongating transcripts (plaNET-seq) to profile co-transcriptional processing of pri-miRNAs according to their biogenesis type. We found that BTL processing has a first co-transcriptional step followed by a post-transcriptional one where mature miRNA is released. Conversely, all LTB processing steps occur co-transcriptionally. Also, by using plaNET-seq data, we defined the processing directionality of pri-miRNAs with unknown profiles and unusual processing mechanisms. We observed that co-transcriptional processing co-exists with canonical post-transcriptional miRNA biogenesis. The ratio between such processing mechanisms changes depending on the RNAPII speed and environmental conditions.

Finally, we showed that R-loops, formed between the nascent pri-miRNAs and the encoding loci, stabilize and anchor the pri-miRNAs allowing co-transcriptional processing. By analyzing ssDRIP-seq data, we found that R-Loop formation near the 5’ ssRNA region of the pri-miRNAs positively correlates with a preference for co-transcriptional processing.

In conclusion, our work demonstrates that plant miRNAs are processed co-transcriptionally and that such mechanism relies on R-Loops formations to displace the balance from canonical post-transcriptional miRNA biogenesis to a co-transcriptionally process.

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BL918SJ
Area: Cell Biology
Tipo de presentación: Poster en formato PDF
Enviado por: Valentina Trionfini

THE ROLE OF THE TRANSCRIPTION FACTOR ATHB22 DURING THE EARLY STAGE OF ARABIDOPSIS GERMINATION AND DEVELOPMENT

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To gain more insight into the role of AtHB22, we studied phenotypic characteristics of Arabidopsis plants with altered expression of this transcription factor at different stages of development. The *athb22* mutant plants exhibit a delay in germination both under control conditions and in presence of Abscisic acid (ABA) in the growth media, showing increased sensitivity to ABA at this stage related to wild-type (WT) plants. To analyze the expression pattern of AtHB22, we generated Arabidopsis plants expressing the *GUS* reporter gene under the control of its putative promoter. We observed GUS expression in embryos at early stages, increasing during the imbibition process and diminishing during the addition of exogenous ABA. In agreement, *AtHB22* transcript levels are higher in imbibed seeds than in dry seeds and are regulated by ABA in WT plants. *AtHB22* expression is increased in the background of *abi4* mutants, while the opposite behaviour is observed during germination in ABI4 overexpressor plants. On the other hand, GUS expression is detected in the shoot apical meristem (SAM) and the leaf margin till 12 days after sawing. The *AtHB22* expression pattern and the phenotype of overexpressor plants are similar to that of its paralog AtHB51. Expression of AtHB51 is deregulated in the background of plants with altered expression of AtHB22. Our results suggest a putative role of AtHB22 during germination and at the early stages of leaf development in Arabidopsis. More experiments are necessary to elucidate the role of AtHB22 and the pathway of plant hormones that regulate these events.

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NC231QH
Area: Developmental Biology
Tipo de presentación: Poster en formato PDF
Enviado por: Nora Graciela UBERTI MANASSERO

The delicate molecular balance under floral formation

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In the inflorescence meristem of *A. thaliana*, TFL1 antagonize AP1 and LFY function. TFL1 restricts LFY and AP1 expression to the cells in the periphery of the meristem, which will be engaged into becoming floral primordia. At the same time, LFY and AP1 repress TFL1 expression and restricted it to the inner cells of the meristem. Here, TFL1 ensures the maintenance of a pool of undifferentiated cells to assure the indeterminate growth of the inflorescence meristem (Bradley et al., 1997; Ratcliffe et al., 1998, Fornara et al., 2010; Hanano and Goto, 2011). The balance between TFL1, LFY, AP1 and their antagonistic roles controls plant architectonics and regulates developmental patterns of vegetative and reproductive organs (Blümel et al., 2015; Krylova et al., 2020).

In this work we discovered that BdRCN4, a TFL1 homologue from *B. distachyon*, negatively regulates floral organ formation by down-regulating AP1, but no LFY *in A. thaliana*. Nevertheless, LFY over-expression restored normal flower formation in the BdRCN4-OE background plants. Wild type flower development also correlated whit normalized AP1 expression levels. With this experiment, we probed that proper floral establishment and floral organ formation depends on a certain threshold of AP1 expression, which is in turn directly related with a determinate TFL1(BdRCN4)/LFY rate. Our results add a new piece of information in order to fully understand the intricated pathway regulating floral development in angiosperms.

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442
PD222SR
Area: Biotechnology, Research Tools, Resources
Tipo de presentación: Poster en formato PDF
Enviado por: camila urriola nuñez

The PavLEAFY promoter from sweet cherry (Prunus avium L.) shows organ-specific expression and their CIS-regulatory elements reveal key regulatory signatures associated with the flower bud differentiation

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In sweet cherry (*Prunus avium* L), flowering induction and flower bud organogenesis determine the number of flower buds per tree and the fertility of buds (number of flowers / bud) which directly influence the productivity of the orchard. Nowadays, the molecular and hormonal mechanisms that govern the first stages of the development of flower buds in sweet cherry are poorly understood. We observed that *PavLFY*, an orthologous of Arabidopsis *LEAFY*, is highly expressed in sweet cherry flower buds and it emerges as a candidate gene with roles during flower induction and organogenesis. To gain insight about the regulation of the transcription of *PavLFY*, we analyzed bioinformatically and functionally its promoter (-1,279 pb to +1 relative to start of translation). We found

CIS-elements involved in the gene response(s) to hormones such as Abscisic acid (ABRE), gibberellins (TAACAAA) and salicylic acid (CGTCA-motif, as-1, TCA), to light signals (G-box), to transcription factors (TATA-box, CAAT-box) and a CIS-element that regulates the gene expression in meristems (CAT-box). Functional analysis of the chimeric *promPavLFY* :: GUS construct in *Arabidopsis* transgenic plants showed restricted expression in organs such as cotyledons, stipules and floral meristem.

The expression of *PavLFY* in flower buds and the functional analysis of its gene promoter suggest that this gene is developmentally regulated and could play a role as an "integrator gene" of the flower signaling pathways in sweet cherry trees

Keywords: Sweet cherry, *LEAFY*, flower induction, hormones, CIS-elements
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443
BC595TN
Area: Biochemistry and Metabolism
Tipo de presentación: video presentacion
Enviado por: María Urrutia

Identification and Functional validation of methyl ketone synthase 2 in woodland strawberry

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Woodland strawberry (*Fragaria vesca*, 2x) is the diploid closest ancestor of the cultivated strawberry (*F. × ananassa*, 8x) and the model species for genetic studies in the Fragaria genus. It is distributed across Europe and it is appreciated for its delicate aroma.

Methyl ketones are compounds with demonstrated insect repellent effects (Antonious *et al*. 2003), highly abundant in the glandular trichomes of wild tomato (*Solanum habrochaites*). Their synthesis derives from fatty acids in a two-step process mediated by a thioesterase (ShMKS2) and a decarboxylase (ShMKS1) (Ben-Israel *et al.* 2009, Yu *et al.* 2010).

High diversity and quantity of methyl ketones are present in the volatilome of woodland strawberry ripe fruits (Ulrich and Olbrich 2013, Urrutia *et al.* 2017). The aim of this study is to reveal the genetic basis of methyl ketone production in strawberry fruit.

We quantified methyl ketones (2-heptanone, 2-nonanone, 2-undecanone), their secondary alcohols and the methyl esters of their fatty acid precursors by GC-MS in a collection of European woodland strawberry (199 accessions genotyped with >1.8 M SNPs). Conducting a GWAS, we identified an associated region and pointed three homologues of *ShMKS2*: *FvMKS2A*, *FvMKS2B* and *FvMKS2C*.

Functional validation of all candidate genes and alleles by transient over-expression and silencing in both *Nicotiana benthamiana* and *F. vesca* has revealed that FvMKS2A and FvMKS2B, are capable of synthesizing methyl ketones, and point to a single SNP in FvMKS2A as responsible for the enzymatic substrate specificity, supporting FvMKS2A as the main MKS2 paralog responsible for methyl ketones in woodland strawberries

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444
QF696GP
Area: Biotic Interactions
Tipo de presentación: Poster en formato PDF
Enviado por: Facundo Uviedo

Understanding molecular mechanisms of action of PthA4AT, a small TAL effector of Xanthomonas citri subsp. citri for the identification of citrus host resistance genes

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Transcription-activator-like effectors (TALE) are secreted by Xanthomonas, acting as eukaryotic transcription factors that can target both susceptibility or resistant genes in the plant cells. They recognize specific DNA sequences in the host promoters through a domain consisting of a variable number of ~34 amino acid repeats following a well characterized code. The main virulence factor of *Xanthomonas citri* subsp. *citri* (*X. citri*), the bacteria causing citrus canker, is PthA4, a 17.5-repeats TAL effector activating susceptibility genes in *Citrus*. We identified a natural variant of *X. citri* triggering a hypersensitive response (HR) in *C. limon* and *C. sinensis* expressing a 7.5- repeat PthA4-derivative TALE (PthA4^{AT}), responsible on activating HR. To further refine PthA4^{AT} targets in the plant cell as an initial step towards the identification of the *C. sinensis* resistance gene responsible for this HR, a library of artificial PthA4^{AT} TALEs were built. Introduction of PthA4^{AT} and specific artificial variants into the reference strain *X. citri* 306 abolished its ability to cause canker symptoms in *C. sinensis*. Notwithstanding, other artificial variants of PthA4^{AT} promotes canker disease. Using a combination of synthetic biology, phenotypic analyses and molecular markers of HR and canker disease, a couple of artificial PthA4^{AT} TALEs were selected. This knowledge will help to rationally exploit the plant immune system with a biotechnological approach to manage citrus canker.

445
RP892CF
Area: Developmental Biology
Tipo de presentación: video presentacion
Enviado por: Paula Vacs

HYPONASTIC LEAVES 1 is required for proper establishment of auxin gradient in apical hooks of Arabidopsis

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Seedlings germinating under the soil surface have evolved to an exquisite developmental program termed skotomorphogenesis. In darkness, seedlings rapidly elongate the hypocotyl toward the surface in a desperate search of light, while protecting the apical meristem against mechanical damage by forming a hook between the hypocotyl and the two closed cotyledons. A proper skotomorphogenic growth must be achieved until seedlings reach the light in order to ensure survival. In our previous work we uncovered that microRNA biogenesis is necessary for proper skotomorphogenesis in Arabidopsis. By studying mutants in the core components of miRNA microprocessor, DICER LIKE 1 (DCL1), HYPONASTIC LEAVES 1 (HYL1) and SERRATE (SE), we surprisingly found a microprocessor-independent function of HYL1 as a repressor of hook development. Our findings have led to hypothesized a possible connection between HYL1 action in skotomorphogenesis and the well-established and crucial function of the phytohormones auxins in hook development. In this work we dissect different aspects of auxin biology in *HYL1* mutants (auxin sensitivity, transcriptional responses, biosynthesis and transport) and found that HYL1 is needed to establish the auxin gradient in apical hooks. Our research led us to propose that HYL1 might integrate light/dark and auxin signals to control skotomorphogenic growth in Arabidopsis.

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SB455NQ
Area: Epigenetics, Chromatin, non-coding RNAs, RNA biology
Tipo de presentación: video presentacion
Enviado por: Anabella Varela

Dynamic of DNA cytosine methylation in the acclimatization of a single clone of Vitis vinifera cv Malbec to contrasting growing environments over a three year study

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DNA cytosine methylation is the most studied epigenetic mechanism, but its role in the acclimatization of the grapevine to different growing environments is unclear. Especially, its stability or dynamics throughout the different growing seasons (inheritance). We previously found that vineyard environments influence *Vitis vinifera* cv Malbec phenotypic traits and DNA methylation patterns in a clone-dependent way. Also, that clone 10 (MB10) showed clear phenotypic differences between vineyards (Agrelo and Gualtallary in Mendoza, 955 and 1343 m a.s.l., respectively) in correlation with DNA methylation patterns. In the present experiment, MB10 cuttings from Agrelo and Gualtallary were planted into a common environment, the Lunlunta vineyard. Then, anonymous genome regions were analyzed using methylation-sensitive amplified polymorphism (MSAP) markers during 2016, 2017 and 2018 seasons in apical apex collected from five replicates from Lunlunta. We found that the different patterns of DNA methylation observed between the original vineyards are gradually decreasing each year in Lunlunta without loosing completely their differences. On the contrary, the level of DNA methylation remained the same through each year. Finally, we discuss how this epigenetic dynamic could be related with the high phenotypic plasticity observed in MB10 cuttings cultivated in Lunlunta.

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447
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Area: Biotechnology, Research Tools, Resources
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Enviado por: Maria Sol Vasquez

Asymbiotic germination and post-germination growth of Epidendrum ibaguense Kunth

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Orchids need a fungus in order to establish the process of symbiosis that allow their seeds germinate and settle in the new seedlings. Through the application of in-vitro culture, seeds may germinate and the plantlets grow in a sterile environment with no presence of fungi. The objective of this study is to evaluate the percentage of pollution, germination and average height of *Epidendrum ibaguense in vitro* seedlings. Due to this fact, seeds of *E. ibaguense* open capsules were sown in Murashige and Skoog culture media (1962) to its 100 % of saline concentration and vitamins as well as supplemented with 30 g/l of sucrose , 7 g /l of Agar Britannia , 0,19g/l of myoinositol , 1g/l of active carbon and Kinetina in two concentrations: : 0,1 ppm (MS0,1Kin), 1 ppm (MS1Kin), BAP: 0,5 ppm (MS0,5BAP) and control treatment (MS) without growth regulators. The cultures were stored in growth chambers at 25+/-2 °C, 40 % of humidity and photoperiod 12/12h. It was registered 18,8 % of pollution due to fungi and bacteria. After 150 days, the level of germination was de MS: 22, 1%, MS0,1 Kin: 21,9%; MS1 Kin 46,7 % y MS0,5 BAP:13,9 %. The average height of the plants was 8,10cm MS, 12,50cm; MS0,1 Kin, 4,50cm to MS1Kin and 3,50cm for MS0,5BAP since the experiment began 270 days ago. The treatment with MS0,1Kin is the best since a higher cauline growth was obtained through this method and not with the others.

Key words: seed, seedlings, *in- vitro* culture
Financing: Facultad de Ciencias Naturales- UNSa

448
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Enviado por: Maria Magdalena Vazquez

Evaluation of brewers yeast (Saccharomyces cerevisiae) supplementation on hydroponic production

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Hydroponics is a technique of growing plants that use a nutrient-rich water solution, without soil. In relation to agricultural production, yeast is one of the potential plant growth-promoting organisms (PGPMs). A wide diversity of soil yeasts have been researched for their potential as bio-fertilizers or PGPMs. However, the potential of brewers' yeast (*Saccharomyces cerevisiae*), a waste product of the brewing industry, and its role as PGPMs have been scarcely investigated in hydroponics. Our aim was to explore how yeasts from the brewing industry residue affects plant growth in hydroponic culture. Analysis by real-time PCR amplification and sequencing revealed that the yeast used in the brewing industry (called S05) was *Saccharomyces cerevisiae* strain J14. We evaluated the effects of addition S05 yeast on plant growth of *Arabidopsis thaliana*, *Eruca vesicaria* y *Lactuca sati*va with this technique. Analyses at stage seed-seedling, showed that *A. thaliana* y *E. vesicaria* inoculated with S05 had higher length of principal root and density of lateral roots than those on control solution. Analyses of *L. sativa* at plant stage, showed an improved in root system performance with S05 yeast as compared to control (hydroponic solution) plant. Our results confirm that *S. cerevisiae* strain J14 from the brewing industry may confer benefits in hydroponics crops with positive effects on root growth. These results validate the potential application of *Saccharomyces cerevisiae* strain J14 in plant cultivation in hydroponic by reducing its cost, improving its quality, and reusing a waste product from the brewing industry as a biotechnological tool.

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449
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Enviado por: Ana Luiza Viana Silva

ADNT1 DEFICIENCY LEADS TO EARLY STRESS RESPONSE IN Arabidopsis PLANTS SUBMITTED TO FLOODING

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ADNT1 is a mitochondrial adenylate carrier that mediates an exchange of mitochondrial matrix ATP by cytosolic AMP and to a lesser extent, cytosolic ADP. It has been shown that *ADNT1* is highly expressed during hypoxic conditions. Here we investigate the role of ADNT1 under flooding conditions *in Arabidopsis thaliana.* For this, we used *adnt1*, a T-DNA insertion line, two *adnt1* antisense lines (10 and 22), and wild-type (WT) plants. Metabolite profiling of leaf and root tissues of *ADNT1* deficient plants indicated decreased levels of tricarboxylic acid (TCA) cycle intermediates besides increased levels of metabolites related with stress responses, such as alanine, aspartate, nicotinic acid, trehalose and inositol, in comparison to WT. For the expression analyses we selected genes encoding proteins associated with energy and stress-related signaling. The expression of SnRK1 was higher in ADNT1 deficient plants already in non-stress conditions, and over time stress period. We also observed that Adenylate Kinase (ADK) and Apyrase (APY) showed higher expression already under non-stress conditions in the ADNT1 deficient lines. Additionally, the greater expression of *PDC1* and *PPDK* during the waterlogging stress period was also observed in the ADNT1 deficient plants, which suggests an early and more expressive induction of the fermentative pathway. We conclude that ADNT1 carrier might play a role in Arabidopsis during waterlogging stress. We hypothesize that the absence of this carrier generates an early “hypoxic status” due to perturbation of the adenylate pool caused by reduced AMP transport to mitochondria.

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450
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Enviado por: María Laura Vidoz

High relative humidity triggers adventitious root primordia elongation in tomato plants

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Tomato (*Solanum lycopersicum* L.) plants are a model horticultural species not only to study fleshy fruit formation but also to unravel plant responses to the environment, such as the formation of adventitious roots (ARs) from submerged stems. We have previously observed that an increase in relative humidity (RH) is enough to induce the elongation of preformed AR primordia. Considering the energetic cost of producing fast-growing roots and the consequent intricate and strict regulation of ARs, it is surprising that a mere increase in water vapor can trigger such a conspicuous response. Therefore, the purpose of this study was to increase our understanding of the mechanism behind high RH-induced ARformation in tomato plants. We have first exposed the base of four weeks old plants to a range of water vapor content in order to determine whether there is a threshold below which AR development does not take place. Following, we assessed the role of auxin, ethylene, gibberellins and abscisic acid on the induction of AR primordia elongation by applying specific inhibitors and exogenous hormones to the hypocotyls, before exposing them to high RH. We have observed that there is no AR induction below 78% RH, and that the number and length of ARs increased proportionally with the RH level. Moreover, the process seems to be regulated by auxin and gibberellins, as the inhibition of both hormones resulted in a reduction in the number and length of ARs.

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451
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Area: Abiotic Stress
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Enviado por: Lissa Vasconcellos Vilas Boas Lissa

Growth of Zeyheria tuberculosa (Vell.) Bureau ex Verl seedlings under excess of iron and manganese

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Soil conditions are fundamental factors for the adequate growth of plants. Deficit or excess of essential elements can affect the growth of plants, hindering their establishment in the environment. Thus, the main of this work was to evaluate the effect of excess of iron (Fe) and manganese (Mn) on growth parameters in *Zeyheria tuberculosa*. For this, seedlings were exposed for 20 days to the following treatments: SNC - Bolle-Jones complete nutrient solution (T1), SNC + Fe 9 ppm (T2), SNC + Mn 18 ppm (T3) and SNC + Fe 9 ppm + Mn 18 ppm (T4). The growth parameters evaluated were aerial and root length, stem diameter, leaf number, aerial and root dry mass, biomass allocation and leaf area. The experimental design was entirely randomized, composed of four treatments and six repetitions. The data were submitted to analysis of variance (ANOVA) and the Tukey test at 5% significance using the R® software. The results of height, stem diameter, number of leaves, leaf area and dry mass of leaves and roots did not present significant statistical differences among treatments. Only the length of the roots at T2 presented a statistical difference, with a 29.80% decrease in length compared to the control. Thus, we conclude that excess manganese did not affect the growth parameters of *Z. tuberculosa*, but iron led to lower root growth in this species.

Keywords: Micronutrients, Ipê-felpudo, Biomass
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452
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Enviado por: Johnatan Vilasboa

Enhanced Eucalyptus spp. cutting productivity under plastic mini-tunnel treatment is associated with specific changes in foliar nutritional status

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Eucalyptus propagation is essential for the global forestry industry. The mini-cutting technique allows low-cost clonal propagation of *Eucalyptus*, but is often hindered by rooting recalcitrance. It has been shown that plastic mini-tunnel (MT) treatments on donor plants may enhance rooting rates in *Eucalyptus* clones. While the mechanism behind this effect remains elusive, an improved leaf nutrient status has been suggested as one of its facets. In this study, easy-to-root *E. urophylla* x *E. grandis* AEC0144 and hard-to-root *E. dunnii* 6201 mini-stumps (donor plants) were cultivated in standard (control) and MT nursery conditions. Both cutting productivity (*i.e.* expected monthly number of successfully rooted cuttings per ministump) and foliar nutrient levels of these clones and treatments were assessed. Over the summer, MTs were set up daily (4pm-10am, including the overnight period) over AEC0144 and 6201 donor plants. Nutrient levels were determined using spectrometric methods. Shoots from 120 cuttings obtained from donor plants under control or MT conditions constituted one biological replicate. For each species, four biological replicates were analyzed. MT treatment enhanced mean cutting productivity in both easy- and hard-to-root species, by 26.1% and 33.6%, respectively. Additionally, this condition increased foliar magnesium levels in both species and calcium and iron levels in 6201. In AEC0144, MT treatment also increased potassium and phosphorus levels. Interestingly, sodium and manganese levels were not affected by MTs, but were higher in AEC0144. These results indicate that foliar nutritional status is associated with and may play a role in the effects of using MTs.

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453
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Area: Abiotic Stress
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Enviado por: Ana Carolina Vilchez

Differential acyl-editing of PA involves the up-regulation of PC -remodelling genes during chilling recovery in barley

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Regulation of the level of saturation and the constitution of glycerolipids is important for plants to maintain the integrity and fluidity of their membranes under temperature stresses and when they are released. A mass spectrometry analysis was performed to compare the lipid profile in barley roots both under chilling stress treatment and in the subsequent recovery to stress. The results indicate that lipid metabolism was significantly affected by chilling. Most of the glycerolipids analysed returned to control values during short- and long-term recovery, whereas several representative phosphatidic acid (PA) molecular species were edited during long-term recovery. Most of the PA molecular species that increased in the long-term had the same acyl chains as the phosphatidylcholine (PC) species that decreased including C34:2 and C36:4 as remarkable changes. To understand the mechanisms underlying the acyl-editing of PC in barley roots, we evaluated the contribution of lysophosphatidylcholine acyltransferases (HvLPCAT) and phospholipase A (HvPLA). In line with the aforementioned results, the expression of the HvLPCAT and HvPLA genes was up-regulated during recovery from chilling. Thus, results showed a differential acyl-editing of PA during recovery, which involves the up-regulation of PC -remodelling genes. Additional biochemical and biophysical analyses will help us to unravel how these recovery formed PA - polyunsaturated species modulate the membrane configuration and properties for further contribute with the knowledge of cold tolerance in barley.

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Enviado por: Victoria Vitali

Root hydraulics adjustment is governed by a dominant cell-to-cell pathway in Beta vulgaris seedlings exposed to salt stress

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Soil salinity reduces root hydraulic conductivity (L_{pr}) of several plant species. However, how cellular signaling and root hydraulic properties are linked in plants that can cope with water restriction remains unclear. In this work, we exposed the halotolerant species red beet (B*eta vulgaris*) to increasing concentrations of NaCl to determine the components that might be critical to sustaining the capacity to adjust root hydraulics. Our strategy was to use both hydraulic and cellular approaches in hydroponically grown seedlings during the first osmotic phase of salt stress. Interestingly, L_{pr} presented a bimodal profile response apart from the magnitude of the imposed salt stress. As well as L_{pr}, the PIP2-aquaporin profile follows an unphosphorylated/phosphorylated pattern when increasing NaCl concentration while PIP1 aquaporins remain constant. L_{pr} also shows high sensitivity to cycloheximide. In low NaCl concentrations, L_{pr} was high and 70 % of its capacity could be attributed to the CHX-inhibited cell-to-cell pathway. More interestingly, roots can maintain a constant spontaneous exudated flow that is independent of the applied NaCl concentration. In conclusion, *Beta vulgaris* root hydraulic adjustment completely lies in a dominant cell-to-cell pathway that contributes to satisfying plant water demands.

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455
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Enviado por: Victoria Vitali

The multifunctional plant PIP aquaporin subfamily: a picture of functional diversity

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An increasingly large number of genes have been identified as multi-functional, being those functions dependent upon biological context. In particular, variations in transported solute specificity impact channels family functions. The PIP (plasma membrane intrinsic proteins) subfamily is the largest of the seven MIP (Major intrinsic proteins, *i.e.* aquaporins) subfamilies found in plants. Though PIP were originally proposed as canonical water channels, there are also reports of permeability to different small solutes, such as hydrogen peroxide, carbon dioxide, and sodium. For years, efforts have been focused on elucidating whether this great multiplicity of PIP isoforms implies functional diversity or a functional overlap. Now it is becoming clearer that different isoforms do not exhibit the same functional properties in terms of solute permeability even with primary sequence identity higher than 80%.

Here, we performed an extensive analysis of the PIP subfamily by implementing a systematic analysis of signature sequences and residues of all PIP isoforms from the PF00230 Pfam database entry (2034 sequences). A sequence similarity network (SSN) for the PIP subfamily was built using the EFI-EST online tool and visualized in Cytoscape 3.8.2. Based on neighborhood connectivity, we characterized the topology of the PIP subfamily within SSN clusters. To go in depth in their functional diversification, we complemented the SSN with the transport specificity reported for PIP in the literature. This approach allows us to get insights regarding their structure-functions relationships, and generate testable hypotheses about the uncharacterized isoforms in the PIP subfamily.

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456
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Area: Biochemistry and Metabolism
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Enviado por: Lea Vojta

Regulation of the electron transfer at chloroplast membranes – what happens when the dual localization of TROL protein converts to the single?

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Thylakoid rhodanese-like protein (TROL), a photosynthetic membrane component, is a hub at the end of the photosynthetic electron transfer chain that in vascular plants influences the preferential electron transfer catalyzed by the enzyme ferredoxin:NADPH oxidoreductase (FNR) for the production of sugars. Investigation of TROL knock-out mutants unraveled its property in the dynamic binding of FNR, with this interaction being a switch influencing photosynthetic electron destination sinks, according to the organelle needs. By monitoring ROS formation and subsequent induction of plant stress-relief responses we clearly demonstrated that plants devoid of TROL cope better with oxidative stress by fast elimination of reactive oxygen species. This property is currently being investigated into more detail, since these plants are potential candidates more resilient plants of the world with aggravated environmental stresses.

TROL is localized in the thylakoids, in its mature form, where it participates in the regulation of photosynthetic electron utilization, and in the inner envelope (IE) of chloroplasts, in its precursor form, where its function is so far unknown. Whether it represents just a storage protein for FNR or is involved in redox sensing and/or in protein import, remains to be resolved. For this purpose, by using the presequence directed mutagenesis and *in vitro* protein import experiments, we managed to arrest TROL at a single location inside the chloroplasts – in the IE membrane. We then engineered Arabidopsis plants with the single-localized TROL. TROL-IE plants should enable investigation of its so far unknown function at the inner envelope.

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457
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Enviado por: Francisco Vázquez Prol

SYMPTOM SEVERITY, INFECTION PROGRESSION AND PLANT RESPONSES IN SOLANUM PLANTS CAUSED BY THREE POSPIVIROIDS VARY WITH THE INOCULATION PROCEDURE

Francisco Vázquez Prol[1], Joan Márquez-Molins[2], Ismael Rodrigo[1], M. Pilar López-Gresa[1], José María Bellés[1], Gustavo Gómez[2], Vicente Pallás[1], Purificación Lisón[1]
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Infectious viroid clones consist of dimeric cDNAs used to generate transcripts which mimic the longer-than-unit replication intermediates. These transcripts can be either generated in vitro or produced in vivo by agro-inoculation. We have designed a new plasmid, which allows both inoculation methods, and we have compared them by infecting *Solanum lycopersicum* and *Solanum melongena* with clones of *Citrus exocortis virod* (CEVd), *Tomato chlorotic dwarf viroid* (TCDVd), and *Potato spindle tuber viroid* (PSTVd). Our results showed more uniform and severe symptoms in agro-inoculated plants. Viroid accumulation and the proportion of circular and linear forms were different depending on the host and the inoculation method and did not correlate with the symptoms, which correlated with an increase in *PR1* induction, accumulation of the defensive signal molecules salicylic (SA) and gentisic (GA) acids, and ribosomal stress in tomato plants. The alteration in ribosome biogenesis was evidenced by both the upregulation of the tomato ribosomal stress marker *SlNAC082* and the impairment in 18S rRNA processing, pointing out ribosomal stress as a novel signature of the pathogenesis of nuclear-replicating viroids. In conclusion, this updated binary vector has turned out to be an efficient and reproducible method that will facilitate the studies of viroid–host interactions.

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458
FN182RP
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Enviado por: Louise Walker

The molecular and physiological link between temperature compensation and the circadian clock in the model legume Medicago truncatula.

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All organisms must adapt to their environment to survive, particularly plants that cannot escape unfavorable conditions. Organisms have evolved an internal timekeeping system, the circadian clock that anticipates the changing environment. The clock synchronizes external cues, mainly light and temperature, with time-of-day specific processes such as growth, starch metabolism and reproduction. Anticipating the changing environment has major benefits for plant survival. Most of our knowledge about the plant circadian clock has come from studies in the model plant *Arabidopsis thaliana*. However, less is known about circadian clock mechanisms in other species.

Legumes are essential as a source of protein for both humans and livestock, and for fixing nitrogen. Our project aims to discover how the circadian clock of barrel-clover (*Medicago truncatula*) can enhance plant fitness in local environments. We identified a wild population with a particularly long internal period (*thermos*). We studied *thermos* in a range of physiological conditions and found it has a strong temperature compensation phenotype. *Thermos* is unable to maintain appropriate clock function in non-stressful changing ambient temperatures. Through qPCR and sequencing of core clock genes, we found downregulation of a PRR family gene and a candidate SNP that could be responsible for the phenotype. More, we found an early flowering phenotype when compared to related populations.

These findings, with further molecular and physiological analysis will highlight the role of clock natural variation in temperature compensation in legumes. Understanding the link between clock period and temperature will help develop plants that can withstand warming climates.

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459
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Enviado por: Florent Weiller

Following cell wall composition modifications in wine and table grapes during Botrytis cinerea infection

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Botrytis cinerea is a necrotrophic fungus responsible for the grey mould disease. It induces important damages to grapes in the field and during postharvest storage, leading to severe loss to the table and wine grapes industries. To develop successful infections, *B. cinerea* first needs to breach plant defences, including the plant cell wall, a polysaccharide and proteins matrix layer protecting plant cells. Surprisingly, despite its importance in plant-pathogen interaction, only limited information is known on grape cell wall during *B. cinerea* infections.

This work followed grape cell wall composition of Sauvignon Blanc, Cabernet Sauvignon, Dauphine and Barlinka cultivars during *B. cinerea* infections. Berries from these wine and table grape cultivars were infected with *Botrytis* spores at three different ripening stages between veraison and ripe stages. Infection development was followed using scanning electron microscopy and X-ray computed tomography while the cell wall of these berries was analysed using comprehensive microarray polymer profiling and gas chromatography.

All grape culltivars were sensitive to *B. cinerea* infection with similar symptoms though slightly more severe for the table grapes. At post-veraison and ripe stages, tissue degradation and maceration were reported, no visible symptoms were observed at veraison. Cell wall of infected grapes showed a decrease of signal for pectin associated epitopes, sign of depectination while their hemicellulose and arabinogalactan proteins content seemed mostly unaffected. Extensins associated signal increased in moderate and severely infected grapes suggesting protein deposition.

460
KH192PC
Area: Abiotic Stress
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Enviado por: H. Martín Winkler

Selection of mutagenized cotton individuals in M4 generation in response to water and saline stress

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Induced mutations techniques are useful tools for crop breeding. Therefore, they could be useful in cotton (*Gossypium hirsutum L.*) for the improvement of its physiological characteristics. In order to select mutagenized plants with a differential response to drought and salinity stress, seeds from 27 M_4 generation individuals were sown in pots at the greenhouse, using the same variety (Guazuncho 3 INTA) without mutagenic treatment as control. Drought and salinity stresses were applied in the vegetative stage (fourth leaf expanded). Morphophysiological characteristics were determined (biomass, relative water content (RWC), water potential, leaf temperature, proline content, Na^+ and K^+ ions), as well as agronomic (fiber yield, lint percentage). The results showed a differential behavior between the individuals evaluated. Differences were observed among materials in the RWC and the K^+/Na^+ ratio under both stresses; while the levels of proline in leaves only showed differences between individuals subjected to water stress, presenting values from 2 to 10.5 nmol/mg of dry tissue. As for agronomic analyzes, significant differences were found among individuals in yield, exhibiting values from 1.50 to 18.50 g/pot and 10.50 to 22.50 g/pot, for salinity and drought stress, respectively. Moreover, lint percentage data showed differences between the plants analyzed under both stresses. The results indicated that there are differences among the M_4 individuals, which allow, based on the variables determined, to make a selection of materials with a differential behavior under water and salinity stress, which could later be incorporated into a breeding program.

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461
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Area: Biotic Interactions
Tipo de presentación: video presentacion
Enviado por: Milagros Yacullo

The Subunit 3 of the Superkiller complex (SKI3) mediates regulation of AP2/NNC1 transcription factor during symbiosis.

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Legumes and rhizobia establish a nitrogen-fixing symbiosis that involves the formation of a lateral root organ, the nodule, and the suppression of the immune response of the plant, which allows the rhizobia to infect the root tissue. The activation and coordination of these two genetic programs requires the reprogramming of root cells, which is accompanied by significant changes in the profiles of gene expression at both the transcriptional and the post-transcriptional levels. Previous studies identified transcripts that change their association to the translational machinery at early stages of symbiosis between the legume *Medicago truncatula* and its symbiotic partner *Sinorhizobium meliloti*. A transcript encoding the Subunit 3 of the *Superkiller Complex* (SKI), designated as *MtSKI3*, was differentially up regulated at the translational level. The SKI complex acts along with the exosome in the 3´-5´ degradation of mRNAs. Functional analysis revealed that *MtSKI3* is required for nodule formation, bacterial survival, and induction of early nodulation genes such as *ENOD40* (https://doi.org/10.1105/tpc.19.00647*).* Recently, a degradome analysis showed that *MtSKI3* affected the miR172-directed endonucleolytic cleavage of the *APETALA 2/ Nodule Number Control 1* mRNA (referred to as *MtNNC1*). Analysis of publicly available expression data showed that *MtNNC1* is down regulated at late stages of the symbiosis, and its expression is restricted to the nodule apex. We are currently using different reverse genetic approaches to elucidate the biological function of *MtNNC1*. The results will allow a better understanding of the mechanisms by which *MtNNC1* exerts its activity during the agronomically important process of nitrogen-fixing symbiosis.

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Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Mauro Yarte

IN VITRO ROOTING OF HANDROANTHUS IMPETIGINOSUS (BIGNONIACEAE) UNDER SALT STRESS CONDITIONS: EFFECT OF BACILLUS SP. AND SPHINGOBACTERIUM SP. INOCULATION

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Salinity is one of main abiotic stresses that causes adverse effects on plant growth and affects millions of hectares around the world. Variability of physical and chemical properties of soils has made field experiments notoriously difficult to evaluate. Plant tissue culture has been used as a model system to study physiological responses induced by salinity. The aim of this work was to evaluate the tolerance to salinity of *Handroanthus impetiginosus* 'pink lapacho' and the effect of inoculation with plant growth-promoting bacteria previously isolated from adult plant roots and rhizosphere. Shoots induced for 3 days in medium with Murashige and Skoog salts at half concentration, Gamborg vitamins, myoinositol 100 mg L^{-1}, sucrose 20 g L^{-1}, agar 6g L^{-1} and 30 µM of indole butyric acid were used. The shoots were transferred to auxin-free medium, supplemented with 0, 40, 80 or 160 mM NaCl and were inoculated or not with 10^8 cfu of *Bacillus* sp. L15 or *Sphingobacterium* sp. L22. At the end of experiments (40 days), 50% Inhibitory Concentracion (IC_{50}) was determined from regression curves constructed with rooting percentages. Bacterization with both strains displaced the IC_{50} to higher concentrations of NaCl (147 and 160 mM) with respect to controls (109 mM). Furthermore, inoculation with *Sphingobacterium* sp. L22 caused significant improvements in root development parameters at 40 mM NaCl. Finally, bacterization and NaCl concentration modified proline content during first 15 days of culture. In conclusion, the studies carried out showed that bacterial inoculation mitigate negative effects from salt stress in *H. impetiginosus*.

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Area: Biotic Interactions
Tipo de presentación: video presentacion
Enviado por: Andrea Alejandra Zanini

Circadian rhythms of sugar metabolism during Cassava common mosaic virus (CsCMV) infection in source-sink cassava leaves

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CsCMV is a potexvirus which causes chloroplasts impairment and metabolic alteration associated with significant yield losses in cassava crops. Crop yield depends on the circadian rhythms since carbon allocation and growth are regulated by the clock. Sugar signalling can affect circadian rhythms, and control growth and stress responses. Here we evaluate the daily metabolism disturbances induced by CsCMV infection in source-sink cassava leaves. The soluble sugar and starch concentration were examined over the 24-hour cycle (16:8 photoperiod), in CsCMV-infected and healthy plants (*var.* IAC-90). Likewise, at the end of the day and night, the expression of an array of carbohydrate-metabolism genes were analyzed. In CsCMV-infected source leaves, at 3-6h light, sucrose content rose with respect to control. The Suc/Hex ratio peaked at 6h light and at 8h dark. Additionally, we found a decrease of expression of starch synthesis and degradation related genes at 16h light and an increase of the starch synthesis gene expression at 8h dark, with respect to control. Meanwhile, the starch content did not change during the 24-hour cycle with respect to control. Regarding sink tissue, Suc/Hex peaked at 16h light while maltose rose at 6h light and decreased at 4h dark. The gene expression of sugar transporters was lower in source and sink tissues at 16h light. Altogether these results demonstrate circadian rhythms of sugar metabolism altered by CsCMV. We suggest that the sucrose spikes could act as sugar-signals in clock-regulated mechanisms involved in the physiological responses during cassava-CsCMV interaction.

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464
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Tipo de presentación: Poster en formato PDF
Enviado por: Diego Zavallo

sRNAs profiling associated with potatoes polyploidy

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The cultivated potato has more than 100 related wild species, and interspecific hybridization is a commonly used tool in genetic improvement. Polyploidy is also a common phenomenon in eukaryotes and is believed to drive ecological and evolutionary success in plants. However, the effects that may produce interspecific hybridization and subsequent whole genome duplication have not been widely studied in potato species. In a recent work, we observed that allotetraploid potato lines showed higher vigor in morphological traits compared to their diploid parental lines (Marfil et al. 2018). Furthermore, in a following experiment with the same lines, a great alteration in the amino acids and volatile organic compounds profiles of the derived tetraploids was found (Cara et al. 2020). On a molecular level, no genetic changes were observed between lines, yet epigenetic differences were found (Marfil et al. 2018).

In this work we dig deeper on the effect of polyploidization on the epigenome by assessing the sRNAs profile of the parental diploid hybrid and its derived allopolyploid. A sRNA-seq experiment was performed and bioinformatic analysis was implemented on 21-22nt-lenght and 24nt-length separately since their distinct biogenesis and mechanism of action. Composition and distribution of different features across the potato genome were assessed and highlighted the ones with differentially accumulated (DA) sRNAs on Circos plot. A subset of genes with DA sRNAs associated were selected to perform mRNA expression to address if the sRNA profile could have an impact on the transcriptome and in consequence on the phenotype.

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Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Fany Zubillaga

Germination response of buckwheat grown in northern Patagonia to different salt stress conditions.

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Buckwheat is a recently introduced crop in the lower valley of Rio Negro. This site is characterised by a great variability of soils and sites with salinity. Germination has been considered the most sensitive stage to salinity in the life of a plant. A saline environment causes a delay in germination, affects plant growth and reduces grain and biomass production.

The objective of this work was to determine the germination response of locally produced buckwheat to different sodium chloride (NaCl) salt solutions: 1) Control: H2O, 2) 0.05M NaCl, 3) 0.1M NaCl, 4) 0.15M NaCl, 5) 0.2M NaCl, 6) 0.25M NaCl and 7) 0.3M NaCl. Each treatment was represented by five Petri dishes with 20 seeds each. They were incubated in the germination chamber at 25°C. Total radicle length (TRL), germination capacity (GC); germination energy (GE); mean germination time (MGT) were quantified,

The GC was 100% for the control and 0.05M, then gradually reduced to a minimum of 20% at 0.30M.

EG decreased with salt concentration, although there was no difference (99%) between the control, 0.05M and 0.10M treatments. For 0.30M EG reached 50%.

TMG tended to increase with salt concentration, doubling the time of the control at the highest concentration (3.6 days).

LTR decreased with salt concentration, the 0.30M treatment decreased more than 95% compared to the control.

Increasing NaCl concentration reduced CG, EG and LTR and increased TMG. However, buckwheat has shown tolerance to salinity up to concentrations of 0.25M with germination rates of 80%.

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466
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Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Fany Zubillaga

Germination response of buckwheat (Fagopyrum esculentum) grown in northern Patagonia at different temperatures.

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The Lower Black River Valley (VIRN) could be considered the southernmost buckwheat growing area in the country. The environmental conditions of the VIRN make its phenological cycle extend from November to April. During this period, the average maximum temperatures (T°) vary between 29 and 21°C and the minimum temperatures between 14 and 7.8°C.

The objective of this study was to determine the germination response of locally produced buckwheat at different germination T°(5; 10; 15; 20; 25; 30; 35 and 40°C). A germination chamber was used and the seeds were placed in Petri dishes conditioned with cotton, paper and adequate humidity. The number of seeds per plate was 20 with five replicates per T°. Germinated seeds were counted every 24 hours for seven days. The parameters evaluated/estimated were: germination capacity (GC); germination energy (GE); mean germination time (MTG), germination rate index (GRI).

At 5, 10 and 40ºC no germination was observed. The variables CG (95%) and EG (99.9%) showed no statistical differences in the 15 to 30ºC range. However, TMG decreased with increasing T°, with the lowest values at 30-35°C (1.46 days±0.08). IVG increased to a maximum at 30°C (17.60±0.74).

These results indicate that 30°C is the optimum T° for germination, since all parameters evaluated were optimal. The results found confirm the optimum T° (20-30°C) proposed by the ISTA standards (2009) for this crop. It is important to note that this crop germinated at T° of 15°C and 35°C which could be due to the environmental conditions where the material was grown.

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467
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Area: Plant Physiology and Ecophysiology
Tipo de presentación: Poster en formato PDF
Enviado por: Paz Estefanía Zuñiga

Overexpression of FaMYC2 increases anthocyanin biosynthesis in strawberry fruits.

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Strawberry (*Fragaria* × *ananassa*) is one of the most popular fruits grown worldwide and a promising model for studying molecular mechanisms involved in fruit biology. Strawberry fruits are an important source of flavonoids such as anthocyanins which can protect plants against stress due to their antioxidant proprieties. Anthocyanins are regulated at the transcriptional level through MBW protein complexes containing R2R3-MYB, bHLH, and WD40-repeat transcription factors (TF). However, little is known about upstream regulatory genes controlling anthocyanin biosynthesis.

MYC2 is a core TF of most aspects of the jasmonate signaling pathway in plants. Also acts controlling the expression of genes that participated in the synthesis of secondary metabolites in a species-specific manner.

In this research, we study the effect of the *MYC2* overexpression on anthocyanin content as well as changes in transcript levels of genes associated with anthocyanin biosynthesis on strawberry fruits. Briefly, the full-length coding sequence of *FaMYC2* was cloned and transiently overexpressed on strawberry fruits by agroinfiltration. We analyzed changes in color, anthocyanin content, and expression levels of genes related to JA signaling (*FaMYC2*, *FaJAZ1*), abscisic acid (*FaNCED1*, *FaNCED2*, and *FaYABBY*), MBW complex (*FaMYB9*, *FaMYB10*, *FaMYB11*, *FabHLH3*, and *FabHLH33*), and anthocyanin biosynthetic genes (*FaANS*, *FaUFGT*).

MYC2 overexpressed fruits show higher anthocyanin content as well an increase in the expression levels of MBW complex-related TF *FaMYB10,* ABA related genes (*FaNCED1*, *FaNCED2*, and *FaYABBY*) and anthocyanin biosynthetic genes *FaANS* and *FaUFGT*. Together, these data suggest that FaMYC2 could be a relevant upstream positive regulator for anthocyanin biosynthesis through *FaMYB10* controlling expression.

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468
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Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Tamires da Silva Martins

Nitrate fertilization decreases oxidative stress in soybean plants exposed to the combined salt and waterlogging stresses

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The combined salt and waterlogging stresses trigger the accumulation of reactive oxygen species (ROS) which leads to extensive oxidative damage in plants. Herein, we hypothesized that NO_3^- decreased the oxidative stress in soybean roots exposed to high salinity during waterlogging and reoxygenation. Nodulated soybean plants were cultivated in a greenhouse and fertilized with a nutrient solution without nitrogen. At the R2 stage, plants were subjected to the following treatments: Water, NO_3^- [$Ca(NO_3)_2.4H_2O$ 1,1 mM + KNO_3 1,2 mM], NaCl (50 mM) and NaCl + NO_3^-. Then plants were exposed to waterlogging for six days and to reoxygenation for 2 days. After waterlogging and reoxygenation periods, roots were harvested to access the levels of NO_3^-, hydrogen peroxide (H_2O_2), and malondialdehyde (MDA). High salinity increased the root levels of MDA during waterlogging and H_2O_2 and MDA during reoxygenation. During these conditions, the NO_3^- supplementation increased the root levels of NO_3^- while decreased the root levels of H_2O_2 and MDA. In conclusion, the NO_3^- fertilization decreases oxidative stress and enhances soybean tolerance to the combined salt and waterlogging stresses.

Financing: Coordenação de Aperfeiçoamento de pessoal de Nível Superior (CAPES), Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), Fundação de Amparo à Pesquisa do Estado do Rio Grande do Sul (FAPERGS),

469
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Area: Developmental Biology
Tipo de presentación: Poster en formato PDF
Enviado por: Mateus de Campos Alves

CARBOHYDRATES PROPORTIONS IN THE CATTLEYA WALKERIANA in vitro FLOWERING

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Among Brazilian native orchid species, *Cattleya walkerina* presents late-blooming which increases production costs. The study aimed to investigate different carbohydrates concentrations in the Catteya walkeriana *in vitro* flowering. The experiment was conducted in a completely randomized design, composed of 0, 10, 15, 20, 25, and 30 g L^{-1} of sucrose, 12 repetitions, with one plant per flask. Knudson medium, 2% sucrose, 5.5 g L-1 agar, 1% activated charcoal was used. The plant material was from in vitro seeding. The plants were grown in a growth room at 25°C ± 2°C, 16 h photoperiod and light intensity of 27 µmol µmol.m $^{-2}$ s $^{-1}$. The chlorophyll content by reading in a spectrophotometer. After four months no flowering induction was observed under the conditions studied. There were no statistical differences for leaves and roots numbers, and aerial part and root length. Plants grown on medium without sucrose and with 10 and 15 g L^{-1} of sucrose showed higher chlorophyll *a, b*, and total and carotenoid contents than the other treatments. It was concluded that the sucrose treatments used in isolation did not induce flowering in of the Cattleya walkeriana orchids species.

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470
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Area: Plant breeding
Tipo de presentación: Poster en formato PDF
Enviado por: Vanessa de Freitas Duarte

THE CHALLENGES OF SPEED BREEDING IN OAT (Avena sativa L.)

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Using the classic methods of plant breeding, it takes about ten years to develop a new oat cultivar. However, the increase in food demand and the fast pathogen evolution require quicker development of new oat cultivars. One option is the adoption of speed breeding, which consists in accelerating the plant development by incrementing light intensity and photoperiod length. The aim of this study was to evaluate oat genotypes under extremely long photoperiods to verify the feasibility of using speed breeding in oat breeding programs. The completely random experiment was performed in a growth chamber, with eight oat genotypes under 25ºC/20ºC diurnal/nocturnal temperature, 200µmol.s^{-1}.m^{-2} of light intensity, two photoperiods (16 and 22 hours), and five biological repetitions. The plant growth was measured by Haun´s scale and the floral transition by Bonnett´s scale. The 22h photoperiod accelerated the floral transition for the majority of the analyzed genotypes, except for URS Altiva and URS 21. The greatest changes in the number of days from emergence to floral transition between the photoperiods were observed to late and super late genotypes. The photoperiod also altered the flowering time of the genotypes, however LA 90105 did not flower at 22 hours, despite the normal floral transition. Other abnormalities in oat development were observed too. Taken together, these results indicate that the speed breeding method could reduce the oat cycle, but its application in the breeding programs requires the development of specific protocols to different oat genotypes.

471
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Enviado por: María José de Leone

The more you know: A role for circadian clock activators in stress responses

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Light signaling pathways interact with the circadian clock to help organisms synchronize physiological and developmental processes to periodical environmental changes. The plant photoreceptors responsible for clock resetting have been characterized, but signaling components that link the photoreceptors to the clock remain to be identified. Members of the family of NIGHT LIGHT–INDUCIBLE AND CLOCK-REGULATED (LNK) and REVEILLE (RVE) genes play key roles linking light regulation of gene expression to the control of daily and seasonal rhythms in *Arabidopsis thaliana*. Particularly, plants defective in LNK (*lnk1;2* and *lnkQ* quadruple mutants) and RVE (*rve8* and *rve4;6;8*) genes were shown to control circadian rhythms, photomorphogenic responses, and photoperiod-dependent flowering time. Despite the large number of processes controlled by these genes, there are no studies that explore their role in responses to stress. In recent work, we found that *lnk* mutants were more susceptible than the WT to bacterial infection. Here we analyze the role of the *LNK* and *RVE* gene families in both biotic and abiotic stress responses. We perform a meta-analysis of whole transcriptome sequencing RNAseq data from *lnk1;2* and *rve8* mutants, and *RVE8* over-expressive transgenic plants, finding that stress-related genes were enriched among the differentially expressed genes in all mutant backgrounds studied. Also, we found that *lnk* and *rve* mutants displayed altered responses to bacterial infection as well as several abiotic stress stimuli when compared to wild-type plants. Our work indicates that members of the *LNK* and RVE *families* have both distinctive functions in the control of stress responses, proving to be an essential link to orchestrate light-regulated plant plasticity in response to an ever-changing environment.

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472
GT981RD
Area: Abiotic Stress
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Enviado por: Talles de Oliveira Santos

Which physiological traits can be used for selection of popcorn germplasm efficient in the use of nitrogen?

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Nitrogen (N) plays an essential role in plant growth and in agricultural production. The excessive use of nitrogen fertilizers causes damage, not only economic, but also to the environment. In the context of the environmental impacts caused by agriculture, the maize breeding programs around the world seek to develop cultivars efficient in the use of nitrogen once this is the most viable strategy from an economic point of view. In this sense, this work aims to evaluate four contrasting popcorn inbred lines for nitrogen use efficiency and to point characteristics with high discriminatory power for selection of germplasm tolerant to conditions of low N in soil. The experiment was carried out in a completely randomized block design and the plants were evaluated in a greenhouse under high (224 mg/L) and low (22.4 mg/L) nitrogen conditions, using the Hoagland and Arnon solution modified for source of nitrate. At stage V6, gas exchange measurements were evaluated with an IRGA and leaf reflectance measurements with a mini spectrometer. Data were submitted to ANOVA and the discriminatory power of the characteristics was estimated using the GT Biplot technique. Under low N conditions, the traits with the highest discriminatory power were SIPI and NDVI, related, respectively, to the presence of carotenoids and leaf health. Under high N conditions, transpiration, photosynthetic rate and stomatal conductance stood out. Therefore, the selection of more tolerant plants under low N conditions is facilitated by non-destructive and fast-measurable leaf indexes, reducing the evaluation time of superior lines.

Financing: Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq/Brasil)

473
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Area: Abiotic Stress
Tipo de presentación: Poster en formato PDF
Enviado por: Romina de San Celedonio

Nitrogen use efficiency and remobilization in wheat and barley plants exposed to waterlogging at different developmental stages

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Waterlogging decreases grain yield in wheat and barley; however, its effect on plant N traits have not been thoroughly analyzed. The study's objective was to evaluate the N utilization efficiency (NUE) and the partitioning to grains in wheat and barley plants exposed to different waterlogging periods throughout the phenological cycle. Two pot experiments under contrasting environmental conditions were performed exposing wheat and barley plants to waterlogging during 15-20 days at five different developmental stages, from emergence to physiological maturity. A well-watered treatment was included as control. Grain N concentration, grain N yield, biomass N concentration at both anthesis and maturity, NUE (grain yield/ total N content in above-ground biomass at maturity), and N remobilization were measured. Both species responded similarly to waterlogging for most N traits. Reductions in grain N yield due to waterlogging were different depending on the moment of occurrence. The greatest reductions in grain N yield (46-77% with respect to the control) were for waterlogging from beginning of stem elongation to anthesis, which also showed the highest reductions in N remobilization, N uptake at maturity, and N partitioning to the grains, but only a slight decrease in NUE. Grain N concentration raised drastically (up to 45 mg N g DW^{-1}) only when grain yield was minimal. N content at maturity was linear and positively correlated to the total biomass (R^2=0.89 $p<0.001$). We concluded that the effect of waterlogging on the N economy of wheat and barley seems indirect and mediated by its impact on biomass production.

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Enviado por: Paulo César de Júnior

Foliar application of Boron in soybean under drought stress

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Micronutrients may act in drought alleviation by activation of certain physiological, biochemical and metabolic processes within the plant. Boron (B), an essential micronutrient, is involved in many processes inside the plants, however its contributions for drought alleviation are not well-defined. We tested the hypothesis that the foliar application of the micronutrient boron (B) can attenuate the effects caused by water deficit in soybean (Glycine max L.) plants, by stimulating the enzymatic antioxidant defense system. The experiment was conducted in an entirely randomized design, under 2x4 factorial scheme, with 5 repetitions. The variation factors were two water conditions (irrigated and deficit water) and four doses/sources of B (Water; B-MEA 150 mg B L^{-1}; B-MEA 300 mg B L^{-1} and H_3BO_3 150 mg B L^{-1}) totaling 8 treatments. The evaluations occurred according to the level of imposition of the water conditions: maximum stress and rehydration. The water stress induced increases in hydrogen peroxide and malondialdehyde levels, and in the activity of the enzymatic antioxidant system. In the leaves, it was possible to observe that the treatment with B-MEA 2, provided an increase in CAT activity in the water deficit condition. The low activity of the enzymes of the enzymatic antioxidant system in plants supplemented with B, is related to the low content of H_2O_2 found in the roots and by the low content of total MDA. This may be an indication that the other strategies were efficient in scavenging reactive oxygen species from the cells, such as the non-enzymatic antioxidant system.

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Stromal ascorbate peroxidase (APX7) silencing enhanced whole-plant transpiration and growth in rice plants

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Ascorbate peroxidases (APXs) are reactive oxygen species (ROS)-scavenger enzymes that act in the conversion of hydrogen peroxide (H_2O_2) to H_2O using ascorbate as specific electron donor. Plant APXs are encoded by a multigenic family, in which seven different isoforms are found in rice. APX7 is found in the stromal and scavenges the H_2O_2 released by redox reactions of the chloroplast electron transport chain. Previous results suggest that APX7 may have an important role during stomatal closure. However, the mechanisms by which rice APX7 modulate stomatal movements and transpiration remains to be determined, specially under stress conditions. Here, we characterized non-transformed (NT) and knockout to APX7 (*Osapx7*) rice plants under well-watered (WW) and water-deficit (WD) conditions. *Osapx7* line showed higher whole-plant transpiration, higher shoot and seed biomass, more panicles per plant and higher number of seeds than NT under WW condition. However, *Osapx7* plants displayed higher number of inviable seeds. This suggests that APX7 knockout disturbs seed development, affecting rice yield. No differences in leaf relative water content and membrane damage between *Osapx7* and NT were observe under WD. Our results collectively suggest that APX7 contribute to regulate whole plant transpiration but this did not affects WD resilience in rice.

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Characterization of carbon and nitrogen metabolisms in fruits of contrasting Acrocomia aculeata accessions

Characterization of carbon and nitrogen metabolisms in fruits of contrasting Acrocomia aculeata accessions

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The Macaúba palm (*Acrocomia aculeata*) has been highlighted by its high quality oil to support the expanding demand for vegetable oil in food, fuel and oleochemical industries. Although a promising alternative, studies on carbon and nitrogen metabolisms underlying development and ripening of its fruits remain scars. Here, we monitored contents of carbohydrates, protein, amino acid and lipids in the mesocarp and endosperm of macauba fruits during the fruit development. To investigate natural variation in fruits composition, we further studied three accessions of Macaúba that differ in the lipid content stored in the mesocarp of ripe fruits. Despite quite different tissues, mesocarp and endosperm exhibited similar trends of metabolites accumulation for most of the analyzed compounds. In the mesocarp, protein, amino acid, sucrose, starch and lipids tended to accumulate towards ripening, while glucose and fructose tended to decline in all accessions. Endosperm differed from mesocarp solely in the amino acid content, which decreased in ripe fruits. In this tissue, accessions accumulated carbohydrates differently. Accession PE showed comparable fructose and starch contents in the endosperm between the beginning of fruit development and ripening, while in accessions MG and MS, both compounds decreased and increased, respectively, towards ripening. Accession MG was highlighted by its highest lipid content in the two tissues indicating its potential for energy and cosmetic industries. These results provide insights into metabolic changes underlying development and ripening of Macaúba fruits and variability in oil content among accessions, which offer targets for breeding programs to enhance oil yield.

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PHA1 proton pump regulates sprout growth and sugar translocation during tuber sprouting in Solanum tuberosum

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After tuber dormancy break, sprouts begin to grow restarting the plant cycle. This process involves a rearrangement of carbohydrate metabolism. From the synthesis of reserve compounds in the tuber (sink), to their degradation, converting the tuber in a source of sugars that will sustain sprouts development.

Plasma membrane proton pump ATPases (PM-H^+-ATPases) play key roles in plants, mainly during growth. They extrude protons out of the cell, generating a membrane potential that provides the driving force for the transport of ions and metabolites through channels and transporters.

In potato, it has recently been described the key role of the PHA1 (*Solanum tuberosum* PM-H^+-ATPase 1) in the regulation of plant growth and tuber development. It promotes stolon elongation and tuber growth, regulating the sucrose-starch metabolism and transport.

In this work we studied the involvement of PHA1 in the regulation of tuber dormancy. We determined sugar content and sprouting progression in tubers obtained from potato plants overexpressing StPHA1 (PHA1-OE). Transgenic tubers showed longer sprouts, lower levels of soluble sugars and starch in the sprouted tubers, and lower levels of soluble sugars and higher levels of starch in the sprouts, compared to wild type ones. These results suggest that the activity of PHA1 might energize the apoplastic transport of sucrose from the tuber to the sprout to support its rapid growth.