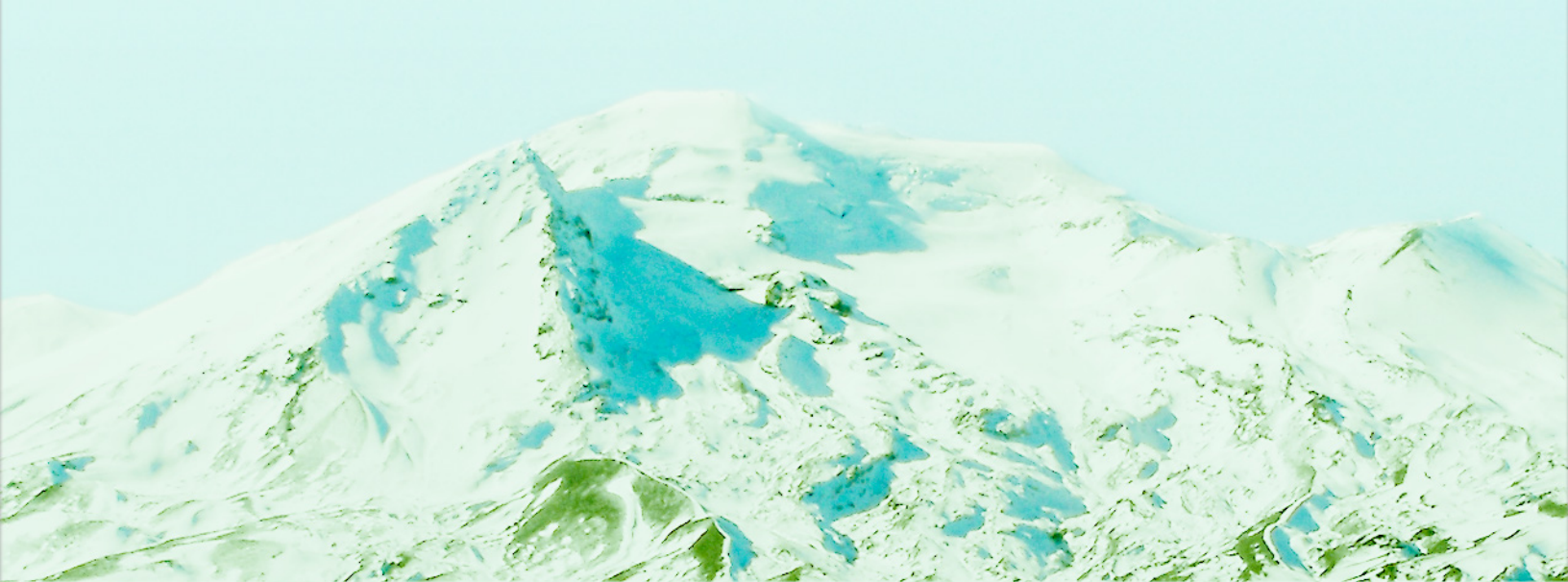




CHILEAN
SOCIETY OF
PLANT BIOLOGISTS

XI REUNIÓN DE BIOLOGÍA VEGETAL

28 de Noviembre al 1 de Diciembre 2016

Hotel Termas de Chillán

www.biologiavegetal.cl



PROGRAM AND ABSTRACTS



CHILEAN
SOCIETY OF
PLANT BIOLOGISTS

XI REUNIÓN DE BIOLOGÍA VEGETAL DE CHILE

28 de Noviembre al 1 de Diciembre 2016

Hotel Termas de Chillán, Chillán. Chile

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CHILEAN
SOCIETY OF
PLANT BIOLOGISTS



Universidad
de Concepción

November 28th to December 1st 2016

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SCIENTIFIC PROGRAM

MONDAY, NOVEMBER 28TH

16:00 - 18:00 **Registration**

18:30 - 19:00 **Opening welcome**

19:00 - 20:00 **Keynote Opening**

Chair: Rodrigo Gutiérrez

Orellana A, Centro de Biotecnología Vegetal and FONDAP Center for Genome Regulation.

Facultad de Ciencias Biológicas, Universidad Andres Bello, Santiago, Chile.

Coping with life in extreme environments: Cistanthe longiscapa, a case of study.

20:00 - 21:00 Welcome Reception

TUESDAY, NOVEMBER 29TH

09:00 - 11:20 **Plenary Session 1: Plant Genome Regulation**

Chairs: Francisca Blanco & Javier Canales

09:00 - 09:50 **Plenary Lecture 1: Plant Genome Regulation**

Saez-Vasquez J. ¹Laboratoire Génome et Développement des Plantes Université de Perpignan Via Domitia (UPVD).

Nucleolus: Structure and functions in plants.

09:50 - 10:20 **Holuigue L**, Herrera-Vásquez A., Seguel A., Ugalde J.M., Fonseca A., del Río V. and Lamig L. Departamento de Genética Molecular y Microbiología, Facultad de Ciencias Biológicas, Pontificia Universidad Católica De Chile.

Regulation of salicylic acid levels and its role in the redox modulation of defense responses against biotic and abiotic stress in Arabidopsis

10:20 - 10:40 **Contreras-López O**¹, Vidal E², Moyano T¹, Alvarez J¹, Sparks E³, Benfey P³, Gutiérrez R¹. ¹Genética Molecular y Microbiología, Ciencias Biológicas, Pontificia Universidad Católica De Chile. ²Centro de Genómica y Bioinformática, Ciencias, Universidad Mayor. ³Biology Duke University.

Spatio-temporal gene regulatory network analyses identify new transcription factors controlling response to nitrate in Arabidopsis roots.

10:40 - 11:00 Castro A¹, **Quiroz D**², Sanchez E³, Miccono M², Aguirre C³, Ramírez A⁴, Montes C³, Prieto H³. ¹Life Sciences Innovation Center University of California, Davis- Chile. ²Biotechnology Laboratory La Platina Research Station, Instituto de Investigaciones Agropecuarias, ³Biotechnology Laboratory La Platina Research Station, Instituto de Investigaciones Agropecuarias. ⁴Chemistry and Biological Sciences Faculty Universidad de Santiago de Chile.

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Synthesis of an artificial Vitis vinifera miRNA 319e using overlapping long primers and its application for gene silencing.

11:00 - 11:20 Gomez-Paez M¹, Corrales AR¹, Dominguez-Figueroa J¹, Carrillo L¹, Renau-Morata B², Molina R.-V², Nebauer S², Vicente-Carbajosa J¹, **Medina J¹**, ¹Centro de Biotecnología y Genómica de Plantas (UPM-INIA). Campus de Montegancedo. Madrid, Spain. ²Universitat Politècnica de València (UPV). Valencia. Spain.
Accelerating Gene Discovery for enhanced use of nitrogen resources and plant biomass production

11:20 - 11:50 **Coffee Break**

11:50 - 12:40 **Plenary Lecture 2: Plant Genome Regulation**

Chair: Rodrigo Gutiérrez

De Lorenzo L¹, Leonhardt N², Ott F³, San Leon D¹, Castrillo G¹, Gil E¹, Leyva A¹, Coupland G⁴, Nussaume L², Weigel D³, **Paz-Ares J¹**. ¹Department of Plant Molecular Genetics, Centro Nacional de Biotecnología, CSIC- Madrid, Spain. ²Institut de Biologie Environnementale et Biotechnologie, CNRS-CEA-Université Aix-Marseille, France. ³Department of Molecular Biology, Max Planck Institute for Developmental Biology, Germany. ⁴Department of Plant Developmental Biology, Max Planck Institute for Plant Breeding Research, Köln, Germany.
Genome wide analysis of targets of PHOSPHATE STARVATION RESPONSE REGULATOR 1 provides novel insights on Transcription factor function and on plant nutrient physiology.

12:40 - 14:10 **Plenary Session 2: Fruit Ripening and Post-Harvest**

Chairs: Raúl Herrera & Reinaldo Campos

12:40 - 13:10 Garrido-Bigotes A^{1,2}, Figueroa P², **Figueroa C²**. ¹Programa de Doctorado en Ciencias Forestales, Facultad de Ciencias Forestales, Universidad de Concepción. ²Phytohormone Research Lab, Instituto de Ciencias Biológicas, Universidad de Talca.
Toward understanding the role of jasmonates during development and ripening of strawberry fruit.

13:10 - 13:30 **Olmedo P¹**, Moreno A¹, Balic I¹, Campos-Vargas R¹, ¹Centro de Biotecnología Vegetal, Facultad de Ciencias Biológicas, Universidad Andrés Bello.
AcPPO: a Golgi localized polyphenol oxidase in cherimoya (Annona cherimola Mill.).

13:30 - 13:50 **Valenzuela-Riffo F¹**, Guajardo J¹, Stappung Y¹, Moya-León M¹, Herrera R¹, Morales-Quintana L¹ ¹Laboratorio de Fisiología Vegetal y Genética Molecular, Instituto de Ciencias Biológicas, Universidad de Talca.
Transcriptional analysis and structural characterization of Xyloglucan endotransglycosylase/hydrolases (XTH) involved in softening of Fragaria chiloensis fruit.

13:50 - 14:10 **Martínez J P¹**, Farias K⁷, Salinas L², Muenza V³, Alfaro J⁴, Gutierrez M³, Fuentes L⁵, Fuentes R⁶, Loyola N⁷, Lutts S⁸, ¹Centro Regional de Investigación La Cruz INIA-CREAS. ²INIA La Cruz. ⁴Centro de Biotecnología Universidad Técnica Federico Santa María. ⁵Centro Regional de

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Estudios de Alimentos y Salud (CREAS). ⁶Departamento de Industrias Universidad Técnica Federico Santa María. ⁷Escuela de Agronomía Universidad Católica Del Maule. ⁸Groupe de Recherche en Physiologie Végétale (GRPV), Earth and Life Institute-Agronomy (ELI-A) Université Catholique de Louvain.

Effect of rootstock on fruit quality in old Limachino tomato under greenhouse conditions in the region of Valparaíso.

14:10 - 15:30 **Light lunch and poster installation (Odd Numbers)**

15:30 - 17:00 **Plenary Session 3: Cell & Developmental Plant Biology**

Chairs: Lorena Norambuena & Rodrigo Gutiérrez

15:30 - 16:00 **Canales J¹**, Contreras-López O², Álvarez J², Gutiérrez R². ¹Instituto de Bioquímica y Microbiología, Ciencias, Universidad Austral De Chile. ²Departamento de Genética Molecular y Microbiología Pontificia Universidad Católica de Chile.

Nitrate control of root hair initiation is mediated by NRT1.1-TGA1/4 in Arabidopsis thaliana.

16:00 - 16:20 Ibeas M A¹, Grant S¹, Vargas-Perez J¹, **Roschztardt H¹**, ¹Genética Molecular y Microbiología Pontificia Universidad Católica De Chile.

Iron localization in seeds.

16:20 - 16:40 **Morales S¹**, Norambuena L¹, ¹Centro de Biología Molecular Vegetal, Facultad de Ciencias, Universidad De Chile.

Endocytic trafficking specifies lateral root founder cells through cell component relocation.

16:40 - 17:00 Gras D¹, Vidal E², Riveras E², **Undurraga S²**, Alabadi D³, Blázquez M³, Gutierrez R². ¹Instituto de Agrobiotecnología del Litoral (CONICET-UNL), Universidad Nacional del Litoral. ²Genética Molecular y Microbiología, Ciencias Biológicas, Pontificia Universidad Católica De Chile. ³Instituto de Biología Molecular y Celular de Plantas, CSIC, Universidad Politécnica de Valencia.

SMZ/SNZ and gibberellin signaling are required for nitrate-elicited delay of flowering time in Arabidopsis thaliana.

17:00 - 17:30 **Coffee Break**

17:30 - 18:20 **Plenary Lecture 3: Cell & Developmental Plant Biology**

Chair: Rodrigo Gutiérrez

Benkova E, Duclercq J, Cuesta C, and Hurny A. Institute of Science and Technology Austria Austria, Austria.

Auxin and cytokinin regulation of the root system architecture – antagonism or synergy?

18:30 - 20:30 **Poster session I: Odd Numbers**

20:30 - 22:00 **Dinner**

WEDNESDAY, NOVEMBER 30TH

09:00 - 09:50 **Plenary Lecture 4: Metabolism and Natural products**

Chair: Marely Cuba

Cernadas A^{1,2}, Conte M², Pivadori M³, Stegmayer G³, Asís R⁴, Sance M⁵, Asprelli P^{5,6}, Peralta I^{5,7}, Valle M. E⁸, Milone D³, **Carrari F^{1,2}**, ¹Universidad de Buenos Aires. Facultad de Agronomía. Buenos Aires, Argentina. ²Instituto de Biotecnología. CICVyA INTA Castelar, Buenos Aires. Argentina. ³Instituto de Investigación en Señales, Sistemas e Inteligencia Computacional (sinc(i)), FICH-UNL, CONICET, Argentina. ⁴CIBICI, Facultad de Ciencias Químicas, Universidad Nacional de Córdoba, Argentina. ⁵Universidad Nacional de Cuyo, Facultad de Ciencias Agrarias, Mendoza, Argentina. ⁶Instituto Nacional de Tecnología Agropecuaria, Estación Experimental La Consulta, Mendoza, Argentina. ⁷CCT CONICET Mendoza, Instituto Argentino de Investigaciones en Zonas Áridas, Mendoza, Argentina. ⁸Instituto de Biología Molecular y Celular de Rosario, CONICET, Universidad Nacional de Rosario, Argentina.

A multi-holistic approach to the understanding of the (epi)genetics and molecular bases determining nutritional quality in fruits.

09:50 - 11:20 **Plenary Session 4: Metabolism and Natural products**

Chairs: Michael Handford & Alejandra Moya

09:50 - 10:20 **Moya-León MA**, Lizana R, Morales-Quintana L, Gaete C, and Herrera R. Instituto de Ciencias Biológicas, Universidad de Talca, Chile.

Understanding the softening of Fragaria chiloensis fruit.

10:20 - 10:40 **Cabeza R¹**, Liese R², Schulze J³. ¹Departamento de Producción Agrícola, Facultad de Ciencias Agrarias, Universidad De Talca. ²Department of Plant Ecology and Ecosystems Research, Faculty of Biology, University of Goettingen. ³Plant Nutrition and Crop Physiology, Faculty of Agricultural Sciences, University of Goettingen.

Similar molecular mechanisms are responsible for the decline in nitrogenase activity in nodules of Medicago truncatula under different treatments.

10:40 - 11:00 **Miranda S¹**, Araya J¹, Handford M¹. ¹Centro de Biología Molecular Vegetal, Facultad de Ciencias, Universidad De Chile.

Solanum lycopersicum possesses mitochondrial and plastidial lipoyl synthases capable of increasing lipoylation levels in vivo.

11:00 - 11:20 **Restovic F¹**, Veloso V², Arce-Johnson P¹. ¹Departamento de Genética Molecular y Microbiología, Facultad de Ciencias Biológicas, Pontificia Universidad Católica De Chile. ²Facultad de Ciencias Universidad De Chile.

Evaluation of the plant biostimulant effect of Arthrospira maxima extracts.

11:20 - 11:50 **Coffee Break**

11:50 - 13:20 **Plenary Session 5: Biotic stress**

Chairs: Loreto Holuigue & Francisca Blanco

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- 11:50 - 12:20 **Dreyer I¹**. ¹Centro de Bioinformática y Simulación Molecular (CBSM) Universidad de Talca.
Cooperation through competition - Dynamics and microeconomics of a minimal nutrient trade system in arbuscular mycorrhizal symbiosis.
- 12:20 - 12:40 **Armijo G¹**, Agurto M¹, Meyer C¹, Nuñez C¹, Solano I¹, Schlechter R¹, Arce-Johnson P¹.
¹Departamento de Genética Molecular y Microbiología, Facultad de Ciencias Biológicas, Pontificia Universidad Católica De Chile.
Molecular characterization of Vitis vinifera resistance to fungal pathogens Botrytis cinerea and Erysiphe necator.
- 12:40 - 13:00 **Silva-Sanzana C¹**, Saez-Aguayo S¹, Salinas H¹, Chorbadian R², Blanco-Herrera F¹. ¹Centro de Biotecnología Vegetal, Facultad de Ciencias Biológicas, Universidad Andrés Bello. ²Departamento de Ciencias Vegetales, Facultad de Agronomía e Ingeniería Forestal, Pontificia Universidad Católica De Chile.
Pectin structure and composition dynamics during early and late plant-aphid interaction.
- 13:00 - 13:20 **Seguel A¹**, Jelenska J², Herrera A¹, Greenberg J², Wildermuth M³ and Holuigue L¹,
¹Departamento de Genética Molecular y Microbiología, Pontificia Universidad Católica de Chile. ²Department of Molecular Genetics and Cell Biology, The University of Chicago. ³Department of Plant and Microbial pathology, University of California, Berkeley.
PHB3 interacts with ICS1 and regulates the SA-mediated defense response controlling the levels of ICS1 in Arabidopsis thaliana.
- 13:20 - 14:10 **Plenary Lecture 5: Plant Stress**
Chair: Marely Cuba
- Graether S**, Boddington K, Clarke M, and Singh K. Department of Molecular and Cellular Biology, University of Guelph, Guelph, Ontario, Canada.
The role of disordered proteins in the protection of plants from abiotic stresses: an examination of the structure and function of dehydrins.
-
- 14:10 - 15:30 **Light lunch and poster installation (Even Numbers)**
-
- 15:30 - 17:00 **Plenary Session 6: Abiotic stress**
Chairs: Marely Cuba & Cristian Balbontín
- 15:30 - 16:00 **Tapia G¹**, Inostroza L¹, Del Pozo A², Vega M V¹, Mendez J¹, Yañez A², Arrey O¹, Cortez D¹.
¹Unidad de Recursos Genéticos Vegetales Instituto de Investigaciones Agropecuarias. ²Departamento de producción agrícola Universidad De Talca.
Traits and genes for drought tolerance: studies in germplasm collection of Lotus spp, tomatoes and wheat.
- 16:00 - 16:20 **Soto D¹**, Varala K², Araus V¹, Carrasco-Puga G¹, Díaz F¹, Nilo-Poyanco R¹, Coruzzi G², Gutiérrez R¹, ¹Departamento de Genética Molecular Pontificia Universidad Católica De Chile. ²Department of Biology New York University.

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Metatranscriptomic approach reveals conserved adaptive processes in Atacama Desert plants.

16:20 - 16:40 **Herrera-Vásquez A¹**, Fonseca A¹, Ugalde J¹, Seguel A¹, Vidal E², Moyano T¹, Gutierrez R¹, Holuigue L¹, ¹Genética Molecular y Microbiología, Ciencias Biológicas, Pontificia Universidad Católica De Chile. ²Centro de Genómica y Bioinformática Universidad Mayor.

Transcription factors from the TGA class II family control the antioxidant response against abiotic stress in Arabidopsis.

16:40 - 17:00 **Yáñez M¹**, Del Pozo A², Tapia G³, Guerra F⁴. ¹Ciencias Agrarias y Forestales Universidad Católica Del Maule. ²Centro de Mejoramiento Genético y Fenómica Vegetal, Ciencias Agrarias, Universidad De Talca. ³Recursos Genéticos INIA. ⁴Instituto de Ciencias Biológicas Universidad De Talca.

Stem carbohydrate dynamics and expression of genes involved in fructan accumulation and remobilization during grain growth in wheat (Triticum aestivum L.) genotypes with contrasting tolerance to water stress.

17:00 - 17:30 **Coffee Break**

17:30 - 18:20 **Plenary Lecture 6: Plant Stress**

Chair: Cristian Balbontín

Schreiber L. Dept. of Ecophysiology, IZMB, Bonn University.

Plant/environment interfaces in leaves and roots: biosynthesis and function of cutin and suberin.

18:30 - 20:30 **Poster Session 2 (Even Numbers)**

20:30 - 22:00 **Dinner**

THURSDAY, DECEMBER 1ST

09:00 - 09:50 **Plenary Lecture 7: Plant Breeding**

Chair: Gerardo Tapia

Sadras V. South Australian Research and Development Institute, Australia.

Understanding and quantifying the drivers of crop yield.

09:50 - 12:00 **Plenary Session 7: Phenomics and ecophysiology**

Chairs: Claudio Meneses & Paula Pimentel

09:50 - 10:20 **Lobos GA¹**, del Pozo A¹, ¹Centro de Mejoramiento Genético y Fenómica Vegetal, Facultad de Ciencias Agrarias, PIEI Adaptación de la Agricultura al Cambio Climático (A2C2), Universidad de Talca.

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Chile, a hotspot for plant phenomic.

10:20 - 10:40 **Mendez-Espinoza A¹**, Garriga M¹, Romero S¹, Estrada F¹, Escobar A¹, Lobos G¹, Del Pozo A¹.
¹Departamento de Producción Agrícola, Centro de Mejoramiento Genético y Fenómica Vegetal, Facultad de Ciencias Agrarias, Universidad De Talca.

Drought effect on leaf gas exchange and chlorophylls contents of four cereals grown in greenhouse.

10:40 - 11:00 **Romero-Bravo S¹**, Méndez-Espinoza AM¹, Garriga M¹, Estrada F¹, Escobar A¹, del Pozo A¹, Lobos GA¹. ¹Departamento de Producción Agrícola, Centro de Mejoramiento Genético y Fenómica Vegetal, Facultad de Ciencias Agrarias, Universidad De Talca.

High throughput phenotyping in an INIA wheat breeding program for drought tolerance selection.

11:00 - 11:30 **Coffee Break**

11:30 - 13:00 **Plenary Session 8: Genetic Resources & Plant Breeding**

Chairs: Claudia Stange & Boris Sagredo

11:30 - 12:00 **Sagredo B¹**, Donoso J¹, Lemus G¹, Almada R², Perez J¹, Bastias A¹, Rojas P¹, Martin C¹, Correa F¹, ¹Biotecnología y recursos naturales, INIA-Rayentué.²Genómica, Centro de estudios avanzados en fruticultura.

Molecular tools for Prunus sp.(L.) improvement

12:00 - 12:20 **Pacheco I¹**, Salazar J², Silva C¹, Shinya P², Morales H³, Peña A³, Infante R². ¹Laboratorio de Bioinformática y Expresión Génica, Instituto de Nutrición y Tecnología de los Alimentos (INTA), Universidad De Chile. ²Departamento de Producción Agrícola, Facultad de Ciencias Agronómicas, Universidad De Chile. ³Departamento de Agroindustria y Enología, Facultad de Ciencias Agronómicas, Universidad De Chile.

Polyphenol profiling in a Japanese plum (Prunus salicina L.) small cultivar collection: towards genetic dissection of functional compound content trait.

12:20 - 13:40 **Muñoz M¹**, Folch C¹, Kalazich J¹, ¹Centro Regional Experimental Remehue Instituto de Investigaciones Agropecuarias INIA.

Use and impact of biotechnology in plant breeding in Chile: experience of the potato breeding program of INIA.

12:40 - 13:00 **Auer C¹**, Rizzitello R¹, Chang C¹, ¹Plant Science University of Connecticut.

Ecological risks and benefits from the novel oilseed crop Camelina.

13:30 - 15:30 **Light lunch**

15:30 - 16:30 **Closure Plenary Lecture: Metabolism and natural products**

Chair: Raúl Herrera

Allan A¹. ¹ Breeding and Genomics Plant & Food Research. New Zealand
Exploring all the options towards engineering an even healthier apple.

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16:30 - 17:00 **Coffee Break**

17:00 - 20:00 **Free Afternoon**

20:30 - 22:00 **Conference Dinner & awards**

22:00 **Conference Party**

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KEYNOTE LECTURES

Keynote Opening

Orellana Ariel¹, ¹Centro de Biotecnología Vegetal and FONDAP Center for Genome Regulation. Facultad de Ciencias Biológicas, Universidad Andres Bello, Santiago, Chile.

COPING WITH LIFE IN EXTREME ENVIRONMENTS: *CISTANTHE LONGISCAPA*, A CASE OF STUDY

aorellana@unab.cl

The Atacama Desert is one the oldest and driest places on earth, with high radiation levels and precipitation levels that range from 100mm to less than 10 mm per year at the hyperarid core. Episodes of rainfall exceeding these levels occur few times every decade and are responsible for triggering the rise of a rich community of plant species in a phenomenon known as "blooming of the desert". *Cistanthe longiscapa*, an annual species from the Montiaceae family, is the most abundant sighted species during this phenomenon and can withstand a prolonged period (3-4 months) without further precipitations. We found that this species exhibits eco-physiological adaptations that are probably related to the high irradiation dry environment it inhabits. To better understand how these adaptations and to detect molecular mechanisms related to its resilience to high irradiation and water scarcity, the genome of this species was sequenced. The predicted genome size was of nearly 800 Mbp and a gene number estimated of 31,133. Both karyotype and kmer analysis suggest that the species is diploid, even though some level of duplication typical of polyploid species was found. This higher than expected number of duplicated genes can be explained by a family level conserved ancient whole genome duplication. Comparative genomics allowed the detection of gene complement size expansion for certain gene families related to response to high radiation protection (xanthophyll cycle and early light-induced proteins). Several of these expanded genes displayed differential gene expression when assessed in six different tissues, supporting their possible neofunctionalization after duplication.

Acknowledgments: Fondap-CRG 15090007, Basal PB-16.

Keynote Closure

EXPLORING ALL THE OPTIONS TOWARDS ENGINEERING AN EVEN HEALTHIER APPLE

Allan Andrew¹, ¹The New Zealand Institute for Plant & Food Research Limited, Private Bag 92169, Auckland, 1142, New Zealand.

andrew.allan@plantandfood.co.nz

Apple is considered historically one of the most convenient and healthy options for the daily diet. With reasonable levels of flavonoids, vitamin C and vitamin A, this perception is not inaccurate. However, most of apple's health benefits are located in the skin, leaving a large volume of flesh ready for "improvement". We have been manipulating levels of secondary metabolites in apple for over a decade, through both conventional breeding and GM approaches. Two new breeding technologies - rapid flowering for plant breeding, and gene editing - produce plants without new DNA. These techniques offer ways of providing large changes in the health potential of apple, if the public will accept the resulting fruit. Exciting new results in regulating levels of vitamin C, anthocyanins, and carotenoids are the targets of our approach, which aims to provide the consumer with new cultivars that have measurable benefits.

PLENARY LECTURES

Plenary Lecture 1: Cell and Developmental Plant Biology

NUCLEOLUS: STRUCTURE AND FUNCTIONS IN PLANTS

Saez-Vasquez J¹, ¹Laboratoire Génome et Développement des Plantes Université de Perpignan Via Domitia (UPVD).

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The nucleolus is the most prominent nuclear substructure. Its functional state has long been known to be intimately linked to ribosome biogenesis, with direct connections to cell growth and proliferation. The driving force for nucleolar assembly is ribosomal DNA (rDNA) transcription and processing of 45S RNA precursors (pre-rRNA) transcribed by RNA polymerase I (RNA pol I). It is also clear that this subnuclear compartment plays wider roles, notably in global chromatin organization, protein sequestering and in cellular responses to intrinsic and environmental changes.

The talk will illustrate findings regarding factors and mechanism controlling ON/OFF switching of transcriptionally competent rRNA genes and molecular processes associated with the activity of the nucleolus. It will be also presented a series of findings that link nucleolus structure and long intergenic non coding rRNA (lincRNA) expression to the heat stress response in Arabidopsis. How these and other activities required for processing of non-coding RNA might affect functional and structural nucleolar organization will be reported.

Plenary Lecture 2: Plant Genome Regulation

GENOME WIDE ANALYSIS OF TARGETS OF PHOSPHATE STARVATION RESPONSE REGULATOR 1 PROVIDES NOVEL INSIGHTS ON TRANSCRIPTION FACTOR FUNCTION AND ON PLANT NUTRIENT PHYSIOLOGY

de Lorenzo L¹, Leonhardt N², Ott F³, San Leon D¹, Castrillo G¹, Gil E¹, Leyva A¹, Coupland G⁴, Nussaume L², Weigel D³, and Paz-Ares J¹. ¹Department of Plant Molecular Genetics, Centro Nacional de Biotecnología, CSIC Madrid, Spain. ²UMR7265, Service de Biologie Végétale et de Microbiologie Environnementales, Institut de Biologie Environnementale et Biotechnologie, CNRS-CEA-Université Aix-Marseille, France. ³Department of Molecular Biology, Max Planck Institute for Developmental Biology, Germany. ⁴Department of Plant Developmental Biology, Max Planck Institute for Plant Breeding Research, Germany.

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Plants evolved an array of adaptive responses to cope with growth under low Pi regimens. These involve developmental and biochemical changes, aiming to increase Pi acquisition and use efficiency and to protect the plant from the stress caused by Pi starvation. PHOSPHATE (Pi) STARVATION RESPONSE1 (PHR1) transcription factor (TF) is a central regulator of plant Pi-starvation responses. We found PHR1 binds 2622 sites in the Arabidopsis genome, 664 corresponding to Pi-starvation responsive genes. These sites are enriched in two motifs, P1BSI and P1BSII, which display high and low intrinsic binding affinity and are bound by PHR1 as dimer and monomer, respectively. Results using fusions of multimers of P1BSII to a minimal promoter showed it is a bona fide Pi starvation response element, although of lower strength than P1BSI, previously studied. Pi-starvation induced (psi) P1BSI and P1BSII targets display significant differences in ontology term enrichment, and these motifs exhibit different evolutionary constraints; nevertheless, P1BSI and P1BSII conservation and enrichment in unrelated TF binding sites surrounding these motifs is not only associated to transcriptional output, but also to site occupancy. These findings inform on the functionality of PHR1 binding sites not producing a concurrent effect on transcription. At the physiological ground, we found that psi PHR1 targets are overrepresented in drought/osmotic stress induced genes. Osmotic stress induction of psi genes was found to be dependent on PHR1. We will discuss on the potential adaptive importance of the cross-talk between the Osmotic stress and Pi starvation signalling pathways.

Plenary Lecture 3: Cell and Developmental Plant Biology

AUXIN AND CYTOKININ REGULATION OF THE ROOT SYSTEM ARCHITECTURE – ANTAGONISM OR SYNERGY?

Benkova E, Duclercq J, Cuesta C and Hurny A. Institute of Science and Technology Austria Austria, Am Campus 1, 3400 Klosterneuburg, Austria.

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The plant hormones auxin and cytokinin are central endogenous signaling molecules that regulate root growth and lateral root organogenesis. Stimulatory effect of auxin is counterbalanced by cytokinin, and thus, tight control and mutual balance of their antagonistic activities are particularly important during the early phases of lateral root organogenesis to ensure continuous lateral root initiation and proper development of lateral root primordia. To investigate the molecular mechanism of the auxin and cytokinin hormonal crosstalk, genome-wide transcriptome profiling was taken as the main strategy. We aimed to identify genes at whose transcriptional regulation auxin and cytokinin pathways converge during early lateral root organogenesis. The SYNERGISTIC AUXIN CYTOKININ1 (SYAC1) gene coding for a protein of unknown function was identified as a gene synergistically regulated by both hormones. Further progress in understanding of SYAC1 role in auxin-cytokinin crosstalk and regulation of the root system architecture will be discussed.

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Plenary Lecture 4: Metabolism and Natural products

A MULTI-HOLISTIC APPROACH TO THE UNDERSTANDING OF THE (EPI)GENETICS AND MOLECULAR BASES DETERMINING NUTRITIONAL QUALITY IN FRUITS

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The thorough understanding of the relationships between the variables that determine productivity and quality in crop species requires holistic approaches based on the collection and analysis of data exposing changes in these variables at different organizational levels: molecular, metabolic and phenotypic. Tomato, in addition to its nutritional and economic importance, is an excellent model for the application of systemic approaches to the understanding of the problems of productivity and quality, since it has a wide genetic variability (natural and induced), sequenced genomes of different accessions and related species, along with a battery of high processivity phenotyping techniques set for the species. By using a germplasm collection from along the Argentine Andean valleys and cultivated ex-situ during several growing seasons an extensive set of data about morpho-agronomic and biochemical characters; including transcriptomics, metabolomics and sensory attributes has been obtained. The application multi-modal clustering algorithms that can fuse such diverse data set without normalization reveals unknown associations between the assayed variables and allow selecting elite accessions that can be used as input for breeding programs of the species.

Plenary Lecture 5: Plant Stress

THE ROLE OF DISORDERED PROTEINS IN THE PROTECTION OF PLANTS FROM ABIOTIC STRESSES: AN EXAMINATION OF THE STRUCTURE AND FUNCTION OF DEHYDRINS

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Plants express a large number of different proteins to protect them from damage caused by drought, cold, and high salinity. One family of proteins, known as dehydrins (dehydration proteins), appears to be key to a plants survival. Our research revolves around understanding the structure and function of dehydrins *in vitro*, with a long-term goal of understanding dehydrins in an *in vivo* environment. Dehydrins are intrinsically disordered proteins, that is, they do not have a defined 3D structure, which also results in overall poor sequence conservation. A bioinformatics analysis of over 600 dehydrin sequences from the Phytozome and Pfam databases shows us which residues are conserved and which are not. Biochemical analysis shows that the disordered nature of dehydrins is important for protection of enzymes from damage caused by freezing. In contrast, dehydrins gain some structure in the presence of membranes, which is necessary for the protein to interact with and protect membranes from cold stress. We will also show unpublished data that suggest that dehydrins are able to protect DNA from damage caused by oxidative stress. Lastly, we will discuss future experiments that will examine the structure and function of dehydrins inside of plant cells using advance NMR techniques.

SPG thanks NSERC for funding this project, and NSERC PCGS and OGS scholarships for KFB.

Plenary Lecture 6: Plant Stress

PLANT/ENVIRONMENT INTERFACES IN LEAVES AND ROOTS: BIOSYNTHESIS AND FUNCTION OF CUTIN AND SUBERIN

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Living plant tissue is separated from the surrounding environment by extracellular lipophilic biopolymers. The interface between the atmosphere and leaves is formed by the cuticle, composed of cutin and cuticular waxes, sealing outer epidermal cell walls and covering fruit surfaces. Soil/root interfaces are essentially formed by exodermal and endodermal tissue, each characterized by a single layer of cells with suberized cell walls. As main function these lipophilic interfaces form barriers regulating water and solute transport between the living plant tissue and the surrounding environment and they significantly help to cope with abiotic and biotic stress factors. Genes and biosynthetic pathways involved in cutin, suberin and wax formation will be presented and discussed. Cuticular transport barriers of Arabidopsis leaves comparing wildtype with wax and/or cutin mutants have been conducted. Results indicated that cuticular barrier properties of Arabidopsis leaves either increased or did not change at all when wax and/or cutin amounts were genetically increased or decreased. An improvement of cuticular barrier properties with enhanced wax and/or cutin amounts was not observed. Chemical composition and barrier properties of suberized roots have been investigated with rice and Arabidopsis. Salt and oxygen stress significantly enhanced suberization in rice roots, thus reducing radial uptake of NaCl and radial loss of oxygen from the root to the soil environment. Arabidopsis mutants with enhanced root suberization were more droughts tolerant, whereas Arabidopsis mutants with reduced amounts of root suberin were characterized by significantly enhanced radial root hydraulic conductivities. On the basis of these results barrier properties of cutinized leaves and suberized roots will be compared and similarities and differences between these two important lipophilic plant environment interfaces will quantitatively be discussed on the basis of permeances.

Plenary Lecture 7: Plant Breeding

UNDERSTANDING AND QUANTIFYING THE DRIVERS OF CROP YIELD

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Yield depends on the technology used to establish, protect, grow and harvest the crop, the environment where it is grown and the interaction between environment and technology. In the short to medium term (5-10 years), the environment over-rides technology. In the long-term (decades), technology increases yield, whereas the environment modulates the rate of technological gain and contributes to often significant deviations around time-trends. Despite its importance, the environment is often characterised superficially, nominally as location and season, high vs low input, etc. This paper outlines methods to quantify and compare the drought environments for wheat, field pea and chickpea in Australia, and their implications for crop improvement and management.

We update discussions on level of organisation and scaling [1], reinforcing the notion that some traits scale from molecular to crop level (e.g. herbicide resistance) but other traits do not scale (e.g. photosynthesis, yield). Natural selection favours competitive plants whereas selection for seed yield in agriculture favours less competitive types, which conform to the phenotype of Donald's "communal plant". Experiments in chickpea showed high-yielding lines are less responsive to competition, in agreement with Donald's theory and Fst genome scan highlights the lack overlap in the genetic architecture underlying yield of crop stands and yield under relaxed competition. The impact of plant-plant interactions is further illustrated in sunflower, where self-organisation of stands mediated by light quality is shown to increase oil production per unit land area.

[1] Sadras V O and Richards R A. 2014. Improvement of crop yield in dry environments: benchmarks, levels of organisation and the role of nitrogen. *Journal of Experimental Botany*, 65:1981-1995.

Plenary Session: Plant Genome Regulation

REGULATION OF SALICYLIC ACID LEVELS AND ITS ROLE IN THE REDOX MODULATION OF DEFENSE RESPONSES AGAINST BIOTIC AND ABIOTIC STRESS IN ARABIDOPSIS

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Since its discovery in the early 90's, the importance of salicylic acid (SA) has been increasingly recognized because of its crucial role in the defense response against biotic and abiotic stress. SA is responsible for transcriptional changes occurring in the infected/damaged tissues, as well as in the neighboring cells, orchestrating the local and systemic defense responses. Evidence also indicates that SA is involved in the redox modulation of the defense response, interplaying with redox signals such as ROS and glutathione. In spite of the importance of SA as a stress hormone, we still ignore essential aspects of its mode of action. Here we show two aspects of our studies on SA function. On one hand, we show evidence for a new mechanism that control SA levels. Our results indicate that prohibitin 3 (PHB3), through its interaction with isochorismate synthase 1 (ICS1), the main enzyme involved in SA biosynthesis, regulates the levels of SA. On the other hand, we will focus in how SA and glutathione interplay during signaling and modulation of redox status in the stressed tissues. Particularly, we will show evidence of the contribution of proteins with antioxidant functions (glutaredoxins and glutathione S-transferases), coded by SA-responsive genes, in the redox modulation of the local and systemic defense response.

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SPATIO-TEMPORAL GENE REGULATORY NETWORK ANALYSES IDENTIFY NEW TRANSCRIPTION FACTORS CONTROLLING RESPONSE TO NITRATE IN ARABIDOPSIS ROOTS

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Genome-wide transcriptional analyses have provided an impressive catalog of N-responsive genes participating in a wide range of processes. The majority of these genome-wide studies were performed at defined time points in whole plants or organs impairing our understanding of cell-specific regulatory gene networks and how they interact to coordinate organ responses over time. In this research, we mapped and characterized dynamic N-regulatory networks acting within cell types in Arabidopsis roots. We combined cell-sorting, transcriptomics analyses and integrative network bioinformatics to identify cell-type-specific gene regulatory networks controlling root responses to nitrate over time. Our experimental design uncovered thousands of new nitrate-regulated genes, most of them regulated in one cell-type and one-time point. Clusters of genes with specific regulation patterns at cell-type level were significantly enriched in different biological processes. Besides the diversity of functions regulated by nitrate, there is a limited repertoire of gene expression patterns indicating highly structured regulatory networks. Analysis of predicted gene regulatory networks revealed that network complexity and specificity varies in cell types and over time. Our data show spatiotemporal analysis not only increases the number of genes involved in an organ response to stimulus, but also show that expression dynamics are cell-type dependent and coordinated at biological processes level. At the core of this regulatory network, we found five main clusters of transcription factor that command the nitrate response in all cell types. We were able to identify new transcription factors controlling response to nitrate in Arabidopsis roots.

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SYNTHESIS OF AN ARTIFICIAL *VITIS VINIFERA* MiRNA 319E USING OVERLAPPING LONG PRIMERS AND ITS APPLICATION FOR GENE SILENCING

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The conserved mechanism of action of micro-RNAs (miRNAs) as regulators of gene expression has allowed the use of artificial miRNAs (amiRNAs) as a powerful tool for candidate gene evaluation in plants. Based on the use of a *Vitis vinifera* miRNA molecule (vvi-miR319e), the present work presents a new methodology for designing artificial miR319e precursors (pre-amiR319e). As a proof of concept, we silenced the green fluorescent protein (GFP) gene in transgenic *Nicotiana benthamiana* plants. This methodology includes a two-step PCR reaction in which overlapping long primers allow for the

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complete generation of pre-amiR319e-GFP molecules that are adequate for recombination into Gateway vectors with no further requirements. The seed region in amiRNA was directed against the 3'-end portion of the GFP gene. Three groups of transformed *N. benthamiana* plants were generated: GFP-, amiR319e-GFP-, and GFP plus miR319e-GFP-expressing vectors. A similar group of wild-type plants was included. Confocal microscopy evaluation of these groups revealed strong silencing of the GFP phenotype in the double GFP plus amiR319e-GFP group. The molecular characterization of silenced plants was achieved via modified 5'RACE of the GFP mRNA and revealed the occurrence of a partial, 3'-end GFP mRNA molecule that was generated *in planta*. In addition, large-scale small RNA sequencing confirmed the occurrence of the expected 21-nt miR319e-GFP species and other 22- and 24-nt species that exhibited sequence relationships with the expected amiRNA. These results highlight the possibility of using vvi-MIR319 as a template for the generation of single amiRNAs as a tool for gene silencing in plants.

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ACCELERATING GENE DISCOVERY FOR ENHANCED USE OF NITROGEN RESOURCES AND PLANT BIOMASS PRODUCTION

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During development plants usually have to encounter simultaneously with multiple nutrient stress conditions. Until now research has been mainly focused in the study of plant responses to individual stresses, and understanding of adaptation to combinatorial stress is reduced, but indicative of non-additive genetic effects. Different of transcriptomic and metabolomic analysis and functional characterization of individual genes has found out a significant crosstalk between signaling pathways for nutrient and water stress adaptation. We are interested in the study of regulatory networks and signaling pathways involved in plant responses to adverse conditions such as limitation of water and nutrients like nitrate and sulfur and to identify new candidate genes that can be used in a new generation of improved-biomass-breeding programs in crops.

The tolerance to these heterogeneous stresses is a very complex phenomenon, which involve a flexible and dynamic metabolic adjustment that implies changes in nutrient use efficiency, partitioning of assimilates and changes in plant organs like roots and cell structures as the plant cell wall and endoplasmic reticulum. We set up comprehensive forward genetic screenings and systems biology approaches that allow us to identified different Arabidopsis transcription factors that might be involved in metabolic adjustment in response to those nutrition limitations. Remarkably, overexpression of some those transcription factors in tomato, enhance tolerance to several nutrient deficiencies and significant increase in biomass production.

Plenary Session: Fruit Ripening and Post-Harvest

TOWARD UNDERSTANDING THE ROLE OF JASMONATES DURING DEVELOPMENT AND RIPENING OF STRAWBERRY FRUIT

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Jasmonates (JAs) are phytohormones involved in stress responses, reproductive development and production of secondary metabolites, although its role in development and ripening of fleshy fruit is not well known. Exogenous methyl jasmonate (MeJA) promotes anthocyanin and lignin accumulation in Chilean strawberry (*Fragaria chiloensis*) fruit. However, until now the role of endogenous JAs has not been reported in strawberry species. In the present study, we characterized the temporal dynamics of JAs biosynthesis during development and ripening of strawberry (*Fragaria xananassa*) fruit. Moreover, we studied whether there is a hormonal relationship between JAs and abscisic acid (ABA), the main ripening-associated phytohormone described in strawberry. The endogenous oxylipins contents such as 12-oxo-phytodienoic acid, jasmonic acid, MeJA and the bioactive JA, jamonoyl-isoleucine (JA-Ile), were quantified by

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chromatography-tandem mass spectrometry (LC-MS/MS). Phytohormone levels were compared with expression of genes encoding for JA metabolism and signalling components. Noteworthy, the expression levels of JA-related genes exhibited a significant decrease concomitant with a reduction of JA-Ile level from flowering to ripe stages, being this behavior inversely correlated to ABA profile. Interestingly, exogenous application of MeJA to immature fruits triggered an anthocyanin accumulation along with increased JA-Ile level and a concomitant downregulation of *FaNCED1*, encoding a rate-limiting step for ABA biosynthesis, besides a decreased level of ABA. Together, these results elucidate JAs homeostasis during strawberry fruit development, suggesting that JA-Ile could participate in early fruit development. Finally, we propose an opposite relationship between JA and ABA during fruit development and ripening that could be relevant to regulate the ripening process in a non-climacteric fruit as strawberry.

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AcPPO: A GOLGI LOCALIZED POLYPHENOL OXIDASE IN CHERIMOYA (*ANNONA CHERIMOLA* MILL.)

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Cherimoya (*Annona cherimola* Mill.) is an exotic tropical fruit with attractive organoleptic characteristics, but highly perishable and susceptible to browning in postharvest. The browning is caused mainly by the activity of the enzyme polyphenol oxidase (PPO). The cherimoya PPO (AcPPO) catalyzes the oxidation of diphenols to quinones, which spontaneously polymerize to form brown pigments that reduce the consumers' acceptability. In the literature, there is no consensus about the biological role of PPO and its subcellular localization has been described in plastids and vacuoles in different plants. In the present work we studied the subcellular localization of polyphenol oxidase in cherimoya leaves. In order to determine where AcPPO enzyme is present, we cloned and performed a translational fusion of this gene previously described (GenBank: DQ990911.1) with the green fluorescent protein (GFP). Confocal microscopy experiments showed that AcPPO-GFP signal co-localized with a Golgi marker (Gm-ManI) in tobacco leaves. Additionally, we carried out sucrose density gradient centrifugations using cherimoya and transiently expressed AcPPO-GFP tobacco leaves. Sucrose density fractionations of cherimoya leaves revealed a correlation between maximum enzyme activity of AcPPO and Golgi apparatus markers. Transient expression assays also shown a correlation of activity of AcPPO-GFP with Golgi markers in tobacco leaves. Moreover, topology analysis of Golgi enriched fractions treated with Triton X-100 and proteinase K in cherimoya and tobacco leaves pointed out that AcPPO is facing the lumen of the Golgi apparatus. These results open new perspectives about the functionality of AcPPO in the secretory pathway, its action on cherimoya fruit physiology and the evolution of this enzyme.

TRANSCRIPTIONAL ANALYSIS AND STRUCTURAL CHARACTERIZATION OF XYLOGLUCAN ENDOTRANSGLYCOSYLASE/HYDROLASES (XTH) INVOLVED IN SOFTENING OF *FRAGARIA CHILOENSIS* FRUIT

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Fragaria chiloensis has potential as an exotic fruit in the international market, however its fast softening produced by changes in the cellulose-hemicellulose fraction take place during ripening of the fruit and this limits its commercialization. Several studies have identified genes encoding proteins named Xyloglucan endotransglycosidase/hydrolase (XTH), which have been associated to fruit ripening. Therefore, in order to provide new data relating to these enzymes in the ripening process of *F. chiloensis*, libraries obtained by RNAseq in different ripening stages were analyzed. From those libraries, 15 putative sequences was identified and classified as XTHs. In order to validate these sequences and have a first approach of their participation in this phenomenon, a transcriptomic profiling of 5 genes coding for XTHs were analyzed by qPCR. Interestingly, differential but overlapping expression patterns was observed for them. With the aim to propose different roles for them, their 3D models were built by comparative modeling methodology. The models obtained were similar and displayed a similar β -jellyroll-type structure that is typical of GH16 enzyme family that comprises a curvature generated by 8 antiparallel β -sheets holds the catalytic ExDxE motif that is oriented towards the central cavity of the protein. The interaction of a set of putative substrates with the protein was

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explored using molecular docking and molecular dynamics simulations, finding a better interaction with xyloglucans than other putative cell wall ligands. Our results provide a view at atomic level of the XTHs role in the cell wall disassembly, which is congruent with the probable participation of XTHs during softening of *F. chiloensis* fruit. Acknowledgments: FONDECYT N° 11150543, Anillo ACT-1110 project and PAI/Academia #79140027 projects supported this work.

EFFECT OF ROOTSTOCK ON FRUIT QUALITY IN OLD LIMACHINO TOMATO UNDER GREENHOUSE CONDITIONS IN THE REGION OF VALPARAISO

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Research on rootstock in terms of productivity and fruit specific quality has not been very developed in local tomato varieties with good organoleptic characteristics (color, taste, and aroma). In this line, our proposal considers the implementation of graft management in the well-known old Limachino Tomato. The purpose of the study was to evaluate the effect of a specific INIA-rootstock on growth, productivity, and specific quality (agronomic, functional, and sensorial) of this specie compared to the long-lived tomato (LV) under greenhouse conditions. The trial took place at INIA-La Cruz in the region of Valparaíso. Three treatments were evaluated: long-lived tomato (LV), self-grafted old Limachino tomato (L/L) and the old Limachino tomato grafted onto INIA rootstock (L/P), with a design of six completely randomized blocks. Growth, productivity, and specific quality (agronomic, functional, and sensorial) of the fruit were evaluated across five harvests of the three treatments. No treatment effect was observed upon fresh biomass nor in dry weight. However, productivity in the first four harvests was better in treatments L/L and L/P of the old Limachino tomato than in the LV one. The treatments L/L and L/P presented smaller sizes, fruit weight and firmness but greater titratable acidity, polyphenols and antioxidant capacity (FRAP) compared to the LV tomato. In both treatments, the old Limachino tomato presented superior taste, color, and aroma, but a worse texture compared to the LV tomato. We conclude that this specific INIA-rootstock did not have a significant effect on the quality of the Limachino tomato fruit, but it presented better health attributes than the LV tomato.

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Plenary Session: Cell & Developmental Plant Biology

NITRATE CONTROL OF ROOT HAIR INITIATION IS MEDIATED BY NRT1.1-TGA1/4 IN *ARABIDOPSIS THALIANA*

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Root hairs are tubular outgrowths of root epidermal cells specialized in water and nutrient uptake. The importance of root hairs for nutrient uptake and plant growth has been reported for phosphate and other nutrients in several plant species. However, the importance of root hairs for nitrogen nutrition has not been addressed in detail. Nitrate, the main source of nitrogen for plants in aerobic soils, has an important signaling role regulating global gene expression metabolic, physiological and developmental processes in plants. In this work, we identified the molecular mechanism by which nitrate controls root hair development in *Arabidopsis thaliana*. We also showed root hairs have an important role in nitrate

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acquisition in *A. thaliana*. Molecular genetics analysis of several mutants reveals the NRT1.1-TGA1/TGA4 nitrate signaling pathway regulates root hair initiation by directly regulating expression of root hair cell fate specification genes in *A. thaliana*. This developmental response represents an important strategy for enhanced nitrogen acquisition when plants reach nitrate-enriched soil patches. The root hair response to nitrate availability and the molecular mechanism described here represents an attractive new target for future breeding programs to enhance nitrogen-use efficiency and crop yield. Acknowledgments: FONDAP 15090007, Millennium Nucleus Center For Plant Systems And Synthetic Biology (NC130030), FONDECYT 1141097 And FONDECYT 11150070.

IRON LOCALIZATION IN SEEDS

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The mechanisms of iron uptake in plant roots are now well described, but those who govern the distribution to organs, cells and organelles targets are still very poorly understood. The development of methods allowing iron visualization in plant tissues has been key in the significant progress observed in our field last years. Recently, a histochemical iron staining method (Perls/DAB) has been used on plant tissues. Thanks to this approach it has been possible to identify new pools of iron in plants. Here, we will show for first time where iron accumulates in different seed plants. Our results open new questions about the mechanisms of iron distribution and accumulation in seeds, and could be used as a basis for the development of novel biotechnological strategies to increasing total iron content in seeds for human consumption.

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ENDOCYTIC TRAFFICKING SPECIFIES LATERAL ROOT FOUNDER CELLS THROUGH CELL COMPONENT RELOCATION

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Lateral roots (LR) are developed postembryonically from the root pericycle cells that acquire the fate to be LR founder cells (LRFC) in a process called priming that involves specification and activation. LRFC activation includes the induction of the transcription factor GATA23, accumulation of the membrane associated-kinase regulator MAKR4 and cellular events in neighboring cells overlying LR primordia. However, the nature of the event that defines LRFC specification is still unclear. Besides, we have shown that the induction of endocytic trafficking towards the vacuole promotes LR formation independently of the auxin receptor SCF^{TIR1/AFBs} by means of the synthetic compound Sortin2. This compound induces *de novo* LR formation suggesting that affects LR priming. With this background, the goal of ourwork is unraveling the role of the endocytic trafficking towards the vacuole in priming events. We have found that Sortin2 promotes the induction of GATA23 and MAKR4. Interestingly, the temporal analysis of Sortin2-triggered events revealed that the induction of trafficking towards the vacuole is detected before LRFC activation events. This evidence strongly suggests that protein trafficking is indeed the leading event for LRFC specification. Furthermore, genetic approach by means of known protein trafficking or LR formation-defective mutants, reinforces the link between these two processes. Indeed, particular trafficking pathways for relocating cell component are important for Sortin2 LRFC specification. Together these results place a cellular process of LR-program where the induction of endocytosis towards the vacuole, as well as, relocation among compartments promote the specification of LRFC, allowing root architecture remodeling in *Arabidopsis thaliana*. Acknowledgments: FONDECYT 1120289. VID Enlace Grant 2016 ENL015/16 Universidad De Chile. CONICYT-PCHA /Magister Nacional/ 2014-22141870.

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SMZ/SNZ AND GIBBERELLIN SIGNALING ARE REQUIRED FOR NITRATE-ELICITED DELAY OF FLOWERING TIME IN *ARABIDOPSIS THALIANA*

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Reproductive success of plants largely depends on the correct programming of developmental phase transitions, particularly the shift from vegetative to reproductive growth. The timing of this transition is finely regulated by the integration of an array of environmental and endogenous factors. Nitrogen (N) is the mineral macronutrient plants require in the largest amount. Therefore, its availability greatly impacts many aspects of plant growth and development, including flowering time. We found nitrate signaling interacts with the age-related and gibberellic acid pathways to control flowering time in *Arabidopsis thaliana*. We show repressors of flowering time belonging to the AP2-type transcription factor family including *SCHLAFMUTZE* (SMZ) and *SCHNARCHZAPFEN* (SNZ) are important regulators of flowering time in response to nitrate. Our results support a model where nitrate activates SMZ and SNZ via the gibberellin pathway to repress flowering time in *Arabidopsis thaliana*.

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Plenary Session: Metabolism and Natural products

UNDERSTANDING THE SOFTENING OF *FRAGARIA CHILOENSIS* FRUIT

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The Chilean strawberry (*Fragaria chiloensis*) fruit is a native species with outstanding quality properties such as its fruity aroma and exotic white-pink color, nevertheless its fast softening limits commercialization. Fruit softening is related to cell wall disassembling and in *F. chiloensis* fruit significant reduction in pectin and hemicellulose fractions are observed during softening. Several cell wall degrading enzymes are taking part in *F. chiloensis*'s softening, including polygalacturonase (PG), xyloglucan endotransglycosylase/hydrolase (XTH1) and expansin 2 (Exp2), among others. The expression level of *FcPG*, *FcXTH1* and *FcExp2* increases as softening is taking place, in addition to their corresponding activities. *F. chiloensis* is a non-climacteric fruit, and the control of its ripening remains unclear. In order to test if ABA could interfere with the ripening of *F. chiloensis*, fruit was treated with 1 mM ABA or 100 µM fluridone (ABA biosynthesis inhibitor). A significant increase in the accumulation of *PG*, *XTH1* and *Exp2* transcripts was observed in response to ABA, and a reduction in response to fluridone. To explain this regulatory mechanism, the promoter regions of these genes were obtained by Genome walker, and the *in silico* analysis reveals putative *cis* regulatory elements responding to ABA. To further explore the participation of these cell wall degrading enzymes their 3D protein models were built through homology modeling, and their interaction with different cell wall polysaccharides was evaluated. The data supports the preferential interaction of XTH1 with hemicellulose, Exp2 with cellulose and PG with homogalacturonan, confirming the hypothesis of a collaborative participation of enzymes in cell wall matrix disassembling. These evidences had provided useful information to understand the softening of *F. chiloensis* fruit and its regulation.

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SIMILAR MOLECULAR MECHANISMS ARE RESPONSIBLE FOR THE DECLINE IN NITROGENASE ACTIVITY IN NODULES OF *MEDICAGO TRUNCATULA* UNDER DIFFERENT TREATMENTS

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The nitrogenase activity in *Medicago truncatula* nodules shows a daily pattern that is common for different treatments that produce N-satiety status in leaves, e.g. a nutrient deficiency or hypernodulation (*M. truncatula* super numeric nodules mutant). The goal of this work was to show that those treatments that induce a daily rhythm in nitrogenase activity have similar molecular mechanisms. We compared the nodule transcriptome of *M. truncatula* in plants growing under P deficiency and in plants treated with nitrate, and we measured the nodule activity in plants growing in an aeroponic system that allows controlled nutrient supply and continuous non-invasive measurement of per plant nitrogenase activity. Plants in the P deficiency treatment developed less dry matter and had lower P concentrations in shoots and nodules, but higher N concentration in shoots. An RNAseq-based comparative transcriptome profiling of nodules during decline of nitrogenase activity revealed similarities between the two treatments (P deficiency versus nitrate supply). In both treatments, the reduction of nitrogenase activity was impaired by a massive reduction in the expression of numerous genes for nodule-specific cysteine-rich peptides (NCR), and probably also by a disturbance of the inner cell iron allocation. In addition, the strong reduction in the expression of leghemoglobin restricted the supply of oxygen for respiration. Additionally, we conducted RNAseq analysis of nodules and roots of *M. truncatula* earlier in time after nitrate addition in order to decipher the first molecular reactions before the nitrogenase activity declines.

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***SOLANUM LYCOPERSICUM* POSSESSES MITOCHONDRIAL AND PLASTIDIAL LIPOYL SYNTHASES CAPABLE OF INCREASING LIPOYLATION LEVELS IN VIVO**

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The powerful antioxidant capacities present in eukaryotic and prokaryotic organisms. LA is the prosthetic group of several key multi-subunit enzymes complexes, including pyruvate dehydrogenase and α -ketoglutarate dehydrogenase of the tricarboxylic acid (TCA) cycle. LA biosynthesis and incorporation into these target proteins (lipoylation) proceeds *de novo* or via a salvage pathway. During *de novo* synthesis, octanoyl transferase (LIP2) uses octanoyl groups linked to an acyl carrier protein to transoctanilate target proteins. Subsequently, lipoyl synthase (LIP1) catalyses the final step by inserting two sulphur atoms into the prosthetic group. Whilst a number of the enzymes have been functionally-characterised in *Arabidopsis thaliana*, the aim of the current work is to identify and evaluate the role of this pathway in a fruit-bearing species. Towards this aim, we identified two proteins in tomato (*Solanum lycopersicum*) with the molecular characteristics of LIP1. We call these proteins SILIP1 and SILIP1p, which possess 78% and 84% amino acid identity with AtLIP1 and AtLIP1p, respectively. Confirming bioinformatic predictions, SILIP1 has a mitochondrial localisation whereas SILIP1p is plastidial, as shown by confocal microscopy. Furthermore, both proteins rescue carbon source requirements and lipoylation levels of an *Escherichia coli* lipoyl synthase mutant (*lipA*), and thus act as lipoyl synthases in this heterologous system. Additionally, stable over-expression of these genes in tomato produces transcriptional alterations in genes encoding proteins involved in LA metabolism, and target proteins of the TCA cycle, which in turn correlate with the increased level of lipoylation measured in these over-expressing lines.

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EVALUATION OF THE PLANT BIOSTIMULANT EFFECT OF *ARTHROSPIRA MAXIMA* EXTRACTS

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Worldwide fertilizer consumption is on the rise, mostly due to an increasing demand associated to a growing global population, which according to the UN, will reach more than 9 billion people in 2050. It has been shown that fertilizer use is directly related to agriculture yield, although, recent studies have established that plants are actually assimilating 10-40% of it. This overuse has been linked to environmental problems such as eutrophication of water bodies, soil degradation, and diseases, among others. In order to counter this, several investigations are focusing on new substances that could increase fertilizer uptake and plant health. Within this we can find a relatively new concept, plant biostimulants. These refer to substances that improve plant nutrient absorption, crop yield, stress tolerance, and the preservation of soil properties. They are not considered nutrients *per se*, but are used as a fertilizer complement. It has been demonstrated that exopolysaccharides from marine algae improve plant growth by enhancing nitrogen assimilation and basal metabolism. Cyanobacteria, oxygenic photosynthetic prokaryotic organisms, represent a major source of polysaccharides and constitute an innovative source of biostimulant compounds (carbohydrate, lipids, glycolipids, glycoproteins, amino acids, etc.) that have been reported to enhance growth, plant phytochemicals accumulation and tolerance against biotic and abiotic stress. In this study, we propose the use of lyophilized extracts of *Arthrospira maxima*, commonly known as Spirulina, as a plant biostimulant in order to improve agronomic traits and stress response, since it contains up to 70% of protein in its dry weight, as well as exopolysaccharides, fatty acids, vitamins, minerals, phytohormones, among others.

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Plenary Sessions: Biotic stress

COOPERATION THROUGH COMPETITION - DYNAMICS AND MICROECONOMICS OF A MINIMAL NUTRIENT TRADE SYSTEM IN ARBUSCULAR MYCORRHIZAL SYMBIOSIS

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In arbuscular mycorrhizal (AM) symbiosis, fungi and plants exchange nutrients (sugars and phosphate, for instance) for reciprocal benefit. Until now it is not clear how this nutrient exchange system works. Here, we used computational cell biology to simulate the dynamics of a network of proton pumps and proton-coupled transporters that are upregulated during AM formation. We show that this minimal network is sufficient to describe accurately and realistically the nutrient trade system. By applying basic principles of microeconomics, we link the biophysics of transmembrane nutrient transport with the ecology of organismic interactions and straightforwardly explain macroscopic scenarios of the relations between plant and AM fungus. This computational cell biology study allows drawing far reaching hypotheses about the mechanism and the regulation of nutrient exchange and proposes that the 'cooperation' between plant and fungus can be in fact the result of a competition between both for the same resources in the tiny periarbuscular space. The minimal model presented here may serve as benchmark to evaluate in future the performance of more complex models of AM nutrient exchange. As a first step towards this goal, we included SWEET sugar transporters in the model and show that their co-occurrence with proton-coupled sugar transporters results in a futile carbon cycle at the plant plasma membrane proposing that two different pathways for the same substrate should not be active at the same time.

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MOLECULAR CHARACTERIZATION OF *VITIS VINIFERA* RESISTANCE TO FUNGAL PATHOGENS *BOTRYTIS CINEREA* AND *ERYSIPHE NECATOR*

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Grapevine (*Vitis vinifera* L.) is greatly affected by a large number of pathogens that cause diseases in pre- and post-harvest periods. This plant is highly susceptible to *Botrytis cinerea*, a necrotrophic fungus that obtains nutrients from dead tissue, and *Erysiphe necator*, a biotrophic fungus that feeds on nutrients obtained from living tissue. Due to the agronomic importance of *V. vinifera*, is essential to introgress resistant traits against these pathogens and to understand how plant respond to the infection. The aim of this work is to generate *V. vinifera* plants with greater resistance to *B. cinerea* or *E. necator* by traditional breeding and to characterize at the molecular level the defense responses against each pathogen. For this, experimental crosses were made using resistant and susceptible plants. Thus, varieties with lower susceptibility to infection by *B. cinerea* or resistance to *E. necator* were selected by phenotypic analysis. These plants were evaluated through biochemical and histological analysis in order to go deeply into the defense response induced by each pathogen. The preliminary results indicate that resistance against *B. cinerea* is mainly due to mechanical barriers, while resistance to *E. necator* is related to an effector triggered immunity (ETI) response. This work will contribute to the study of plant-pathogen interactions at molecular level in agronomical important crops.

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PECTIN STRUCTURE AND COMPOSITION DYNAMICS DURING EARLY AND LATE PLANT-APHID INTERACTION

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Feeding strategy employed by aphids represents a particular challenge for plants in terms of defense activation due to the low tissue damage caused by these insects. Aphids possess a specialized mouthpart within which a slender structure called stylet allows them to penetrate the different tissue layers of plant organs until a single sieve element is reached. Aphids carry out several probing events during early stages of interaction with plants in order to choose the most suitable host for colony settle. During aphid probing, cell wall and intercellular matrix are mechanically and enzymatically disrupted by stylet progression toward phloem. Despite that probing pathways are known, little attention has been paid to these plant structures. Since pectins represents 30 to 35% of total polysaccharides that buildup cell wall and intercellular polymers, the present study focuses on the analysis of pectin matrix dynamics during *Myzus persicae* infestation process in *Arabidopsis thaliana*. Our results reveals significant changes in pectin related enzymes and polymers at 6 and 72 hours of aphid-plant interaction. Global activity of pectin methylesterases (PMEs) significantly increased at 6 and 72 hours in local infested tissue. In accordance with these results, methyl esters content decrease at 6 and 72 hours in local infested tissue. Additionally, LM19 and LM20 immunohistochemistry reveals that Homogalacturonan chains were demethylesterified during aphid attack in local infested tissues. Our results suggest that pectin modifications observed at early (6 hours) and late (72 hours) stages could represent a key step during aphid host selection and colonization. Therefore, pectin polymers and associated modifying enzymes could be considered as suitable molecular targets for biotechnology and agronomic studies that points to reduce the detrimental impact of aphids in commercial crops.

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PHB3 INTERACTS WITH ICS1 AND REGULATES THE SA-MEDIATED DEFENSE RESPONSE CONTROLLING THE LEVELS OF ICS1 IN *ARABIDOPSIS THALIANA*.

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Salicylic acid (SA) is a phytohormone widely known for its role in the regulation of plant defense responses. It accumulates in plant tissues during a variety of biotic and abiotic stress conditions including pathogen infections and UV-C light exposure. In *Arabidopsis thaliana*, the main source of SA biosynthesis under such stress conditions is a chloroplastic pathway from chorismate, in which isochorismate synthase 1 (ICS1) is, so far, the only enzyme known to be involved. However, it is known that in some bacteria ICS1 forms a complex with other proteins in order to produce SA. Therefore, we hypothesized that ICS1 could work in a similar way in plants. To test this possibility, we performed immunoprecipitation of ICS1 and used mass spectrometry to identify ICS1-interacting proteins. In this analysis, we found a large number of peptides from a protein family that was previously described as mitochondria-localized, called Prohibitins (PHBs). Here we confirm the interaction between PHB3 and ICS1 and report that PHB3, like ICS1, localizes into the chloroplasts. We evaluated the defense response of *phb3-3* mutant plants subjected to treatments with UV-C and avirulent strains of *Pseudomonas syringae* DC3000 (*Pst*). Under both stress conditions, we detected a reduced increase in the SA levels in *phb3-3* mutant compared to WT plants. Furthermore, accumulation of PR-1 protein after these stress conditions was also reduced in the mutant compared to WT plants. Accordingly, the *phb3-3* mutant plants also show higher susceptibility to avirulent strains of *Pst*. Using an antibody against ICS1 we found that the absence of PHB3 gene produce a decrease on the levels of ICS1 protein compared to WT plants. All these phenotypes were reverted in *phb3-3* plants complemented with pUBQ10:PHB3-V5 gene. This evidence shows that PHB3 is involved in the regulation of SA biosynthesis in the chloroplasts and is therefore required for proper SA-mediated defense responses to stress in *Arabidopsis thaliana*. Supported by FONDECYT (1141202) and Millenium Nucleus Center for Plant Systems and Synthetic Biology (NC130030)

Plenary Sessions: Abiotic stress

TRAITS AND GENES FOR DROUGHT TOLERANCE: STUDIES IN GERMLASM COLLECTION OF LOTUS SPP, TOMATOES AND WHEAT.

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Drought stress is the most limiting factor in plant development affecting directly crop productivity and yield. Dramatic reduction of water availability has been evidenced by the climatic change in several region of the world, where our country is included. The rainfall reduction as well as other water resource restrictions show that the improvement of the water use efficiency through the utilization of drought tolerant crops, urge to develop in zones affected by water scarcity. Our research is focused in an integral vision of drought stress tolerance from the point of view of morphology, physiology, biochemistry, and molecular biology linked to specific traits that confer drought tolerance in three main plant groups: cereals, wild and cultivated tomatoes and forage legumes.

We have screened germplasm collections of *Lotus* spp., *Solanum* spp. and wheat for the identification of contrasting relevant traits associated with drought tolerance. Additionally, for specific genotypes of tomato we have developed RNAseq studies and identified enriched GO categories in overexpressed and repressed groups of genes between cultivated

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tomato and wild species for “transcription factor activity”, “photosynthesis” and “enzyme inhibitor activity” between others. In *Lotus* spp. we have identified QTLs associated with important physiological traits such as osmotic potential or crop water stress index. Additionally, other researches have been directed to characterize the role of genes coding for lipid transfer proteins in cuticle formation of tomato as much as *Lotus japonicus*.

Studies in wheat have been conducted to reveal the role of sugar accumulation and mobilization during grain filling mediated by terminal drought stress. The involving of genes that coding for fructans metabolism enzymes has been evaluated.

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METATRANSCRIPTOMIC APPROACH REVEALS CONSERVED ADAPTIVE PROCESSES IN ATACAMA DESERT PLANTS

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Atacama Desert is the oldest and driest desert, and represents one of the harshest environments on Earth. It has been estimated that Atacama Desert has remained extremely hyperarid for at least the past eight million years, a sufficiently long time for plants to adapt and colonize this environment. To exploit the genomes of these plants adapted to thrive in marginal soils in the arid Chilean Andes desert, we sequenced and *de novo* assembled the transcriptome of 32 selected species, covering a wide range of plant families present in the study site. To identify candidate genes and processes that have had a role in the adaptation of these extremophile plants, we used a unique phylogenomic approach. This strategy rebuilds the evolutionary divergence by comparing the sequences of Atacama Desert plants with 32 phylogenetically related species and 6 model species. Key genes involved in the divergence of Atacama and non-Atacama species were identified and analyzed, revealing discriminative molecular mechanisms underlying Atacama Desert plants adaptability. Acknowledgments: Center For Genome Regulation, Howard Hughes Medical Institute, Conicyt, Department Of Energy United States Of America, European Comission.

TRANSCRIPTION FACTORS FROM THE TGA CLASS II FAMILY CONTROL THE ANTIOXIDANT RESPONSE AGAINST ABIOTIC STRESS IN ARABIDOPSIS

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The TGA family of transcription factors in *Arabidopsis* is composed of 10 members grouped in 5 classes. TGA class II factors, which include TGA2, TGA5 and TGA6 proteins, have a redundant function in the regulation of some defense genes. Nevertheless, their role in constraining oxidative stress has not been studied yet. In this work we assess the importance of TGA2/5/6 factors in the plant tolerance response to stress treatments with methyl viologen and UV-B radiation, using a triple mutant line (*tga256*). We found that *tga256* mutant plants are more susceptible to the different abiotic stresses than wild type (WT) plants, showing a higher accumulation of reactive oxygen species. In order to evaluate the genes controlled by TGA2/5/6, a transcriptomic analysis was performed. For this, WT and *tga256* mutant plants were irradiated with UV-B light. Non-irradiated plants were used as control. We found 717 genes regulated by both genotype and treatment. In this group of genes, two types of induction profiles are particularly interesting. 1st. Genes controlled positively by TGAs in the stress condition. The biological process over-represented in this group is *toxic metabolic process*

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and includes genes coding for glutathione *S*-transferases (GSTs). 2nd. Genes controlled negatively by TGA in the stress condition. This group don't show GO overrepresented terms, nevertheless genes involved in salicylic acid biosynthesis are included. These results indicate a key role of TGA2/5/6 as a node for redox regulation in response to abiotic stress in plants. Acknowledgements: FONDECYT 1141202 And Scientific Millenium Initiative PSSB NC130030.

STEM CARBOHYDRATE DYNAMICS AND EXPRESSION OF GENES INVOLVED IN FRUCTAN ACCUMULATION AND REMOVAL DURING GRAIN GROWTH IN WHEAT (*TRITICUM AESTIVUM* L.) GENOTYPES WITH CONTRASTING TOLERANCE TO WATER STRESS

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The genetic and physiological mechanisms underlying the relationship between water-soluble carbohydrates (WSCs) and water stress tolerance are scarcely known. This study aimed to evaluate the main WSCs in stems, and the expression of genes involved in fructan metabolism in wheat genotypes growing in a glasshouse with water stress (WS; 50% field capacity from heading) and full irrigation (FI; 100% field capacity). Eight wheat genotypes (five tolerant and three susceptible to water stress) were evaluated initially (experiment 1) and the two most contrasting genotypes in terms of WSC accumulation were evaluated in a subsequent experiment (experiment 2). Maximum accumulation of WSCs occurred 10-20 days after anthesis. Under WS, the stress-tolerant genotype exhibited higher concentrations of WSCs, glucose, fructose and fructan in the stems, compared to FI. In addition, the stress-tolerant genotype exhibited higher up-regulation of the fructan 1-fructosyltransferase B (1-FFTb) and fructan 1-exohydrolase w2 (1-FEHw2) genes, whereas the susceptible cultivar presented an up-regulation of the fructan 6-fructosyltransferase (6-SFT) and fructan 1-exohydrolase w3 (1-FEHw3) genes. Our results indicated clear differences in the pattern of WSC accumulation and the expression of genes regulating fructan metabolism between the tolerant and susceptible genotypes, under WS.

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Plenary Session: Phenomics and ecophysiology

PHENOMICS, AND THE NEW CHALLENGES IN PLANT SCIENCES

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Understanding the link between genotype and phenotype is at present one of the major challenges in plant breeding in order to improve traits of agriculture importance related to high yield, fruit quality, disease resistance and the plant capacity to grow in unfavourable environmental conditions. In this work we analyzed the phenotype-genotype relationships in a segregating progeny of a cross of Ruby × Sultanina grapevine cultivars by phenotyping for berry quality and cluster architecture traits. The QTLs detected indicated that these traits have a clear genetic basis and that they are good candidates to determine phenotypic traits of interest for grapevine breeding. We also analyzed the role that roots play in determining the adaptability of plants to water stress. Phenotyping root architectural traits in a quinoa population, correlations and differences among ecotypes for all the traits analyzed were found. In our analysis we emphasize that the

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main goal of a quantitative phenotyping approach is to link the genotype and the environment to morphological, functional, and yield characteristics of plants.

DROUGHT EFFECT ON LEAF GAS EXCHANGE AND CHLOROPHYLLS CONTENTS OF FOUR CEREALS GROWN IN GREENHOUSE

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One of the most immediate plant responses to water deficit is the progressive closure of the stomata, limiting carbon assimilation and plant growth. Stomatal conductance (g_s) responds very quickly and sustainably to changes in soil water potential, so it could be considered as an indicator of plant response to water deficit. The impact of drought on crop performance depends on the intensity of the stress and plant species and cultivars. A comparative study between small grains cereals, bread wheat, durum wheat, triticale and barley under water stress (WS) and full irrigated (FI) conditions was conducted in a greenhouse. The measurements were performed every seven days for four weeks since barley anthesis. Under WS triticale exhibited the highest g_s and leaf photosynthesis (A_n). Barley presented the lowest xylematic water potential and leaf gas exchange under WS. The relationship between g_s and A_n showed a clear separation between durum wheat and barley. It can be concluded that barley was more sensitivity to soil water deficit.

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HIGH THROUGHPUT PHENOTYPING IN AN INIA WHEAT BREEDING PROGRAM FOR DROUGHT TOLERANCE SELECTION

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In Mediterranean environments water deficit is the most common factor producing abiotic stress in plants, causing reduced yields. This effect is even greater when stress events occur during flowering and grain filling, commonly called late stress. Plant breeding focused on water stress tolerance is a complex matter due to the lack of fast and accurate evaluation methodologies. Different techniques exist for monitoring the water status of plants, such as the modulated chlorophyll a fluorescence, gas exchange, and leaf water potential among others. However, these methods are not feasible (technically and economically) to use due to the high number of genotypes to evaluate within a breeding program. Currently, there is equipment, techniques and forms of non-destructive analysis, which have proved to be helpful in phenotyping oriented to plant breeding (phenomics). We have used hyperspectral reflectance to generate mathematical models for predicting in a fast and non-destructive way, physiological and agronomical traits closely related with drought tolerance. For that, a collection of 368 advanced lines and cultivars of spring wheat were evaluated under three different water regimes (severe water stress, mild water stress and full irrigated). Traits evaluated were grain yield (GY), carbon isotope discrimination ($\Delta^{13}C$), LAI, spectral reflectance, among others. Spectral indices and 4 mathematical modelling technics were tested (PCR, PLS, RIDGE and SVR). GY, LAI and $\Delta^{13}C$ were the traits best correlated with SRI and the models, particularly when there were measured during grain filling stage.

CHILE, A HOTSPOT FOR PLANT PHENOMIC

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The success of breeding programs is reflected in the number of individuals released at the end of the selection process. Breeders must generate thousands of hybrids annually and evaluate them for a number of years. Because of the large number of genotypes, deep phenotypic characterizations of the material often becomes impractical due to the time and costs involved. For this reason, conventional breeding generally focuses on different visual characteristics and a few that require measurements of average complexity. To effectively develop cultivars well adapted to fluctuations in environmental stresses, breeders will have to evaluate a number of morpho-physiological and physicochemical traits. The only reasonable way to fulfill all these needs is through acquisition of high-dimensional phenotypic data (high-throughput field phenotyping) or 'Phenomics'. The Plant Breeding and Phenomic Center (University of Talca – Chile) have focused its efforts on the prediction of these traits (e.g. gas exchange, modulated chlorophyll fluorescence, pigments concentration, stem water potential, hydric and osmotic cell potential, cell membrane stability, lipid peroxidation, proline content, C and O isotopic composition) by spectrometry and thermography on several breeding programs (wheat, blueberries, alfalfa, strawberries, and quinoa) oriented to abiotic stresses (salt, water deficit and high temperature). We have also developed a software for exploratory analysis of high-resolution spectral reflectance data on plant breeding. Last year, our institution also organized First Latin American Conference on Plant Phenotyping and Phenomics for Plant Breeding and set up the Latin American Plant Phenomics Network (LatPPN).

Plenary Session: Genetic Resources and Plant Breeding

MOLECULAR TOOLS FOR PRUNUS SP.(L.) IMPROVEMENT

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Usually a breeding strategy for *Prunus sp.* (L.) tree fruit starts with creation of desirable genetic combinations by crossing plants with desired traits, then it is followed by a long process of selection among progenies for individuals predicted to have the required genetic components of superior performance to become potential cultivars. Thereby, dependent to a considerable extent on subjective evaluation and empirical selection, the development of a new variety usually takes 10–15 years or more. The DNA marker technology, derived from research in molecular genetics and genomics, offers great promise for plant breeding. Based on genetic linkage, the DNA markers (DM) can be used to detect the presence of allelic variation in the genes underlying these traits. Since the first published genetic map of Peach by 1994 using isoenzymes and RAPD, a large number of genetic maps for *Prunus spp.* have been developed to identify DM associated to different desired breeding traits. Despite of great technological advances, such as the developing of new high-throughput markers and genome sequencing capacities, the use of DM in *Prunus* breeding still low. Advantages and limitations of molecular assisted selection method in *Prunus* breeding programs carried out by INIA will be discussed.

FONDECYT 1161377; INNOVA-CORFO: 09PMG-7243

POLYPHENOL PROFILING IN A JAPANESE PLUM (*PRUNUS SALICINA* L.) SMALL CULTIVAR COLLECTION: TOWARDS GENETIC DISSECTION OF FUNCTIONAL COMPOUND CONTENT TRAIT

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Japanese plum has an excellent place in the fruit production in Chile, being an interesting target for fruit quality and functional-food value improvement. Related with the latter aspect, one of the objectives of University of Chile Japanese plum-breeding program is to develop new selections with enhanced fruit functional compound content. A suitable strategy to improve the efficiency of selection process (a slow and expensive relatively long generational time and the presence of self-incompatibility in the species) is the use of molecular markers genetically associated to mutations responsible for phenotypic variation. In the year 2015, we started to explore the phenotypic variability of plum fruit polyphenol content as a first step in the characterization of the genetic mechanisms underlying this complex trait. For this aim, we are analyzing the anthocyanin and low-molecular weight phenols (LMWP) profile in a small collection of 12 Japanese plum commercial varieties. For each cultivar, skin and flesh tissues of fruits sampled at two different ripening conditions (E1 and E2), were subjected to methanolic maceration and organic extraction to obtain extracts enriched in anthocyanins and LMWP, respectively. HPLC-DAD analysis of the extracts is revealing the presence of 8 anthocyanin-related and 16 LMWP-related peaks. In the former, and employing HPLC-qTOF-MS² qualitative analysis, we have detected the presence of cyanidin 3-rutinoside, as well as 3-monoglucosides of cyanidin, petunidin, peonidin, pelargonidin and delphinidin. Peaks putatively associated to cyanidin 3-glucose and cyanidin 3-rutinoside show the highest concentration in all red-skinned cultivars. As expected, the compound distribution across fruit tissues and ripening conditions is strongly dependent on the cultivar. Correlation of phenolic compounds and phenological and fruit quality traits (determined on the same analyzed fruits) is also shown. These preliminary data confirm a genotype-dependent phenolic content, suggesting that breeding for health-promoting fruits is a completely feasible activity.

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USE AND IMPACT OF BIOTECHNOLOGY IN PLANT BREEDING IN CHILE: EXPERIENCE OF THE POTATO BREEDING PROGRAM OF INIA

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The national potato breeding program of Instituto de Investigaciones Agropecuarias (INIA) Chile has developed eleven varieties. It is estimated that these varieties have 50% of the Chilean potato market and are being evaluated in 7 foreign countries. The program has incorporated biotechnology techniques at different stages of breeding and initial seed production for output to market. The aim of this work is to summarize the current importance and scope of biotechnology in breeding in Chile, by presenting a program that has generated widespread material among farmers and consumers. The biotechnological techniques used in the program are presented. Moreover, we cover the processes of breeding assisted by biotechnology, improved characteristics involving biotechnology, number of potato varieties developed and released to market with the assistance of biotechnology techniques. The program has implemented six biotechnological techniques, these are applied in the stages of characterization of the gene bank, selection of parents, marker assisted selection, characterization of varieties, and propagation of material for seed production. One hundred percent of the varieties have been released involving biotechnology, especially by the use of in vitro culture techniques to produce pathogen free material for initial stages of seed production of advanced lines. Biotechnological techniques have participated in the improvement of 2 of the 13 main characteristics associated with the program objectives. Two of the 11 varieties were characterized by molecular fingerprint at the time of their release. Biotechnological techniques such as in vitro culture, molecular fingerprint, and molecular diagnosis of diseases are used to produce primary multiplication of reproductive material for 100% of the varieties currently on the market.

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ECOLOGICAL RISKS AND BENEFITS FROM THE NOVEL OILSEED CROP CAMELINA

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Camelina (*Camelina sativa* L.) is a Brassica oilseed crop from Europe that has been genetically engineered (GE) for the production of biofuels, dietary supplements, and industrial products. With little history of cultivation in the Americas, there are questions about its potential ecological risks and benefits. Like rapeseed, camelina might be able to escape from cultivation, or transfer transgenes and traits to native plants or weeds. Our research projects in Connecticut (USA) are focusing on camelina gene flow, insect-crop interactions, and weediness. Camelina grown under low-input field conditions produced yields of 531-1096 kg/ha (2014-2016) consistent with other published field trials. In 2015, low rainfall and high temperatures after seeding reduced seed germination and caused crop failure. Various experiments showed that camelina plants were competitive with agricultural weeds, and volunteer seedlings were observed after harvest. The opening of camelina flowers coincided with the visitation of many insect pollinators from the orders Hymenoptera, Diptera, Lepidoptera, and Coleoptera. Hymenoptera collected in the field included honey bees, mining bees, sweat bees, bumble bees, and leaf cutter bees. Overall, the pollinator population was 33% honey bees and 25-33% syrphid flies. Camelina clearly provided pollen and nectar resources for both native insects and honey bees. These experiments will help government regulators, farmers, and companies make decisions regarding the future use of GE camelina. Acknowledgments: Biotechnology Risk Assessment Program Grant from the US Department of Agriculture.

Poster session

PS 1

QUANTITATIVE PHOSPHOPROTEOME ANALYSIS OF THE PRIMARY NITRATE RESPONSE

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Nitrogen (N) is one of the main limiting nutrients for plant growth and crop yield. Despite its role as a nutrient, nitrate can also act as a signaling molecule that modulates gene expression of a wide range of plant processes. It is well documented that changes in nitrate availability, the main N source found in agricultural soils, influences a myriad of developmental programs and processes including plant defense responses. Although transcriptional responses in response to nitrate have been characterized by a number of groups, the nitrate-signaling pathway is yet to be discovered. Most signaling pathways involved post-translational modifications of key components. Among these, protein phosphorylation is one of the most abundant, affecting protein-protein interactions and thus providing a framework for signaling networks. As a first step to identify potential regulatory factors involved in early signaling events in response to nitrate treatments, we performed quantitative time-course analyses of the Arabidopsis root phosphoproteome in response to nitrate by liquid chromatography with tandem mass spectrometry detection (LC MS/MS). This large-scale approach allowed us to identify peptides with changes in their phosphorylation level after nitrate treatments. The nature of the proteins identified differ significantly from genes implicated in transcriptome studies. The new proteins found implicated in nitrate responses include mainly signaling-associated proteins, kinases, transcription factors and transporters. Our data provide new insights into the phosphoproteome of Arabidopsis roots and identify putative novel components of the nitrate-signaling pathway. (Sponsored by Sponsored By Nucleo Milenio BSSV NC 130030, Fondecyt 15090007, Howard Hughes Medical Institute, Fondecyt-11110095, Fondecyt-1141097).

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PS 2

EVALUATION OF RESISTANCE TO CAVITATION OF INTER-SPECIFIC POPLAR (POPULUS) HYBRIDS UNDER WATER STRESS

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Both the decrease of water in the soil and the increase of temperature, change the evapotranspiration breaking the continuity of the water flow through the xylem. It has associated the generation of negative pressure hydraulic and the alteration in water metastability, producing a change from liquid to air (nucleation) within xylem cells. The accumulation of air in those cells affects the normal flow of water, in a phenomenon known as cavitation. Poplars (*Populus* spp) are one of the woody plant species proposed as a model of study to revert the cavitation. The aim of this work was to analyze the response of hybrid poplars to water deficit stress. We studied a set of inter-specific poplar hybrids, and selected two with contrasting tolerance to water stress. For this purpose, ten different hybrids were grown in pots, in a nursery, and subjected to water stress. The following physiological parameters were analyzed: net photosynthesis, evapotranspiration, and stomatal conductance. The treatment consisted; control (irrigation every 2 days (500mL)), moderate (irrigation every 2 days (250mL)) and severe (unirrigated). Additionally, stems were sampled after treatment, before bud flushing and analyzed for embolism resistance, at INRA, Clermont-Ferrand, France. Results indicated that [*P. Trichocarpa* x *P. Deltoides*]x *P. Deltoides* hybrids did not show a significant decrease in physiological parameters evaluated under any conditions. Furthermore, they showed a higher resistance to cavitation. While hybrids most affected by stressful conditions were *P. trichocarpa* x *P. deltoid*. We concluded that these contrasting hybrids will allow us know the mechanisms involved in tolerance to water stress.

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PS 3

GENOME-WIDE IDENTIFICATION, CHARACTERIZATION AND EXPRESSION ANALYSIS OF GENES PUTATIVELY INVOLVED IN POLLEN DEVELOPMENT IN *Vitis vinifera*

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The adequate pollen development and its germination capacity are essential for reproductive success in *Vitis vinifera*. However, the molecular mechanisms that regulate this process in grape remain unclear. In *Arabidopsis thaliana* the floral organs are specified by the combinatorial action of transcription factors under the ABC model. In whorl 3, the activity of the class B APETALA3 (AP3) and PISTILLATA (PI) together with the class C AGAMOUS (AG) homeotic regulators are required for stamen development. Anther cell differentiation and early sporogenesis, is initiated by the activation of SPOROCTELESS/NOZZLE (SPL/NZZ) gene by AG and the induction of downstream target genes by the encoded transcription factor. The identification of homologues for the above mentioned genes in grape genome suggest that the molecular mechanisms may be common among species. In this study, bioinformatics methods were used to carry out genome-wide analysis of a complete set of candidate genes in grape, including sequence analysis, identification of conserved domains in encoded proteins and phylogenetic analysis. Homologues for 13 genes involved in the pollen development regulatory network in *Arabidopsis*, have been found in the grape genome. However, homologues for *BAM2*, *DUO1* and *NOZZ* genes were not identified, suggesting that other genes may be regulating this process in grapevine. The expression timing for the identified genes as well as for floral organ identity genes along the inflorescence and flower development was screened by qRT-PCR, providing a framework about this group of regulatory genes in grape for further characterization of their roles in pollen development.

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PS 4

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EFFECTS OF SIMULATED REGIONAL CLIMATE CHANGE ON NATIVES (*COLOBANTHUS QUITENSIS* AND *DESCHAMPSIA ANTARCTICA*) AND NON-NATIVES (*POA ANNUA* AND *JUNCUS BUFONIUS*) ANTARTIC PLANTS

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The Antarctic continent has extreme weather conditions such as freezing temperature, high solar radiation, strong winds and low nutrient availability. This has contributed at low colonization of species and the simplicity of the terrestrial ecosystem in the Region. However due to regional climate change caused by global warming, factors such as temperature increasing and water availability have been modifying. The effect of these factors over the survival and expansion of the species living in Antarctic needs to be evaluated. The native species (*Colobanthus quitensis* and *Deschampsia antarctica*) and the non-native (*Poa annua* and *Juncus bufonius*) were maintain in controlled conditions at 6°C and then were subjected to two irrigation regimes, field capacity (H₂O) and increased irrigating (+H₂O) during 74 days, a period of dehydration between days 30th and 44th was made in order to simulate periods of dehydration caused by freezing in Antarctica. Variables such as leaves and root length, leaves number and Fv/Fm were evaluated. Native species were able to recover following drying period, what was most significant in *D. antarctica* in increased irrigation treatment. Non-native species showed a sustained growth in both irrigating regimes; however, *J. bufonius* was significantly affected after drying period on field capacity irrigation treatment. All species (native and non-native) growing individually seem favored by the climate changes regarding water availability but it is imperative to evaluate the behavior when they are growing together (Competency analysis).

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PS 5

CHARACTERIZATION OF THE SILENCING MECHANISMS INVOLVED IN TRANSGENIC PLUM POX VIRUS (PPV)-RESISTANT HERBACEOUS (*NICOTIANA BENTHAMIANA*) AND WOODY (JAPANESE PLUM) HOSTS: A LARGE-SCALE SMALL RNA SEQUENCING APPROACH.

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Gene silencing is an important technique used in the development of pathogen resistance strategies for Plum pox virus (PPV), a high impact disease of *Prunus* spp. In addition, the availability of large-scale small RNA analysis facilitates studies that aim to elucidate the process of RNA interference (RNAi). In this study, the pPPViRNA silencing vector, which harbors two regions of the PPV coat protein (CP) gene that are predicted to be rich in silencing motifs, was evaluated in transgenic *Nicotiana benthamiana* (NB) and *Prunus salicina* (Japanese plum) (JP) plants. From the generated transgenic populations, resistant NB and JP individuals were selected and the RNAi process further analyzed. Large-scale small RNA sequencing with a focus on molecules with known activity (i.e., 21- to 24-nt small interfering RNAs; siRNAs) revealed important differences between control and resistant NB and JP plants. In controls, the observed siRNAs were nearly exclusively 21- and 22-nt siRNAs that targeted the whole PPV genome. Importantly, 24-nt siRNAs were absent in these individuals. In contrast, challenged resistant- NB and JP plants, accumulated a “full set” of 21- to 24-nt siRNAs, which all targeted the CP gene segments used in the construct. Sequence similarities between 21-nt siRNAs and the 22-, 23-, and 24-nt RNA molecules generated by these plants were also analyzed using BLAST to identify 22- to 24-nt siRNAs that included full or partial 21-nt siRNA core sequences. The results demonstrated that in susceptible lines, the 22-nt siRNAs and the rare 23- and 24-nt molecules generated during PPV infection were largely associated with 21-nt molecules; in resistant plants, both NB and JP, most of the observed 22-, 23- and 24-nt siRNAs contained these 21-nt siRNA core sequences. These results strongly suggest that 21-nt siRNA species play a role in the biogenesis of 22- to 24-nt siRNA during RNAi in plants.

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PS 6

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EFFECT OF THE WATER STRESS IN THE PHOTOSYNTHETIC ACTIVITY OF *SOLANUM PERUVIANUM* AND *SOLANUM LYCOPERSICUM*

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Changes in environmental conditions associated to low water availability affect negatively crop yield in the entire world. Here, the challenge is the generation of varieties with improved traits for tolerate drought. On the other hand, cultivated tomato at difference that any wild relative is sensitive to several abiotic and biotic stresses including water deficit. The drought affects hardly the yield, which is primarily mediated by the inhibition of photosynthesis. Wild relatives to tomato such as *Solanum peruvianum* are capable to maintain a high stem growth rate under moderate drought stress. A process of acclimation to water deficit mediates this. The aim of this research was evaluate the behaviour of photosynthesis and electron transport chain (ETC) in *Solanum lycopersicum* var Money maker (MM) and accession QUI957 from *S. peruvianum*, comparing two levels of water supply and a previously period of acclimation to drought. The results shows that acclimated plants of *S. lycopersicum* and *S. peruvianum* suffered an important reduction in the electrons transport rate (ETR) and the opening of reaction centers percentage (ql), both under water deficit. In the other hand, MM showed higher NPQ than QUI957 in all the comparisons. Additionally, only in acclimated plants the NPQ was higher during RW compared with WW. The net assimilation of CO₂ (A) at 400 uM of referential CO₂ had a significant reduction in acclimated and non-acclimated plants of *S. lycopersicum* in RW but not in *S. peruvianum*. The results suggest that *S. peruvianum* present an improved ability to maintain a higher photosynthesis under WW and RW conditions and acclimation process is required for activate certain defense mechanisms in both species.

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PS 7

INTERACTION BETWEEN *ARABIDOPSIS THALIANA* AND *SINORHIZOBIUM MELILOTI* FOR IMPROVED PLANT GROWTH AND NITROGEN NUTRITION

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Nitrogen (N) is an essential macronutrient and a major factor limiting plant growth in natural as well as in agricultural environments. Plants acquire N directly from the soil and in a few cases N can be provided by N-fixing bacteria. Plant:bacteria interactions associated with N-nutrition are well described in legumes, but are also observed in some non-legume plant species. We found *Arabidopsis thaliana* growth under N-limiting conditions is enhanced by *Sinorhizobium meliloti* RMP110. This growth enhancement is in part mediated by bacterial N-fixation. Dilution of ¹⁵N labeling when *Arabidopsis* plants were grown with *S. meliloti* indicated *Arabidopsis* plants indirectly acquired atmospheric N, where ¹⁴N isotope predominates. *Arabidopsis* homologs of key regulatory genes involved in legume:rhizobium interactions are required for *Arabidopsis* growth promotion mediated by *S. meliloti*. Our results suggest conserved molecular mechanisms exist in plants to interact with N-fixing bacteria for improved growth under N-limiting conditions.

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PS 8

VALIDATION OF REFERENCE GENES FOR REAL TIME QRT-PCR NORMALIZATION IN ROOT TISSUE DURING WATER STRESS IN GENOTYPES *EUCALYPTUS GLOBULUS* TO ANALYZE THE GENE EXPRESSION OF *WRKY* TRANSCRIPTION FACTORS

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The expansion of eucalyptus plantations is limited to regions with favorable climatic conditions, where drought is one of the most important factors limiting growth and forest production. Transcription factors regulate the response of the plant against changing environmental conditions, affecting positively or negatively the expression of their effector genes. *WRKY* transcription factors have been linked to the response of the plant against biotic and abiotic stress, being induced by water and osmotic stress, regulating stomatal movement. Housekeeping genes with stable expression are required for quantitative Real-time RT-PCR. Measurements of photosynthetic rate, stomatal conductivity, transpiration and water potential in the xylem for two genotypes of *Eucalyptus globulus* under control and drought conditions were performed. In this work the gene expression stability of six housekeeping genes (*PP2Aa*, *H2B*, *SAND*, *UBC-2010*, *UBC9* and *EF1-a*) and the expression of *WRKY* genes in root tissue of *Eucalyptus globulus* subjected to drought stress for 5 weeks were evaluated. According to the expression analysis, the *EF1-a* and *PP2Aa* genes are the most stable genes. The expression of transcription factors *WRKY* is induced by water stress in root tissues of *E. globulus*, showing differences between the two genotypes evaluated, these results are correlated to the physiological analysis performed during the experiment.

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PS 9

WHOLE-TRANSCRIPTOME AND GENETIC ANALYSIS REVEALS THAT SEED AND BERRY DEVELOPMENT IN GRAPEVINE ARE CONTROLLED PRINCIPALLY BY GIBBERELLINS SUPERPATHWAYS, CELL WALL METABOLISM AND CYTOSKELETON GENES, AND SPECIFIC DEVELOPMENTAL TRANSCRIPTION FACTORS

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Seedless varieties are preferred among costumers for fresh consumption and thus one of the main targets for breeding. However, under natural conditions seedless berries are smaller and require the application of growth regulators, mainly GA₃. It is believed that endogenous gibberellins are the main responsible for differences in berry size. An integrative approach, that included transcriptome analysis using RNAseq during seed and berry development over seedless and seeded genotypes that differ in berry size, and a fine mapping QTL experiment based in the analysis of a F1 biparental population that segregates for these traits, was performed. Based in two statistical tests (EDGE and Baggerley with a FDR p-value <0.05 and 2-fold cutoff) to identify differentially expressed genes in RNAseq results from an Illumina HiSeq 2000 sequencing experiment, we identified 376 and 675 genes up and down-regulated respectively in seedless genotypes. The most significantly altered pathways are related to the superpathway of gibberellin biosynthesis, most genes from this pathway were significantly down regulated confirming a possible role during early berry growth. Several families of transcription factors related to developmental processes as well as genes related to hormones biosynthesis and their signal transduction were also differentially expressed. Cytoskeleton, cell-wall-modification and regulation of water intake genes were generally down-regulated. QTL mapping experiments for berry size (berry weight and ecuatorial diameter) identified up to 15 QTLs that explain between 1.0 and 26.6 % of phenotypic variation, within their boundaries most of the identified Candidate Genes are related to growth regulator biosynthesis and signal transduction, transcription factors related to flower, and fruit development, cell wall organization, modification and biogenesis. Search for differentially expressed genes within QTLs allowed the identification of better Positional Candidate Genes to understand berry development in the seedlessness context.

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PS 10

JASMONATE MEDIATED DOWNREGULATION OF ABSCISIC ACID GENE EXPRESSION RESPONSE LEADS TO THE SLOW-DOWN OF THE CELL ELONGATION RECOVERY PHASE DURING SALT STRESS IN *ARABIDOPSIS* ROOT

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Soil salinity is a relevant problem limiting crop production worldwide. Plants have developed response mechanisms against salt stress, being abscisic acid (ABA) a major player. Recently, we have reported that jasmonate (JA) signaling pathway is activated by salt stress, leading to cell elongation inhibition in *Arabidopsis* primary root. To obtain insights into how JA regulates root growth inhibition, we studied the changes in root transcriptome between *coi1-2* JA-signaling mutant and WT during salt-stress response by RNA-Seq. We found that salt stress and ABA responsive genes were upregulated in *coi1-2* roots with respect to WT ones after 150 mM NaCl treatment for 3 h. A contrasting gene expression profile between JA- and ABA-response genes was found, suggesting a negative relationship from JA to ABA at a transcriptional level during salt stress for 3 h in roots. Finally, the attenuation of cell elongation inhibition observed in JA-related mutants (e.g. *aos*, *coi1-2* and *jai3-1*) compared to WT under salt stress was impaired by fluridone, an inhibitor of ABA biosynthesis, thus supporting the idea of an antagonistic JA/ABA crosstalk at a phenotypic level in roots. Together, these results are in agreement with a JA-mediated downregulation of ABA pathway, leading to the slow-down of the cell elongation recovery phase during salt stress root growth inhibition in *Arabidopsis*. Further studies will be necessary to underpin mechanistic aspects related to the JA/ABA crosstalk at a spatio-temporal basis in roots.

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PS 11

ARABINOGLACTAN PROTEIN DIFFERENTIALLY EXPRESSED GENES IN TILT YOUNG SEEDLINGS OF RADIATA PINE BY RNA-SEQ ANALYSIS

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Arabinogalactan-proteins (AGPs) are a class of proteins likely to be involved in the development of wood. AGPs are widely distributed throughout the plant kingdom and reside predominantly in the plasma membrane, cell wall and extracellular matrix, which may be involved in cell interactions, cell adhesion and cell wall biosynthesis. AGPs are abundant and specific in xylem differentiation. Wood is largely composed of tracheids, and its properties depend primarily on the composition and morphology of tracheid cell walls.

RNA-Seq strategy was used to identify genes differentially expressed in response to inclination, where 4 different genes showed identity to AGP. A contig named PrAGP1 was found with 98% identity to PtaAGP6, with higher FPKM values after 10 h of inclination in the lower stem side. Similarly, PrAGP2 showed high FPKM value after 10 h of inclination and 99% identity to p14A9 arabinogalactan-like protein. On the other hand, PrAGP3 with 98% identity to p3H6/CDM8 showed a variable FPKM like, similarly to what is observed for PrAGP4.

The phylogenetic analysis reveals that AGP sequences from pine grouped in sub-category of fasciclin-like proteins. This protein is categorized in A-B-C- and D, according to the number of FAS domain, the number of AGP-like domain, and the presence or absence of GPI anchor signal in the C-terminal.

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PS 12

EXPRESSION OF *GSTU7* AND *GSTU24* GENES CODIGN FOR GLUTATHIONE S–TRANSFERASES IS IMPORTANT FOR THE CONTENTION OF THE OXIDATIVE DAMAGE PRODUCED UNDER STRESS CONDITIONS IN *ARABIDOPSIS THALIANA*

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Salicylic acid (SA) is a phytohormone involved in the establishment of defense responses against biotic and abiotic stress, responses that are developed through controlling the expression of a high number of genes. Under stress conditions, plants accumulate reactive oxygen species (ROS) and SA, signals that play a feed forward loop generating an oxidative burst that is essential for the defense response. However, uncontrolled accumulation of ROS is dangerous for plants. Evidence suggests that SA has also an antioxidant effect that constrains the oxidative burst and prevents the consequences of the accumulation of ROS. It is still unclear how SA mediates this effect. We performed an extensive analysis of available

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microarray data looking for SA-inducible genes with antioxidant functions that were also induced under stress conditions, and that could be responsible for the ROS contention mediated by SA. Two genes coding for the enzymes GLUTATHIONE S-TRANSFERASES TAU 7 and 24 (GSTU7 and GSTU24) were found. We hypothesize that *GSTU7* and *GSTU24* genes expression is important for the SA-mediated contention of the oxidative burst produced under stress conditions. Here we show that knock out mutants in these genes are impaired in their capacity to resist treatments with the herbicide methyl viologen (MV), which induces superoxide accumulation in the chloroplasts. We also show that over-expressor lines in these genes improved their capacity to resist the oxidative stress caused by MV. These results indicate that *GSTU7* and *GSTU24* genes are important for the contention of the oxidative damage caused by MV.

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PS 13

NITRATE-DEPENDENT TRANSCRIPTIONAL REGULATION OF THE *ARABIDOPSIS* NRT2.1 NITRATE TRANSPORTER

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Nitrate is one of the most important nitrogen sources for plants. Nitrate acts as a signaling molecule that modulates the expression of a wide range of genes, with an impact in plant physiology, metabolism, growth and development. The nitrate response starts with nitrate sensing which triggers a transcriptional response mediated by a number of transcription factors. Although some transcription factors induced by or regulating nitrate responses have been comprehensively described, there are still nitrate-signaling components and pathways yet to be identified. The modulation of the expression levels of nitrate transporters such as *NRT2.1* is key for the regulation of nitrate uptake. Furthermore, the *NRT2.1* gene has a 150 bp cis-acting element in its promoter that confers its response to nitrate. As a first step to identify components involved in nitrate signaling, we performed a large-scale Y1H screen to identify transcription factors binding to this 150bp regulatory element. We identified 35 transcription factors binding to this element. These belong to the main transcription factor families that include Zinc-finger (ZFs), ethylene response factors (ERFs), basic leucine-zipper (bZIP), No Apical Meristem (NAC), WRKY and MYB among others. We further characterized the role in nitrate response of one of the transcription factors and proposed a working mechanism. Our data provide new insights into the transcriptional response underlying nitrate uptake in plants.

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PS 14

IDENTIFICATION AND EVALUATION OF PUTATIVE WRKY GENES INVOLVED IN COLD STRESS RESPONSE IN *E. globulus*

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Eucalyptus spp. is an important genus in the forest industry at global and national level. *Eucalyptus globulus* is one of the most important species due to its rapid growth and excellent quality for kraft pulp production. However, *E. globulus* is susceptible to some abiotic stresses, mainly to freezing stress conditions. The regulation at the transcriptional level is an important mechanism in the response to abiotic stress in plants. Several transcription factors (TFs) have been involved in the response to abiotic stress. WRKY TFs, are one of the largest families of TFs in plants, that have been extensively investigated in recent decades and associated to cold stress response but currently there is no information in *Eucalyptus* species. Previously in our laboratory leaf tissue transcriptome of *E. globulus* subjected to a profile of cold acclimatization was obtained in which some *E. globulus* WRKY (*EuglWRKY*) genes were found, however, they have not been studied in

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their role in cold stress response. In this work we identified putative *EuglWRKY* genes and assessed the expression levels of *EuglWRKY33* and *EuglWRKY57* in leaves from contrasting *E. globulus* genotypes (resistant/intermediate/susceptible) submitted to cold stress. Quantitative real-time PCR (qRT-PCR) analysis showed that these genes were up-regulated in the plants material studied when submitted to cold stress in the resistant and intermediate genotypes. In other hand, no variations were observed in the treatment of cold in the susceptible genotype. These data was correlated with the lethal temperature 50 (LT₅₀) value and survival and damage rate of the plants. Therefore, these two putative *EuglWRKY* genes could be involved in the response to cold stress tolerance in *E. globulus*.

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PS 15

THE GRAPEVINE *VvPSZ3* GENE AND ITS HOMOLOGUE *AtZAT4* FROM *ARABIDOPSIS THALIANA*, ENCODE FOR ZINC-FINGER C2H2-TYPE TRANSCRIPTION FACTORS INVOLVED IN POLLEN AND SEED DEVELOPMENT

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Fruit yield and quality are essential for winemaking and some grapevine cultivars (i.e. Merlot and Carménère) exhibit high tendency to fruitlet abscission and parthenocarpy, reproductive disorders seriously affecting these traits. Since structural abnormalities in pollen grains that reduces their germination capability, seems to be one the causes of these phenomena, the pollen developmental process and its regulation is of great importance for a better understanding of these disorders. In models species, pollen development is regulated by a complex regulatory network involving the participation of several types of transcription factors, which are sequentially expressed along this process. Among them, key roles are played by zinc-finger C2H2-type transcription factors and a gene coding for a representative of this family. *VvPSZ3* (*Vitis vinifera* Pollen and Seed Zinc Finger 3) has been identified and characterized in grapevine. The encoded protein shows high structural similarity with *AtZAT4*, a zinc-finger protein with unknown function in *Arabidopsis thaliana*. To determine if both proteins also have functional similitude, promoters of both genes were compared by fusion to *GUS* reporter gene and expression analysis in tobacco transgenic plants. Similar tissue-specific and hormone-regulated (ABA and GA) *GUS* expression pattern was driven by *VvPSZ3* and *AtZAT4* promoters. Also, an *Arabidopsis* line defective in *AtZAT4* expression and showing a reduction in the seed/silique ratio was successfully complemented by overexpression of the grapevine *VVPSZ3* gene, indicating that both encoded transcription factors regulate similar target genes.

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PS 16

EXPRESSION ANALYSIS OF THE GENES INVOLVED IN FRUCTAN BIOSYNTHESIS AND DEGRADATION IN THE PEDUNCLE OF BARLEY RECOMBINANT CHROMOSOME SUBSTITUTION LINES UNDER LONG-TERM MILD DROUGHT STRESS

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Water-soluble carbohydrates stored in the stem can make a significant contribution to final grain yield and grain weight under drought conditions. In cereals, the main carbon storage form in the stem is fructan. Carbohydrate content and expression of genes involved in fructan metabolism were determined in the peduncle of the main stem of three RCSL barley lines and the parental Harrington under long-term mild drought stress at the beginning of the grain growth stage and late milk stage. At both developmental stages, drought stress decreased the level of fructans in association with increased transcripts for 1-FEH and decreased those for 6-SFT, but increased the sucrose content. Fructan content was higher in RCSL-89 than in the other genotypes, and in cv. Harrington and RCSL-8 higher than in RCSL-76. At the beginning of the grain growth stage, drought stress increased transcripts for 1-FFT in RCSL-89 and, in lesser extent, 1-SST and 6-SFT, indicative of an induction of fructan biosynthesis. The pattern of changes described for the expression of genes linked to fructan biosynthesis in line 89 disappeared at late milk stage. Number of grains and grain weight per ear were decreased

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by drought. RCSL-89 showed the highest grain weight of all the genotypes but lower grain yield per plant. It can be concluded that enhanced capability of fructan storage might help into the stress conditions.

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PS 17

REDOX REGULATION OF TRANSCRIPTION FACTOR TGA2 AND ITS INFLUENCE IN SALICYLIC ACID-MEDIATED GENE EXPRESSION

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Salicylic acid (SA) is an essential phytohormone in the establishment of immune responses against biotrophic pathogens. SA accumulation by stress conditions results in changes in the cellular redox state and in the induction of a set of genes involved in defense responses. The transcription factors TGA2, TGA5 and TGA6 play an important role in SA-mediated transcriptional responses. Plants of the tga256 triple mutant line show higher susceptibility to infection by biotrophic pathogens compared to wild type plants. These factors have been described as regulators of an important group of genes, acting downstream of SA production. In Arabidopsis, the TGA family of transcription factors is composed of 10 members. Two of them, TGA1 and TGA8, have been described as redox-regulated proteins. On the other hand, TGA2 protein interacts with the glutaredoxins GRXC9 and GRXS13, suggesting that GRXs could catalyze the redox modification of TGA2. To assess this hypothesis, we generated plants that constitutively express the wild-type TGA2 protein, or a mutant version in the unique cysteine -TGA2(C186S)-, in the tga256 mutant background. The SA-mediated induction of the TGA-regulated genes (PR1, GRXC9) was evaluated in these plants. In order to evaluate the possible post-translational redox modification of TGA2, we expressed, purified and determined the glutathionylation of a recombinant wild-type TGA2 protein and the TGA2(C186S) mutant version. This work allows us to determine the importance of redox modifications of TGA2 for transcriptional regulation.

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PS 18

ANTIOXIDANT SYSTEM AND GROWTH RESPONSES OF WHEAT CULTIVARS SUBJECTED TO Mn EXCESS UNDER ACIDIC CONDITIONS

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Manganese (Mn²⁺) is an available ion and essential micronutrient for plants. However, under acidic soil conditions, as Andisols, an excess of Mn²⁺ can cause negative effects in crops as wheat, an important cereal cultivated in central and south of Chile. Thus, an excess of Mn²⁺ can be an important limiting factor for cereal production in Chile. Damage oxidative (lipid peroxidation, LP) and decrease of activity superoxide dismutase (SOD) enzyme, relative growth rate (RGR) and plant biomass are some negative effects that can produce Mn excess. In this experiment, we evaluated the effect to Mn excess on LP, SOD activity and RGR and biomass of six wheat cultivars (Dollinco, Rupanco, Fritz, Bakan, Maxwell, Paleta) mostly grown in south-central Chile. Increasing Mn treatments (as MnCl₂): control (2.4), 150, 350, 750 and 1500 µM Mn were applied, in nutrient solution by seven days, adjusting to pH= 4.8. Results showed that Dollinco decreased RGR and biomass both shoots as roots with the highest Mn treatment (1500 µM) compared with control. On the other hand, Bakan enhanced these growth parameters, mainly in shoots. With respect to antioxidant system, Dollinco had increasing LP values with all Mn treatments in shoots and until the 750 µM Mn in roots, whereas that Bakan and Fritz were not altered or decrease the oxidative damage with increasing Mn treatments. The results suggest that according to the evaluated

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parameters and conditions used in this study, wheat cultivar Bakan and Fritz were higher tolerant to Mn excess and Dollinco, the most sensitive one.

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PS 19

TRANSCRIPTOMIC ANALYSIS BY RNA-SEQ DURING FRUIT DEVELOPMENT IN AVOCADO (*Persea americana* Mill.) CV. HASS

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Persea americana is a basal angiosperm from the *Lauraceae* family. This species possess a diploid genome with an approximated size of ~920 Mpb and produces a climacteric and fleshy fruit. Avocado fruit have a high content of vegetable oils (mainly mono-saturated fatty acids) that are beneficial for human health and they are used as harvest index. The fruit development is a particularly long process, having a blooming stage for about 2 months and a fruit development of 8-12 months. Thus, the long bloom process produces fruits with significant differences in physiological ages within the same tree. The objective of this work is to identify candidate genes associated with fruit development that could be used as biomarkers in order to estimate the physiological age of the fruits. For this, we proposed to carry out a RNA-Seq approach during 4 stages of fruit development; 150 days after flowering (DAF), 240 DAF, 300 DAF (harvest) and 390 DAF (late-harvest). The avocado *de novo* transcriptome contains 62,203 contigs ($\bar{x}$ =988bp, N50=1,050bp). We found on the avocado *de novo* transcriptome over 99% (CEGMA) and 85% (BUSCO) ultra-conserved genes in eukaryote and *plantae* database. Annotation was performed with BLASTx and Trinotate resulting in a 58% of annotated contigs (90% of differentially expressed genes (DEGs) were annotated). DEGs analysis (FDR≤0.01) found 7,650 genes during all development stages. Finally, we have assembled a high quality transcriptome and this is the first step to explore and discover genes associated to fruit development.

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PS 20

SUBCELLULAR LOCALIZATION OF AQUAPORIN SMALL INTRINSIC PROTEIN FROM *PRUNUS* ROOTSTOCK (PcxPmSIP10591)

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Prunus rootstocks are classified as hypoxia-sensitive, although tolerance degrees among genotypes have been reported. Waterlogging limits the water absorption thus leading to an internal water deficit. The water flow is modulated by proteins called aquaporins, proteins belonging to the membrane intrinsic proteins (MIP) family, which facilitates the transport of water through the cell. These transmembrane proteins can be classified in different subfamilies: PIP, TIP, NIP, SIP, XIP and LIP. It has been shown that these have a differential expression against abiotic stress. Recent studies in the SIP (Small Intrinsic Protein) subfamily proteins found that its N-terminal tail is smaller than in the other subfamilies of aquaporins. We study the subcellular localization of the aquaporin PcxPmSIP10591 identified from the root hypoxia-tolerant *Prunus* rootstock (Mariana 2624). In our approach we used a vector containing the coding sequence of this gene fused to GFP and a vector with a marker of endoplasmic reticulum (ER) co-transfecting the heterologous system, *Nicotiana benthamiana* in a transient transformation assay.

Microscopy analysis showed an ER localization of PcxPmSIP10591, specifically in the cortical ER and plasmodesmata. These results provide new information of this aquaporin subfamily and this suggests a possible relationship between aquaporin PcxPmSIP10591 activity and water transport via symplast.

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PS 21

MARCHANTIA POLYMORPHA AS A MODEL SYSTEM TO DISSECT THE NITROGEN SIGNALING PATHWAY IN PLANTS

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Marchantia polymorpha is a hepatic that rapidly gain adepts in biology to become the next plant model system. It belongs to the bryophyte taxa, the first land plants, characterized by absence of vasculature, haploid genetic, low genetic redundancy and both asexual and sexual reproduction. All these characteristics together with the recent sequencing of its whole genome and easy of transformation, makes *Marchantia* an attractive model system to address fundamental questions in plant biology. Nitrogen (N) is an essential macronutrient for plant growth and development. N is a structural component of biomolecules and different N metabolites/nutrients are known to have signaling functions. Despite enormous efforts in recent years, the N signaling pathway is still not clearly understood in plants. Here we evaluate *M. polymorpha* as a model system to dissect the N signaling pathway in plants. We characterized phenotypic and molecular characteristics of this plant in response to various N treatments, using different sources and regimes. Using existing transformation protocols and CRISPR/CAS9 technology, we generated KO mutants in the main known genes implicated in N responses in plants. In a relatively short amount of time, we were able to recapitulate years of research in higher plants. We believe *Marchantia polymorpha* is an ideal model system that should accelerate the rate of discoveries in the plant N field.

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PS 22

STUDYING ATA6PR1 AND ATA6PR2, PUTATIVE ALDOSE-6-PHOSPHATE REDUCTASES, UNDER ABIOTIC STRESS CONDITIONS IN ARABIDOPSIS THALIANA

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Sorbitol is the main phloem-translocated photosynthate in many species of the Rosaceae family. The key regulatory step in the synthesis of this acyclic polyol is catalysed by aldose-6-phosphate-reductase (A6PR) in source organs, which reduces glucose-6-phosphate. The resulting sorbitol-6-phosphate is then hydrolysed to form sorbitol, via sorbitol-6-phosphatase. In sink organs (like roots and fruits), NAD⁺-dependent sorbitol dehydrogenase (SDH) oxidises sorbitol to fructose. Polyol translocation has several advantages including more efficient carbon use, osmoprotection in abiotic stress (cold, osmotic, salt), and phloem-remobilisation of boron in boron-deficiency conditions. Interestingly, even though *A. thaliana* (Brassicaceae) is a non-sorbitol translocating species, we have nevertheless identified bioinformatically two proteins with structural characteristics and ~70% amino acid identity with known A6PRs from plants where sorbitol is a primary end product of photosynthesis. We call these two proteins AtA6PR1 and AtA6PR2. Unlike in Rosaceae, our studies have demonstrated that AtA6PR1 and AtA6PR2 are ubiquitously-, but differentially-expressed under normal growth conditions. In order to establish their physiological role in this non-sorbitol translocating species, we are now studying the relative expression of both genes in wild-type plants grown under diverse abiotic stresses (cold, salinity, osmotic, and boron deprivation), stresses known to induce expression in Rosaceae species. We are also performing experiments to determine the effect of over-accumulation of AtA6PR1 in *sdh1-1* plants in the distribution and allocation of carbon, with the overall aim of analysing the consequences that a potential mis-balance in sorbitol metabolism has on the plant. Additionally, we have recently obtained *Arabidopsis sdh1-1* mutants transformed with AtA6PR2 as a tool for complementing these studies.

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PS 23

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EFFECT OF EXOGENOUS ABSCISIC ACID (ABA) AND METHYL JASMONATE (MeJA) APPLICATIONS ON GROWTH AND QUALITY PARAMETERS OF SWEET CHERRY FRUITS (CV. BING)

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Sweet cherry (*Prunus avium* L.) is a non-climacteric fruit with high commercial value. Fruit quality is a determinant factor in consumer acceptance, which depends on fruit size, ripening index and integrity. Then, the aim of this research was determine the effect of exogenous applications of abscisic acid (ABA) and methyl jasmonate (MeJA) on growth and quality parameters of sweet cherry fruits (cv. Bing). The applications in two doses of these hormones ABA, MeJA and ABA+MeJA; were evaluated during the three stages of development of sweet cherry fruit (I: fruit set, II: pit hardening and III: ripening). The effect on growth fruit size, soluble solids content (SSC), titratable acidity (% malic acid) and susceptibility to cracking was examined. The results showed significant effects on fruit size towards the end of the fruit development, regardless of the dose applied. Also, applications during stage I, II, III and I+II+III, modified significantly some parameters of fruit, such as increasing the SSC and/or % malic acid during ripening. Finally, when both hormones were applied at the three stages (together or separately) an increase in cracking susceptibility in sweet cherry fruits was observed.

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PS 24

EVALUATION OF TWO INTERSPECIFIC HYBRIDS ROOTSTOCKS OF THE GENUS *PRUNUS* IN THE RESPONSE OF TOLERANCE TO WATER DEFICIT CONDITIONS

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Water deficit is a severe environmental stress for fruit production. The climate change will decrease precipitation and increase temperature in the central zone of Chile, the main production zone of stone fruits. Rootstocks tolerant to water deficit can be an interesting alternative to deal with this scenario, but its contribution must still be evaluated. In this study, two commercial interspecific hybrids rootstocks (ROOTPAC[®] 40 [(*P. dulcis* Miller x *P. persica* (L.) Batsch) x (*P. dulcis* x *P. persica*)] and ROOTPAC[®] 20 (*P. besseyi* Bailey x *P. cerasifera* Ehrh)) were evaluated. Rootstocks were kept 30 days under deficit irrigation and then 7 days of recovery. It was observed that ROOTPAC[®] 40 (almond x peach hybrid genotype) was the most tolerant genotype being less affected in its biomass production and showing greater water use efficiency at the whole-plant level. In comparison, ROOTPAC[®] 20 (sensitive genotype) declined earlier their leaf relative water content and the stomatal conductance (g_s). In addition, g_s failed to recover to the level of the control plants in the recovery period. Besides, biomass production decreased to less than half in roots, stems and leaf compared to well-watered plants. PIP aquaporins gene expression was analyzed in the roots during the most stressed period and it was observed that the sensitive genotype decreased the expression of two of these genes. The future challenge is to determine how many of these responses are kept when commercial varieties are grafted on these hybrid rootstocks.

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PS 25

IDENTIFICATION AND MOLECULAR CHARACTERIZATION OF THREE NAC GENES (NAM, ATAF, CUC) TRANSCRIPTION FACTOR DURING *FRAGARIA CHILOENSIS* RIPENING

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Fragaria chiloensis fruit has been characterized since possess different organoleptic attributes as intense flavor, attractive color and pleasant aroma. Nevertheless, fast fruit softening is one of the main problem. We have identified the differential expression of three fruit specific NAC genes (FcNAC1, FcNAC2 and FcNAC3) and we have obtained their complete amino acid sequences from fruits RNA-seq libraries. All of these sequences contain the highly conserved NAC domain and is subdivided into 5 subdomains (A to E). Phylogenetic analyzes showed high evolutionary proximity with others NAC transcription factors related to secondary wall formation (FcNAC1), related to NAC-regulated seed morphology 1 (FcNAC2) and related to CUC2 and Fc NAC3 was 332, 346 and 551, respectively. The latter showed a transmembrane region in the N-terminal predicted by TMHMM server tools. The analysis of transcription profile at different fruit stages of maturation (C1, C2, C3 and C4) showed a peak of transcripts rate at fruit ripening stage C3. On the other hand, FcNAC1 gene shows high transcript levels in flowers and FcNAC2. FcNAC3 showed high transcripts levels in roots, stem and runners but low level of transcript was accumulated in flowers and leaves. Confocal microscopy analysis showed nuclear localization of FcNAC1 in transient transformation system in young leaves of *Nicotiana benthamiana*. Finally, the involvement of NAC genes during fruit softening and senescence is still unknown, and these data allow us to understand a biological process of particular interest.

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PS 26

EFFECT OF WATER STRESS ON BUD CARBON RESERVES, YIELD COMPONENTS AND FRUIT MINERAL STATUS IN GRAPEVINES (*VITIS VINIFERA* L.)

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Water stress in plants reduces photosynthesis affecting the capacity for carbon gain and storage. Also, water shortages limit the capacity of plants to incorporate minerals. Little is known, however, if grapevines under limited water supply will affect the carbon reserves at the bud sites, in turn reducing yield on the following season, and if the eventual reductions in water supply will affect the nitrogen status of berries. In the present study we have assessed the effect of different irrigation levels, from 30% of potential evapotranspiration (ET₀) to 90 % ET₀ starting on veraison until harvest in *Vitis vinifera* L. cvs Cabernet sauvignon, Carmenere and Syrah, on the starch content in dormant buds, the impact on yield of next season, and the nitrogen concentration in berries at harvest. Despite the difference in irrigation and photosynthetic capacity between irrigation regimes, no differences were found in starch concentration in buds, bud fertility and flower abscission in any of the varieties. But for Syrah, differences in yield components were found, affecting yield upon water stress. On the other hand, no differences in nitrogen concentration as for weight basis were found between treatments. We conclude that water stress does not affect bud reserves in winter. Syrah is affected in next season yield, however, due to yield components at the clusters level. Other minerals in berries are being analysed, such as calcium, which are directed straightforward into berries, unlike nitrogen, which is partly remobilized from other plant parts.

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PS 27

MORPHOLOGY AND GENE EXPRESSION CHANGES IN TABLE GRAPE BERRY PEDICELS FROM CONTRASTING PHENOTYPES IN BERRY DROP

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Most seedless table grapes (*Vitis vinifera* L.) require gibberellic acid (GA₃) applications to obtain an adequate berry size in order to satisfy market requirements. However, the GA₃ treatment also produces severe berry drop in some cultivars, occurring mainly after a cold storage period after harvest. Berry drop caused by GA₃ has been related to the hardening and thickening of berry pedicel, which produce a cellulose accumulation, and lignification of this tissue. The goal of this work is to study the morphology and gene expression change(s) in pedicel samples from contrasting phenotypes in berry drop susceptibility: i.e. 'Thompson Seedless', that usually exhibits a low incidence of berry drop, and the line P23, belonging to the INIA's breeding program, that have shown a high incidence of this disorder at harvest and after storage, especially in bunches applied with GA₃ for berry growth. Different parameters for the study of this phenomenon were measured during fruit growth and postharvest storage, including fruit detachment force (FDF), hardness, thickness and berry drop. The observation of pedicel structures under a light microscope showed differences between both genotypes in the size of cells and accumulation of lignin in the cortex zone, in samples treated with GA₃, during berry development and harvest. Gene expression analyses by qPCR are currently underway, focused in the genes related to cell wall metabolism (mainly new genes associated with lignin biosynthesis) in order to infer on the possible molecular mechanisms affecting the hardness of the pedicel. The work will help us to understand the developmental mechanisms of berry drop, which could have a significant impact in table grape breeding.

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PS 28

DIFFERENTIAL RESPONSES OF ROOT GROWTH AND OXIDATIVE DAMAGE IN RYEGRASS CULTIVARS UNDER ALUMINIUM TOXICITY

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Aluminum (Al) toxicity in Chilean Andisols is one of the major limiting factors for pasture species growth, including ryegrass. Inhibition of root elongation and oxidative stress are early symptoms of Al toxicity. Previous studies have demonstrated a genotypic variation for Al tolerance in ryegrass cultivars. However, researches are scarce in ryegrass cultivars currently on the market. Our experiments were conducted to evaluate Al-tolerance of four ryegrass cultivars (Nui, One 50, Expo and Bealey) in a nutrient solution (pH 4.8) for 7 days with two Al concentration (0 and 200 µM). Lipid peroxidation (TBARS), radical scavenging activity (RSA), Al content and relative root length (RRL_{AL}) was measured. In general, all ryegrass cultivars accumulated a similar amount of Al in root tissues (around 1400 µg Pot⁻¹). Nui and One 50 were the least affected by Al (200 µM), according to root growth inhibition (2% and 17% respectively). In contrast, Expo and Bealey were the most affected by Al, showing root growth inhibition of 31% and 21%, respectively. The level of lipid peroxidation in roots of Nui exposed to Al, is significantly smaller compared with the other three cultivars. Higher RSA was found in One 50 and Nui cultivars compared with Expo and Bealey cultivars. These results suggest that Nui and One 50 were the most Al-tolerant cultivars, whereas Expo and Bealey were the most sensitive ones.

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PS 29

INHIBITION OF BIOACTIVE JASMONATE BIOSYNTHESIS IN STRAWBERRY (*FRAGARIA X ANANASSA*) FRUIT: EFFECTS ON ANTHOCYANINS AND PROANTHOCYANIDINS ACCUMULATION

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Exogenous jasmonate (JA) application increases anthocyanins accumulation in the non-climacteric strawberry (*F. x ananassa*) fruit. However, the role of the bioactive JA, jasmonoyl-isoleucine (JA-Ile), on anthocyanins and proanthocyanidins (PAs) accumulation in strawberry fruit is not well known. Anthocyanins and PAs accumulation is regulated at a transcriptional level through R2R3 MYB and bHLH transcription factors (TFs) in different plant species. However, the relationship between JA-Ile biosynthesis and the transcriptional regulation of the MYB and bHLH TFs encoding genes still remains to be studied in strawberry fruit. In this work, we assessed the effect of jarin-1, a specific inhibitor of JA-Ile biosynthesis, on the anthocyanins and PAs accumulation in strawberry fruit. We applied jarin-1 and methyl jasmonate (MeJA) to immature fruits using an *in vitro* ripening system during 48 h. It was found a higher α^* value (which indicates redness of strawberry receptacle) and anthocyanin content in MeJA-treated fruits respect to jarin-1-treated ones. Inversely, the PAs content was higher in jarin-1-treated fruits than in MeJA-treated ones. The application of jarin-1 to pretreated MeJA fruits resulted in upregulation of several PAs-related genes (*FabHLH33*, *FaMYB9* and *FaMYB11*) and JA-Ile and MeJA biosynthetic ones (*FaJAR1* and *FaJMT*). In contrast, the transcriptional levels of *FabHLH3* and *FaMYB10* remained unaltered in the latter treatment. We propose that PAs biosynthesis-related genes are upregulated in an unexpected way by both inhibitions of JA-Ile biosynthesis or increase of JA-Ile levels. Further studies are necessary to elucidate mechanistic aspects into how JA-Ile regulates anthocyanin and PAs biosynthesis in strawberry fruit.

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PS 30

Physiological and Molecular Changes Associated to Drought Tolerance in Tomato Genotypes

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Drought stress is one of the main causes that limit plant metabolism and growth, causing a reduction in crop yields. Numerous biochemical reactions have been described to be sensitive to drought. While it is difficult to estimate the magnitude of the loss in production due to drought stress, it is considered that water deficiency is the main abiotic stress in agriculture, which can affect up to 50% of the world production. This study analyses the physiological and molecular response of six commercial tomato varieties to moderate and strong drought stress.

Our results indicated that there exists a positive correlation a physiological level between drought tolerance and leaf water relative content, relative growth rate and stomatal conductance; on the other hand, at a molecular level the plant drought tolerance is correlated with an increase in metabolites of phenyl propanoid pathway, up-regulation in genes that encode to proteins involved in proline and ABA biosynthesis, and an increase in activity of antioxidant enzymes, indicating the importance of ROS metabolism in drought tolerance in tomato genotypes.

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PS 31

IDENTIFICATION AND EXPRESSION ANALYSIS OF CELL WALL-RELATED GENES POSSIBLY INVOLVED IN TEXTURAL CHANGES DURING POSTHARVEST OF Highbush Blueberries (*Vaccinium corymbosum* L.) CV. 'BRIGITTA'

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Blueberry (*Vaccinium corymbosum* L.) is a climacteric fruit characterized by a very short postharvest life, highly dependent on ripening stage and storage conditions, with a characteristic loss of firmness as one of the main factors limiting for its storage, transport and marketability. Ripening-associated softening of fleshy fruit is a direct consequence of enzyme-mediated cell wall and middle lamella degradation, where pectin solubilization is considered to be one of the main factors implicated in fruit softening. To gain insight into blueberry firmness and texture, our goal is to study cell wall metabolism

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in blueberry, its changes at molecular and structural levels and their relationship with texture changes during postharvest under different storage conditions. In this work experiments were performed using Highbush blueberries cv. 'Brigitta' collected from an orchard in 'Los Lagos' Region and stored under regular air and modified atmosphere up to 45 days at 0°C. Samples fruits were analyzed for quality parameters (texture, fresh weight loss and soft fruits incidence), pectin content by AIR (Alcohol Insoluble Residue) and gene expression. To date, we identified and characterized several genes encoding putative proteins related to cell wall metabolism (and putative housekeeping genes), by using ESTs sequences from *V. corymbosum* available in NCBI and BBGD (Towson). The transcript abundance of eighteen cell wall-related genes identified in this study was analyzed by qPCR and correlated with texture pattern and pectin content in order to infer on the possible molecular mechanisms affecting the blueberries softening during storage at 0°C at two different gas composition conditions. The finding of transcripts that could be correlated with blueberry firmness and/or texture would help to understand texture phenotype. This will provide a starting point for the selection of a better technology to maintain the quality of a blueberry fruit shipped to distant markets.

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PS 32

XYLEM MORPHOANATOMY IN VINES (*VITIS VINIFERA* L.), UNDER DIFFERENT IRRIGATION LEVELS AND ITS EFFECT ON THE HYDRAULIC CONDUCTIVITY

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The xylem network determines the capacity of plants to supply water from the soil to the evaporative sites in leaves and is permanently under variable tension forces along the day and seasons. The capacity of the xylem to efficiently conduct water, but also to avoid hydraulic failure, depends on its morphoanatomical properties and must be coupled to stomatal function. In grapevines (*Vitis vinifera* L.), differences in stomatal responses have been observed. Cabernet Sauvignon and Carmenere are known as isohydric and Syrah as anisohydric. In order to investigate possible morphological and functional characteristics of xylem vessels to stomatal behaviour, and its plasticity upon water stress, we have assessed the effect of different irrigation levels, starting on veraison until harvest, in *Vitis vinifera* L. cvs Cabernet Sauvignon, Carmenere and Syrah, on the vulnerability to cavitation and xylem anatomy in fruit bearing shoots. The number of xylem vessels and the frequency distribution of the size of xylem vessel per unit section area were equal between varieties. However, the area of vessel per driving area is higher in Syrah. Furthermore, vulnerability curves show that Syrah is less vulnerable to cavitation ($\Psi_{50} = -2$) compared to Cabernet Sauvignon ($\Psi_{50} = -1.25$) and Carmenere ($\Psi_{50} = -1.1$). This trait could be associated to a difference in the spatial distribution of vessels in the xylem, where Syrah could present a lower percentage of vessels isolated compared to the other two varieties. Other anatomical characteristics of the xylem and whether they are correlated with the vulnerability to cavitation, will be discussed.

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PS 33

EFFECTS OF THINNING ON SUGAR AND ORGANIC ACID PROFILES OF EARLY AND LATE *PRUNUS PERSICA* (L.) BATSCH VARIETIES AT HARVEST AND STORAGE

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Chile is the main exporter of peaches and nectarines to the Northern hemisphere in counter season. Since the markets are usually overseas the fruit should be transported at 0 °C for around a month. In these conditions some fruits can present postharvest disorders after prolonged cold exposure evidenced as mealiness and flesh browning mainly. We believe that agronomic handling such as thinning could affect the final fruit size and flesh composition. Therefore, the aim of this work was to analyze the effect of thinning treatments in fruit quality at harvest and cold storage in an early (Magique) and late (Red Pearl) variety. The treatments were commercial thinning (34 leaves/fruit) and control without thinning (10

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leaves/fruit). The fruit were harvested with similar flesh firmness (12 lbf) and kept at 0°C for 21 days and 0 °C for 21 days plus 5 days at 20 °C. The fruit from thinned trees of both varieties presented increased size and higher amount of soluble solids compared to fruit from unthinned control trees. Thinning also advanced Red Pearl fruit development. Sugar and organic acid contents were analyzed by HPLC pulsed amperometric and diode array detection respectively. Red Pearl presented significant variations in the concentration of metabolites due to thinning mainly sugars and organic acids. Magique was not affected by thinning in these parameters, suggesting that the changes in metabolites in flesh fruit induced by thinning are variety dependent.

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PS 34

EXPRESSION ANALYSIS OF CRUCIAL FRUCTAN GENES (*1-SST*, *6G-FFT* AND *1-FFT*) IN ALOE VERA PLANTS SUBJECTED TO WATER STRESS AND A POSSIBLE REGULATION OF THESE GENES BY ABA

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The monocot CAM plant *Aloe barbadensis* Miller, also known as Aloe vera, is well adapted to live in arid environments. Xerophytic plants have developed diverse response mechanisms to cope with the abiotic stresses produced by these environments. The synthesis and accumulation of different polysaccharides e.g., fructans, in plants has been shown to protect the integrity and function of cell membranes and proteins during dehydration caused by water stress.

Previous results from our group have shown that Aloe vera plants subjected to moderate (50% field capacity (FC) irrigation) and severe water deficit (25% FC irrigation) have higher concentrations of fructans. Glycosidic linkage analysis indicated that fructans from water stressed Aloe plants increased in a highly branched sub-type of fructans, neo-fructans. We also found a significant increase in the degree of polymerization in fructans from 25% FC plants.

In our current study we have analyzed the expression of three crucial genes involved in fructan biosynthesis in Aloe vera; *1-sst*, sucrose: sucrose 1-fructosyltransferase which synthesizes the trisaccharide 1-kestose; *6G-fft*, fructan: fructan 6G-fructosyltransferase that produces the trisaccharide neo-kestose and *1-fft*, fructan: fructan 1-fructosyltransferase which elongates the fructan polymer. By RT-qPCR we determined the effect of water stress and the plant stress hormone ABA have on the expression of these genes in *Aloe vera*. The presence of all three fructan genes (*1-sst*, *6G-fft* and *1-fft*) in Aloe vera plants has been confirmed by preliminary PCR results. RT-qPCR analysis so far has indicated a significant increase in expression for both *1-sst* and *6G-fft* genes in water stressed plants. Meanwhile we have observed a significant effect in *1-sst* expression induced by an external ABA solution.

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PS 35

HETEROLOGOUS EXPRESSION AND ENZYMATIC ACTIVITY OF A RHAMNOGALACTURONAN ENDOLYASE ENZYME OF *FRAGARIA CHILOENSIS*

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Rhamnogalacturonan endolyase (RG-lyase; PL4 family; EC number 4.2.2.23) is an enzyme with catalytic β -elimination mechanism acting on the α -1,4-glycosidic bond between rhamnose (Rha) and galacturonic acid (Gala) that exists in the main backbone of rhamnogalacturonan-I (RG-I). RG-I is a type of pectin present in the cell wall of fruit tissues, which is subjected to disassembling during softening of *Fragaria chiloensis* fruit. *FcRGL4* was isolated from *F. chiloensis* with a length of 2028 basepairs; the protein sequence has 676 aminoacids and a molecular weight of ~75,5 kDa without post-translational modifications. Relative expression analyses indicate the increase in the level of transcripts of *FcRGL4*

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throughout the ripening of *F. chiloensis* fruit, with maximum values at the turning and ripe fruit stages. The coding sequence was heterologously expressed in the methylotrophic yeast *Pichia pastoris*. The recombinant protein was purified through cation exchange (CMC) and affinity (His-tag) consecutive chromatographies. Enzymatic activity assays were performed with RG-I from potato as substrate, detecting the formation of a double bond in GalA at 235 nm. Furthermore, the recombinant RG-lyase enzyme is able to breakdown the mucilage of *A. thaliana* germinating seeds, which is rich in slightly branched RG-I. The role of *FcRGL4* is discussed in terms of its participation during softening of *F. chiloensis* fruit. Acknowledgments: Anillo ACT-1110 And CONICYT-Doctoral Fellowship N°21130658.

PS 36

PHYSIOLOGICAL IMPACT OF SALT STRESS IN *PRUNUS* ROOTSTOCKS

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Fruit production is one of the agricultural items with greater dynamism and growth in Chile and one of the engines of the export industry. In this context, stone fruit tree orchards are one of the most important fruit producers representing a 25% of the total area planted with fruit trees. However, environmental problems imposed by the actual global climate scenario could restrict the cultivation of these species. Salinity is an important environmental stress and salinization of agricultural soils is a critical issue that must be faced in front of a world food demand steadily rising. In an IRGA-based physiological measurement, the plant response to saline condition was characterized on nine *Prunus* rootstocks. We selected two rootstocks with contrasting tolerance to salt stress for deepening our study of their salt adaptive response. Mariana M2624 (*P. cerasifera* x *P. munsoniana*), the salt-tolerant genotype, when exposed to saline irrigation showed an early drop in its CO₂ assimilation (*A*) and stomatal conductance (*gs*) values, but they reached steady levels which were kept till the end of the assay (day 30). In contrast, Mazzard F12/1 plants (*P. avium*) under saline condition showed *A* and *gs* values closer to control levels in earlier sampling times. However, this salt-sensitive genotype evidenced a very sharp decline in these values after day 14 and 5, respectively. These interchange gas parameters are in consonance with biomass production registered for both genotypes under control and salt stress conditions.

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PS 37

RELATIONSHIP BETWEEN CELL WALL CHANGES AND CRACKING INDEX DURING DEVELOPMENT AND RIPENING OF SWEET CHERRY (*PRUNUS AVIUM*) FRUIT

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Cracking in sweet cherry (*Prunus avium*) fruit can be induced by rain during fruit ripening or by an abrupt increment of fruit size. Development of sweet cherry fruit follows a double sigmoid pattern with two peaks of maximum growth, which coincide with the onset of fruit set and fruit color change. In these stages the fruit cell wall extensibility might play an important role, allowing the elongation under periods of tensile force. Previous studies in developing sweet cherry fruits have suggested that primary causes of fruit cracking could be related with the increase in fruit surface area during fruit development. In order to understand the relationship between cherry fruit cracking and cell wall metabolism during fruit development and ripening, we carried out a chemical sequential fractionation of fruit cell wall of the varieties 'Kordia' and 'Bing', which are tolerant and susceptible to cracking, respectively. During early stages of fruit development, 'Kordia' showed greater uronic acid (UA) and neutral sugars (NS) contents in the CDTA-soluble (CSF), Na₂CO₃-soluble (NSF) and KOH-soluble (KSF) fractions than those observed in 'Bing'. This observation along with that at ripe stage no significant differences were observed between most of the UA and NS contents in the different fractions between both varieties,

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suggests that differences in cell wall polymers contents at early fruit development could be related with cracking index. We concluded that greater UA and NS contents in the CSF, NSF and KSF fractions at immature stages could be related with a lower cracking index at ripe stage of sweet cherry fruit.
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PS 38

INVOLVEMENT OF *SCHGDI1* FROM *SOLANUM CHILENSE* IN VESICULAR TRAFFICKING AND TOLERANCE TO SALT STRESS IN *ARABIDOPSIS THALIANA*

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Plant adaptation to abiotic stress may involve rearrangement of molecules from various cellular compartments. Transport of material to and from the specific compartments is carried out by an intracellular vesicle trafficking system, regulated by members of the large superfamily of small GTPases. RabGTPases determined the intracellular membrane trafficking in the secretory and endocytic pathways and operate as a molecular switch that cycle between “active” and “inactive” state. GDP dissociation inhibitor (GDI) protein is key in the regulation of the cycle of the Rabs as they would be responsible for their extraction, recycling and maintaining a cytosolic reservoir of Rab proteins to be delivered to membranes. *Solanum chilense* is considered tolerant to salt and drought stress. The *Solanum chilense* gene *SchGDI1* codified a protein with high homology to a RabGDI and is strongly induced by salt and drought stress. In order to evaluate the role of *SchGDI1* in salt stress, plants of *Arabidopsis thaliana* (Col-0) were transformed with *p35S::SchGDI1* and then stressed under *in vitro* conditions with [50, 75 and 100mM] NaCl. Our results showed that the germination rate, endocytic rate and fresh weight were higher in transgenic than wild type *Arabidopsis* plants. In contrast ROS content was significantly higher in the wild type *Arabidopsis* than in transgenic plants. Therefore, the overexpression of *SchGDI1* increases the vesicular trafficking and salt tolerance in *Arabidopsis thaliana*.

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PS 39

ANALYSIS OF THE INTERACTION DFR - DIHYDROFLAVONOLS BY MOLECULAR DYNAMICS SIMULATIONS

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Dihydroflavonol 4-reductase (DFR) is a pivotal enzyme in the flavonoid biosynthesis pathway catalyzing the last common step that leads to anthocyanins and proanthocyanidins. DFR promotes the reduction of three dihydroflavonols: dihydrokaempferol (DHK), dihydroquercetin (DHQ) and dihydromyricetin (DHM) to leucoanthocyanidins. These substrates differ only in the number of hydroxyl groups on the B phenyl ring: DHK only one, DHQ two, DHM three. Recently, a new variant of DFR (DFR1), which showed an unusual preference for only DHK was identified in strawberry, meanwhile DFR2 can convert any of the three dihydroflavonols. A region of 26 amino acid residues could be relevant to identify the substrates, proposed as the binding pocket of B phenyl ring of dihydroflavonols, where an asparagine residue could be critical. We analyzed FcDFR1 and FcDFR2 isolated from the Chilean white strawberry (*F. chiloensis* spp. *chiloensis*) at sequence and structural level to identify differences in substrate binding (DHK and DHQ).

Phylogenetic analyses grouped FcDFR1 and FcDFR2 into separate clades. FcDFR1 and FcDFR2 sequences consist of 341 and 350 amino acid residues respectively, and share 78.6% sequence identity. The most important differences were found in the region that is important for substrate identification. FcDFR1 and FcDFR2 structures were obtained through comparative modeling, showing a RMSD of 2.39 Å. Regarding protein-ligand interactions, in FcDFR2 a strong and stable interaction between Asn133 and the 3'-OH group on ring B of DHQ was determined by molecular dynamics simulations, but not in FcDFR1, where the equivalent residue is Ala135. In contrast, DHK without 3'-OH group could be transformed by both enzymes as stable interactions were determined. The data provides an explanation of why DFR1 could interact with DHK and not with DHQ.

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EFFECTS OF EXOGENOUS APPLICATION OF ABA AND WATERLOGGING ON AQUAPORIN GENE EXPRESSION IN *PRUNUS* ROOTSTOCKS

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Several species of the *Prunus* genus used as rootstocks are particularly affected by waterlogging stress. Aquaporins play a key role in root water uptake capacity, which would provide a molecular basis for fast and reversible regulation of transmembrane water transport. ABA is one of the most important hormones involved in the plant signaling and responses under several abiotic stresses, but is not clearly elucidated its role on waterlogging stress. In roots, the mRNA expression of most aquaporins genes is affected under waterlogging stress and a putative link with ABA regulation is presumed. To evaluate the role of ABA on the responses of *Prunus* rootstocks to waterlogging stress, exogenous applications of ABA and ABA biosynthesis inhibitor (NGDA) were performed. These treatments were applied to whole roots three hours before waterlogging stress. Roots samples were collected at 3, 6, 24 and 72 hours and physiological parameters were measured at 3, 24 and 72 hours after waterlogging stress. Differences in photosynthesis and stomata conductance between treatments and rootstocks were observed. Gene expression of PIPs aquaporins in responses to these treatments was assessed by quantitative PCR (qPCR). qPCR results showed differences in the gene expression of PIPs aquaporins subfamily. ABA role in *Prunus* rootstocks under waterlogging stress are discussed.

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BIOINFORMATICS AND MOLECULAR ANALYSIS OF FACTORS INVOLVED IN DEVELOPMENTAL AND CRACKING TOLERANCE IN DIFFERENT VARIETIES OF SWEET CHERRY

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Chile is the main exporter of sweet cherries (*Prunus avium*) from the south hemisphere. Unfortunately these fruits suffer a series of superficial problems such as cracking that is one of the major reasons of losses in the worldwide production. The damage is produced when the fruit became in contact with rainfall. We hypothesize that susceptibility to cracking in these fruits could be related to structural components of exocarp and differential expression of genes associated with this physiopathology. Five varieties of sweet cherry (Bing, Kordia, Lapins, Rainier and Regina) were compared in terms of their RNAseq profile in unripe and ripe fruit as well as ripen fruit of two varieties (Bing and Regina) when subjected to cracking assays *in vitro*. Previous analysis by GC-MS enabled identification and quantification of n-alkanes. Varieties with significantly higher concentrations of nonacosane (Kordia, Regina and Lapins) were more tolerant to cracking compared to varieties with lower amounts (Bing and Rainier). The transcriptome analysis allowed the assembly of 47,524 and 76,185 contigs for ripe and unripe fruit, were 75% of them had functional annotation. Our results show that ripe fruit of these five cherry varieties express a core of 20,256 genes (42.6%) and unripe fruit express a core of 18,721 genes (24.6%). We also performed a differential expression analysis from *in vitro* cracked fruits where we observe that Bing (less tolerant) have 271 genes up regulated and 933 genes down regulated under the stress, meanwhile Regina (more tolerant) have 5,060 genes upregulated and 3,165 down regulated. Enrichment analysis of functional annotation allowed us to identify metabolic pathways and genes involved in variety specificity and ripening processes and to explore correlations between differences in alkane concentration and gene expression. Candidate genes are being tested for these five cherry varieties from different locations, seasons, developmental stages and treatments.

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HETEROLOGOUS EXPRESSION OF *RabG3e* AND *GDI1* OF *Solanum chilense* HAVE A SYNERGIC EFFECT IN SALT STRESS TOLERANCE IN *ARABIDOPSIS THALIANA*.

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Plants under environmental stresses activate different mechanism to restore homeostasis and to protect and repair damaged proteins and membranes, which require removal of existing molecules from various cellular compartments and replacement with newer ones. This recycling and deposition of macromolecules is carried out by a complex intracellular vesicle trafficking system that is regulated by RabGTPases. To perform their action, RabGTPases cycle between inactive GDP-bound states and active GTP-bound states. In this cycle other accessory proteins are involved as GDI, GAP and GEF. RabGDI are responsible for removing RabGTPases membrane proteins once occurred GTP hydrolysis, letting RabGTPases free to start a new cycle. The involvement of RabGTPases in salt stress has been studied, relating the overexpression of these genes to salt tolerance in plants. Previous studies in our laboratory show that *SchRabG3e* and *RabGDI1* expression is induced in *Solanum chilense* when subjected to salt stress. Furthermore, we have demonstrated that *SchGDI1* overexpression in *Arabidopsis thaliana* confers salt tolerance. Considering that separately these genes have a positive effect on salt stress tolerance, a synergistic effect would be expected when both genes are expressed together. For this we generated transgenic plants overexpressing *SchRabG3e* and *SchGDI1* and submitted them to different concentrations of NaCl. To evaluate the performance of these double transgenic plants we measure different physiological parameters, comparing *Arabidopsis thaliana* plants expressing these genes separately and together. The results show that the overexpressions of *SchRabG3e* and *SchGDI1* together have a synergic effect in the plant grow and development. The double transgenic plants are stronger, since under salt stress conditions they have a better germination rates and longer and robust roots than the single transformant plants.

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ANALYSIS OF FLAVOR DETERMINANTS IN TABLE GRAPE AND THEIR IMPACT OVER QUALITY THROUGH GENETIC AND METABOLIC CHARACTERIZATION

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In grapevine, flavor and aroma have been widely studied for their role in the winemaking processes; nevertheless, flavor determined by volatile monoterpenes in table grapes has not been genetically characterized. The accepted hypothesis states that the presence of flavor in table grapevine leads to physiological disorders such as browning or non-uniform coloration in berry skin; however, this apparent correlation remains unstudied. Muscat flavor production is mainly controlled by a SNP mutation in the *VvDXS* gene, which leads to an increased accumulation of GPP, the main substrate for monoterpene synthesis. In order to elucidate the complex nature of flavor in grapevines; metabolic, genetic and expression analyses of both an experimental progeny derived from the cross of Muscat of Alexandria and Crimson Seedless and common Muscat varieties used for distillation of *pisco*, revealed that Muscat flavor is detectable in absence of the aforementioned mutation; and that only half of the individuals bearing the mutation are able to produce Muscat flavor; suggesting the existence of additional genetic determinants involved in the process. mQTL analysis based on the quantification of volatile compounds in a population (~200 individuals) bearing the mutation allowed us to identify at least four minor QTLs for the main volatile monoterpene in Muscat flavor composition, linalool, that combined explain 52,76% of the phenotypic variation. Finally, a negative correlation of more than 30% was discovered between linalool content and color variation in presence of the *VvDXS* mutation, suggesting the possibility to develop flavor in absence of the mutation and its secondary effects, due to the enhanced expression of genes different of *VvDXS* involved in the accumulation of volatile monoterpenes.

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INDUCTION OF EXPRESSION OF NSLTP GENES IN FRUIT AND DROUGHT STRESS IN LEAVES SUGGEST A DUAL ROLE IN TOMATO

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The plant cuticle is an extracellular hydrophobic layer that covers the aerial epidermis of plants, providing protection against desiccation and external environmental stresses. The past decade has seen considerable progress in assembling models for the biosynthesis of its two major components, the polymer cutin and cuticular waxes, and the complex regulatory networks that control cuticle synthesis, assembly and transport. Plant non-specific lipid-transfer proteins (nsLTPs) are small, basic proteins present in abundance in higher plants, they have the ability to bind or transfer several types of hydrophobic molecules (fatty acids, fatty acyl-CoA, phospholipids, glycolipids, and cutin monomers). In order to determinate the specific function of these proteins in tomato drought tolerance we analyzed the expression of several genes coding for nsLTPs. Initially we used RNAseq dataset generated from leaves of *S. peruvianum* (Sp), and *S. lycopersicum* var. *Money Maker* (Sl) under moderate (MD) and severe drought (SD) treatments. From 117 genes coding for nsLTPs in the tomato genome, 33 were differentially regulated and significantly in the four combinations (Sp-MD, Sp-SD, Sl-MD, Sl-SD) compared with well watered plants. We analyzed the expression of five of them, where three (TomLTP1, TomLTP2 and TomLTP5) were previously described for us to be induced during fruit development.

TomLTP1 was induced in both species under MD, while TomLTP2 and TomLTP5 were induced in Sl but not in Sp. The other two genes TomLTP70 and TomLTP50 were induced in both species, although under different drought severities. Additionally, we related the effect of acclimation to drought and cuticle permeability to the expression of the genes for suggests a putative function in cuticle formation.

The results suggest that some of these nsLTPs can be implicated in more than one function in tomato, such as fruit morphogenesis and drought stress tolerance.

PS 45

COMPUTATIONAL STUDY OF FCEG1, AN ENDOGLUCANASE INVOLVED IN FRUIT SOFTENING OF *FRAGARIA CHILOENSIS*

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Endo-β-1,4-glucanases belonging to the glycosyl hydrolase family 9 (GH9) have roles in cell wall synthesis, remodeling and degradation. These enzymes are associated to several processes including fruit ripening. In our group, changes in the cellulose-hemicellulosic fraction have been previously reported during ripening, and match with softening of *Fragaria chiloensis* fruit. A full-length sequence was obtained for *FcEG1*, and using qRT-PCR, transcript accumulation was determined during fruit ripening. Phylogenetic analyses suggest that *FcEG1* belongs to α group of GH9 family with other proteins previously described with roles in elongation, ripening, and abscission. To gain insight about the protein structure of FcEG1 and its mechanism of action at the molecular level, the structure of the protein was built by comparative modeling methodology, and was validated and refined through molecular dynamics simulation. The model obtained display a β-barrel-type structure that is typical of GH9 enzyme family that comprises 12 α-helix, 2 3₁₀ helices and 6 β-sheets; and an open groove in the center of the enzyme where the catalytic residues is oriented to the solvent. Additionally, the interaction of FcEG1 with a set of putative substrates such as xyloglucans (XGs) and cellulose was explored

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using molecular docking simulations. The results of the interaction between FcEG1 protein with these potential substrates suggest that stable conformational complexes are formed, with favourable affinity energies for the binding of hemicellulose. The data is congruent with a probable role of FcEG1 protein in the disassembling of the cellulose-hemicellulosic fraction during ripening of strawberry fruit.

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PS 46

WATER TRANSPORT RESPONSES OF ISO- AND ANISOHYDRIC GRAPEVINE VARIETIES: IMPLICATIONS FOR THE SAFETY IN THE CARBON GAIN TO WATER LOSS TRADE OFF

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The hydraulic system of plants has evolved increasing the capacity to supply water to evaporative leaves, but incorporating resistances to avoid hydraulic failure upon water shortages and/or increased evaporative demand. At the stem to leaf continuum, major resistances are stomatal conductance (g_s) with two divergent behaviours: iso- (safe) and anisohydric (risky); and leaf hydraulic conductance (k_{leaf}), strongly determined by vein density, a long-term adaptation. In order to evaluate iso- and anisohydric grapevines responses to water limitation in a commercial vineyard, we have assessed gas exchange responses and water potential status to water availability on the isohydric grapevines Cabernet Sauvignon (CS) and Carmenere (C) and the anisohydric Syrah (S). Across the 3 varieties, S showed a higher stem to leaf water potential gradient ($\Delta\Psi_{stem-leaf}$), independent of the soil water content. Also, all the varieties showed a negative $\Delta\Psi_{stem-leaf}$ to Ψ_{leaf} correlation but S responding up to a higher extent. Moreover, the stronger reductions in k_{leaf} upon decreases in Ψ_{leaf} , was observed in S. On the contrary, C is capable of simultaneous reductions of k_{leaf} and g_s implying plasticity in the water transport system at the leaf level, different from vein density adaptations and/or embolism. The tight control of g_s in C led to higher assimilation rates (A_N) at a lower transpiration rates (E) compared to CS and S, suggesting a higher water use efficiency, even though the three varieties had the same A_N to g_s ratio. These results will be discussed in relation to xylem morphology, veins and stomatal density and the susceptibility to embolism, from observations made in the same plants.

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PS 47

DOES SUGAR MATTER? THE ROLE OF GLUCOSE IN GRAPE BERRY RIPENING

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Grapevine fruit development can be divided into three stages: the formation stage, the lag phase (veraison), and the ripening stage; during which physiological and biochemical changes occur that allow cell differentiation and the accumulation of different solutes. Interestingly, during veraison, a fast glucose and fructose accumulation begins together with anthocyanin biosynthesis allowing the color change of berries, which remains during the whole ripening process. The anthocyanin accumulation together with other processes like size increase, turgor, acidity decrease and hormonal variations, allow the full berry development.

Despite there is widespread knowledge about berry grape development, the nature of the signal that initiates and facilitates the coordination of the ripening process still remains unknown.

Sugars have been studied not only as an energy source, but also as a signaling molecule able to control gene expression. It has been demonstrated that glucose and fructose induce anthocyanin biosynthesis in cell cultures of grape. So, in order to determine which is the signal that initiates and regulates the ripening in grape berry, this work is mainly focused on

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understanding the role of glucose and fructose during berry development, due to the increment of these molecules in the beginning of this stage.

Genetic and phenotypic analysis was used in order to determine the degree of ripening of the berry. The results of this work allowed us to demonstrate the importance of glucose in the regulation of the beginning of ripening, because pre-veraison berries treated exogenously with glucose matured 20 days earlier than fruit treated with water. Moreover, sugar treatment in cell cultures of grape showed that the expression of the *MybA1* gene, which is essential for anthocyanin biosynthesis, is induced in response to glucose.

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PS 48

KINETICS OF SILICON AND ALUMINIUM UPTAKE IN BARLEY PLANTS

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Barley (*Hordeum vulgare*) is highly consumed due to energetic and nutritional content. However, the acidic conditions of soils and the presence of toxic aluminum (Al) are important growth-limiting factors for barley plants. It has been demonstrated that silicon (Si) attenuates Al phytotoxicity, as well as it promotes the production of phenolic compounds with antioxidant or structural (e.g. lignin) function. The aim of this research was to evaluate Si and Al uptake, phenols concentration and antioxidant capacity of barley plants cultivated under Al stress conditions. A hydroponic experiment was conducted by using two barley cultivars (Scarlet and Sebastian), which were treated with Al (0 or 0.2 mM Al) and Si (0 or 2 mM) at different harvest times (2, 4, 8, 12, 24, 48 hours). At harvest, Si and Al concentration, total phenols, lipid peroxidation and lignin accumulation were determined in plants. The concentrations of Si and Al increased for the two cultivars when 2 mM Si or 0.2 mM Al was applied, respectively. Aluminium concentration decreased at all harvest times when Al was supplied in combination with Si. The highest concentration of soluble phenols was found at 2 mM Si and 0.2 mM Al addition after 8 hours in both cultivars. Lipid peroxidation decreased in Si-treated plants at all harvest times compared with non-treated plants. Finally, increased lignin accumulation was found when Si was applied in combination with Al.

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PS 49

ENZYMATIC PROPERTIES OF PRXTH1 ENZYME, A XYLOGLUCAN ENDO-TRANSGLYCOSIDASE/HYDROLASE INVOLVED IN THE MOLECULAR RESPONSE TO INCLINATION OF RADIATA PINE

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Several enzymes related to inclination response have been identified in radiata pine, and previous studies suggest that xyloglucan endotransglycosidases/ hydrolases (XTH) might play a key role in the molecular response to inclination of radiata pine. XTHs may have two activities: transglycosidase (XET) and hydrolase (XEH). The full-length complementary DNA of *PrXTH1* was isolated and characterized from radiata pine. Phylogenetic and gene structure analyses suggest that *PrXTH1* belongs to group I of XTHs with putative XET activity. The aim of this work was to study the enzymatic properties of *PrXTH1*. Firstly, *PrXTH1* was cloned and heterologous expressed in *P. pastoris*. The purified recombinant protein is active

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and this activity has only XET activity with 37.86 [a.u./mg protein]. The optimal pH was 6.0 and optimal temperature was 37°C. A Km value of 29.5 µM was determined for XGO (xyloglucan oligomer). To gain insights the mechanism of action of PrXTH1 enzyme at the molecular level, comparative modeling methodology was used to build the structure. The model obtained display a β-jellyroll-type structure that is typical of GH16 enzyme family that comprises 2α-helix, 4 3₁₀α-helix and 15 β-sheets; and a curvature generated by 8 antiparallel β-sheets holds the catalytic ExDxE motif that is oriented towards the central cavity of the protein. The interaction of a set of putative substrates with the protein was explored using molecular dynamics simulations, finding a better interaction with xyloglucans than cellulose. The data provided allow us to propose that PrXTH1 might be hydrolase involved in the molecular response to inclination of radiata pine.

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PS 50

TRANSCRIPTIONAL CHARACTERIZATION OF MYB TRANSCRIPTION FACTORS INVOLVED IN THE MOLECULAR RESPONSE TO INCLINATION AND PUTATIVE REGULATION OF FLAVONOID TRANSPORTER TARGET GENES

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It has been proposed that flavonoids block polar auxin transport. This mechanism regulates the distribution of the phyto-hormone auxin, which is responsible for the differential stem growth during gravitropic response. Flavonoid biosynthesis, performed in the cytosol is transcriptionally regulated by MYB transcription factors. To maintain the cytosolic flavonoid homeostasis, vacuolar compartmentalization of these compounds is needed, which is carried out by specific flavonoid transporters. Transcriptional characterization of MYB transcription factors in response to inclination was studied in order to determine their participation in the biosynthesis of flavonoids and their transport. To this aim, RNA-Seq libraries of plants exposed to different times of inclination were analyzed. Eleven R2R3-MYB full-length sequences, with a differential expression profile according to their FPKM values, were found. Multiple sequence alignment and phylogenetic analysis were performed. Expression analysis of *PrMYB2*, *PrMYB5*, *PrMYB6*, and *PrMYB8*, by qPCR assays, showed an induction in response to inclination in the upper half at 10 hours of inclination. Finally, promoter regions of flavonoids transporter MATE and ABCC genes were isolate and sequenced by "Genome-Walker" technique, revealing the presence of several MYB-related *cis*-acting elements. Results suggest that PrMYB TFs may be regulating flavonoid biosynthesis and, on the other hand, be putative gene expression regulators of flavonoid transporters MATE and ABCC to modulated the flavonoid homeostasis in radiata pine seedlings under inclination stimuli.

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PS 51

ROLE OF UDP-URONIC ACIDS TRANSPORTERS IN THE BIOSYNTHESIS OF NON-CELLULOSIC POLYSACCHARIDES IN *ARABIDOPSIS THALIANA*

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The synthesis of cell wall matrix polysaccharides occurs in the Golgi apparatus through the concerted action of hundreds of glycosyltransferases. The activity of these enzymes depends, in turn upon nucleotide-sugar synthesizing/interconverting enzymes in the cytosol, and also of the nucleotide-sugar transporters (NSTs) necessary for sugar transport into the lumen of Golgi. UDP-Glucuronic acid (UDP-GlcA) is a key molecule involved in this process since it serves as precursor for the synthesis of several polysaccharides of the cell wall. To date, no UDP-GlcA transporter has been

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identified so their role in non-cellulosic polysaccharides remains unclear. In this work we identified a family of UDP-GlcA transporters (UUATs) located in Golgi apparatus. To determine their contribution to non-polysaccharide synthesis, we studied UUATs family members and determined their expression pattern using RT-qPCR experiments. We confirmed UUATs are Golgi localized proteins and analyzed their contribution to non-cellulosic polysaccharides biosynthesis, analyzing the cell wall composition of plants presenting altered expression levels of UUATs genes by High Performance Anion Exchange Chromatography (HPAEC) and we analyzed xylan structure and composition by Polysaccharides Analysis by Carbohydrates Electrophoresis (PACE). Overall results suggest UUATs participate in pectin polysaccharides biosynthesis rather than hemicellulose biosynthesis.

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PS 52

SILICON AMELIORATES ALUMINUM STRESS BY REGULATING ALUMINIUM UPTAKE AND ANTIOXIDANT RESPONSES IN RYEGRASS PLANTS

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Aluminium (Al) toxicity limits crop production in acidic soils, and there is evidence that silicon (Si) can ameliorate the negative effects of Al in some plant species. Nevertheless, there are few reports about the role of Si in regulating the antioxidant system of plants growing under Al stress. We investigated the impact of Si against Al toxicity in ryegrass by analyzing the growth responses, Si and Al concentrations, lipid peroxidation and antioxidant enzyme activities in plants hydroponically cultured with Al (0 or 0.2 mM) and Si (0, 0.5 or 2.0 mM). Aluminum stress reduced dry matter production of roots by about 28%, while applied Si improved the growth of shoots and roots by 22 % and 12%, respectively. Aluminum supply also raised Al accumulation mainly in roots, but Al concentration in shoots and roots was progressively reduced in response to increasing Si doses. By contrast, Si concentration of shoot and roots increased as the Si dose rose, but this increment was less noticeable when plants were simultaneously supplied with Al and Si. Likewise, Si supply significantly counteracts (in about 35% in shoots and 28% in roots) the increase of Al-induced lipid peroxidation. Moreover, the activation of superoxide dismutase, catalase, peroxidase and ascorbate peroxidase enzymes was found as a consequence of Si application to plants subjected to Al stress.

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PS 53

ANALYSIS OF TRANSCRIPTION FACTORS FAMILIES INVOLVED IN STEM INCLINATION ON *P. RADIATA* PINES.

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Gravity plays an important role as environmental stimulus, particularly responding to loss of verticality, and triggering differential cellular responses. Molecular events in response to inclination promote cell wall modifications, such as, synthesis of hormones like Auxins and Ethylene, and gene expression of transcription factors (TFs) as MYB and NAC families, which control lignin biosynthesis during wood formation.

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In this study, RNA-seq library was built from inclined *Pinus radiata* D. Don. Samples were taken at 2.5, 10 and 24 hours after inclination, keeping upright stem as control. A total of 101575 contigs were *de novo* assembly by Trinity, then, GO annotation was performed. A Transcription factors categorization was obtained using Plant TFDB. Twenty-six thousands four hundred and twenty four different TFs belonging to 47 families were identified. After filtering the data, we used 2622 TFs; from which 27 were differentially expressed in at least one of the conditions. These 27 genes belong to only 16 transcription factor families, and finally 11 genes were selected for qRT-PCR analysis. Subsequently, a regulatory network was built using, *A. thaliana* orthologous genes, in order to evaluate the interaction between those TFs. Interestingly, the two WRKY and GRAS genes showed a higher expression in the upper stem halves, on the other hand, bHLH, NAC and HDZip genes in the lower stem halves.

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ANTIOXIDANT RESPONSES IN WHEAT (*TRITICUM AESTIVUM*) BAKAN CULTIVAR UNDER ALUMINUM TOXICITY

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Acid soils represent about 40% of world arable land, having high availability of toxic aluminum (Al³⁺), which limits plant growth. Wheat is the main crop and food in the world, being the base of nutrition in many populations. The aim of this work was to determine the antioxidant responses in wheat (Bakan cultivar) under aluminum toxicity. Nineteen-days-old plants of wheat Bakan (Baer) cultivar were treated with Al as AlCl₃ (5 mM) at 4.2 pH for 48 h in greenhouse. During seven-days, plants were grown in a Hoagland nutrient solution with and without (control) toxic Al. Thereafter, in shoots and roots lipid peroxidation (LP) by TBARS method, antioxidant activity (AA) by DPPH method, and total phenols (TP) by Folin-Ciocalteu method were determined. Results showed that the LP did not show statistically significant differences between control and Al treatment in shoots and roots. However, AA and TP increased in shoots (37.7 and 37.6%, respectively) and in roots (28.1 and 41.7%, respectively) under Al treatment compared to control. Thus, it is concluded that wheat Bakan cultivar could be an Al-resistant cultivar, due to its increase of AA, TP and low oxidative damage (LP). However, more studies are needed to determine the mechanisms involved in this resistance.

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GENETIC CONTROL OF IRON LOADING IN *ARABIDOPSIS* EMBRYOS

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The molecular mechanisms that regulate iron allocation in plant seeds are poorly understood. It has been shown that iron accumulates in endodermis, a cell layer that surround provascularature, during Arabidopsis embryo maturation. In order to better understand the genetic control of iron accumulation and distribution in seed embryo, we used mutants in transcription factors known involved in embryo development and seed maturation. We initially focus on *FUSCA3* (*FUS3*),

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ABSCISIC ACID INSENSITIVE3 (ABI3) and *LEAFY COTYLEDON2 (LEC2)* mutants. These three proteins belong to B3 domain-containing transcription factors family. Thanks to Perls/DAB staining we were able to determine that *fus3*, *lec2* and *abi3* mutant embryos have different iron distribution patterning and/or accumulate less iron than wild-type embryos. Also, preliminary results indicate that iron content decrease in *bzip63* mutant seeds, a member of bZIP group C transcription factors. Finally, regarding hormonal control, it is known that abscisic acid has an essential role during seed maturation, and so far, there are not reports about hormonal control of iron loading in seed. Our results indicate that *abi3* mutant embryos have low iron content suggesting a possible role of abscisic acid in iron accumulation in seeds. We propose to analyze iron distribution and accumulation in abscisic acid biosynthetic pathway mutants (*aba* mutants), in order to characterize the possible role of ABA in embryo iron loading. This is the first description of a genetic control involved in iron accumulation and distribution in Arabidopsis embryos.

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PS 56

INCREASE IN WATER USE EFFICIENCY IN CITRUS PLANTS THROUGH STOMATA OVEREXPRESSION OF THE TRANSCRIPTION FACTOR MYB61

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Citrus are perennial plants that are known worldwide for its juice and pulp cultivated in tropical, subtropical, and Mediterranean climates, being the most relevant Brazil, United States, India, Mexico and Spain. Drought is the main abiotic stress factor limiting the yield in fruits. One of the first plant responses to drought is the stomatal closure in order to prevent desiccation. It has been shown that some transcription factors are involved in this process, such as *AtMYB61*, which is related to the stomatal closure induced in the absence of light. Considering this background, we wanted to assess whether over-expression of the homologous gene of *AtMYB61* in citrus (*CsMYB61*), under the transcriptional control of a specific stomatal promoter, increases the EUA in citrus plants under water stress. To do this we identified, isolated and sequenced the *CsMYB61* coding region. The protein encoded by this sequence has characteristic domains and motifs of other MYB61 proteins. Similarly, we isolated the 1.2 kb promoter region of the gene *CsMYB15* (*pCsMYB15*) containing regulatory elements for expression in guard cells, and other possible ABA and light responsive elements. In transgenic plants of Arabidopsis and citrus, *pCsMYB15* directs the expression of the reporter gene *GUS* in stomata. Valencia orange lines over-expressing *CsMYB61*, have a normal phenotype under *in vitro* and greenhouse conditions. WUE assessment under water stress is currently under evaluation.

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IRON DISTRIBUTION IN EMBRYO OF CLOSELY RELATED ARABIDOPSIS SPECIES

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Iron is an essential micronutrient for most living organisms, including plants. The role of iron in seed production is an important agronomical trait because iron deficiency affects plant reproduction and limits crops yield. According to the World Health Organization, 30% of the population is anemic, and biofortification is a possible alternative to combat iron

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deficiency, and seeds with higher mineral content may contribute to this goal. Using *Arabidopsis thaliana* as model plant, it has been described that iron accumulates during embryo maturation in vacuoles of endodermis cell layer. Using Perls/DAB staining we were able to find that others seed embryos from relatives species to *Arabidopsis*, have a different iron distribution pattern. In those embryos, iron accumulates in two cell layers in hypocotyl. Using epifluorescence microscopy we identify one of these cell layers as endodermis. This is the first description of plant embryos with different iron distribution compared to *Arabidopsis*. Our results open new questions about the molecular mechanism controlling iron loading in seeds.

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PS 58

EFFECT OF SILICON ON ANTIOXIDANT CAPACITY OF RYEGRASS PLANTS SUBJETED TO PHOSPHORUS DEFICIENCY

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Phosphorus (P) is an essential nutrient for plant growth. However, in acidic Andisols of Southern Chile, P availability is limited. Some researches indicate that Si can alleviate P deficiency, which is highly detrimental to grassland production. This study aims to assess the effect of Si on antioxidant capacity of ryegrass cultivated under different P supply. A pot experiment was conducted with ryegrass (*Lolium perenne* L.) grown on an acid Andisol supplied with Si (0, 250, 500 mg Si/kg soil), applied as either calcium silicate (SiCa) or sodium silicate (SiNa), and P (0, 150 and 300 mg P/kg soil) using Triple superphosphate. At the end of the experiment, antioxidant activity, total phenols and superoxide dismutase (SOD) activity were evaluated in shoots tissues. Plants growing under P deficiency showed a significant decrease of antioxidant activity, while an increase of antioxidant activity was observed in plants treated with 150 or 300 mg P/kg soil, irrespective of Si treatments. By contrast, both Si sources raised total phenol production of plants subjected to P deficiency, but no differences in total phenols were detected under optimal P nutrition. A significant decrease of SOD activity occurred when plants were grown at the highest P doses, and no changes in SOD activity were observed in plants supplied with Si.

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PS 59

NEW MASTER REGULATORY FACTORS IN NITRATE CONTROL OF POST-EMBRYONIC PLANT DEVELOPMENT

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Nitrogen is an essential macronutrient for plant development and growth. Synthetic fertilizers are the main source of N applied to crops. Unfortunately, plants are not able to use the entire N deposited and 50 to 70% is lost contaminating terrestrial and aquatic systems. The most abundant inorganic N source for plants in agronomic soils is nitrate. Beyond its role as a nutrient, nitrate can act as a signal that regulates global gene expression. However, most studies have focused in root organs and we know relatively little about how nitrate regulates physiological and developmental processes in shoots. We aim to understand of nitrate modulates vegetative shoot development. Nitrate deficiency has a direct impact in aerial surface and shoot fresh weight early in post-embryonic development. Despite a clear growth and developmental phenotype, no correlation is observed at the level of nitrate reductase activity, suggesting nitrate as a signaling molecule

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modulates shoot vegetative growth and development. Detailed transcriptome analysis using RNA- seq technology and transcriptional network modeling allowed us to identify new transcription factors that are candidate master regulators of Arabidopsis growth and development in response to nitrate. To understand how these master regulators are regulated by nitrate could help us to improve the nitrate use with direct influences in a more efficient and ecological agriculture.

PS 60

GRAIN QUALITY OF TWO WHEAT SPECIES IN RESPONSE TO CLIMATE CHANGE SCENARIO: A SHORT HEAT STRESS ON A KEY PHASE OF SEEDS DEVELOPMENT

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For the end of this century, it has been predicted an average increase of the surface global temperature of 1.7 – 4.9 °C. Furthermore, a higher frequency of short episodes of heat stress is expected as a direct consequence of the climate change. Therefore, temperature will be one of the main factors affecting the development and productivity of crops in Chile and worldwide. Wheat is the most widely cultivated cereal and an essential component of global food security. Temperature increases during grain filling will impact on yield components, weight and quality of the final grains. In this work we analyze the effect of temperature on grain quality at the molecular and physiological level in two agronomical wheat species: the hexaploid *T.aestivum* (bread wheat) and the tetraploid *T.durum* (pasta wheat) exposed for 4 days to the high temperature (32°C for the treatment and 24°C for the control plants in average) at the post-anthesis (flowering). Heat stress rapidly induces the expression of Heat Shock Proteins (HSPs) in the seeds 3 hours after treatment. However, the expression of glutenins and gliadins (the main components of the storage proteins in wheat endosperm) and several starch synthesis genes are not altered, at least in the first 24 hours of heat stress. In both species, the thermal stress generated a reduction of 30-32% in grain weight, one of the main components of yield. Seed viability is not affected by heat stress. Conversely we observed a decrease of 35% in seed size, with an important effect in the grain width. A drastic reduction of the grain length was observed only in *T.durum*. These results suggest the existence of different mechanisms of response to heat stress in both wheat species.

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PS 61

RELATIONSHIP BETWEEN THE IMPLIED GENES IN VEGETATIVE PHASE CHANGE AND THEIR METHYLATION PROFILES ON *EUCALYPTUS GLOBULUS* LABILL

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On the life cycle of some plants, the heteroblasty phenomenon is observed, which consists in a marked transition of juvenile-to-adult traits. These plants allow us to study vegetative phase change (VPC) as a model, which are characterized by changes in morphology, physiology and biochemistry that are specific for every species. *Eucalyptus globulus* Labill. is a good genetic model to study heteroblasty because of a delimited VPC. The molecular control of heteroblasty remains unknown, although it has been shown in *Arabidopsis thaliana* L. that there are epigenetic mechanisms involved. Among these mechanisms, non-coding RNA (ncRNA) has a regulatory role. miR156 inhibits transcription factors SQUAMOSA PROMOTER BINDING PROTEIN-LIKE (SPL). SPL3 and SPL9 have a role in juvenile-to-adult VPC in different plant species. To determine the relationship between the expression of some regulatory genes from VPC and its possible epigenetic control on *E. globulus*, we contrasted expression profiles from selected genes with their methylation profiles based on genome-

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wide methylation profile (previously published results) comparing adult and juvenile leaves. The results show that expression of miR156 decreases during VPC, which coincides with the increase of genes expression from SPL3 and SPL9 in adult tissues. Comparing the patterns of relative expression from SPL3 and SPL9 with methylation profiles in adult and juvenile tissues, we found an apparent relationship with methylation from promoter regions, in which there is more methylation on juvenile tissues, coinciding with a lower expression from the studied genes. In miR156 we did not observe differences on methylation profiles. These results provide a framework for further studies of the epigenetic regulation in VPC.

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PS 62

RESPONSES OF TWO POPULATIONS OF *Embotrium coccineum* J.R. et G. Forster (PROTEACEAE) TO THE LIMITATION AND CO-LIMITATION OF PHOSPHORUS AND NITROGEN

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Embotrium coccineum (Notro), is a shade-intolerant pioneer specie that colonize full light exposed areas and grows in soils with low nutrient availability. It is characterized by a special type of root adaptation called Cluster Roots (CRs), which exudes organic compounds that improve the acquisition of nutrients from the soil. It has been reported that the formation of these CRs increases in phosphorus (P) deficiency. However, there is still no clarity for the effect on CRs formation with low nitrogen (N) availability or the co-limitation for both P and N. Due of its wide geographical distribution, we wonder if the response to both low P and N (co-limitation) may show variation from different populations. In order to search for those differences, we compared morphological responses of Puerto Montt (PM) and Punta Arenas (PA) populations, maintained the seedlings in hydroponics growing under different nutritional conditions. Moreover, we seek genes such as AFB3, PHT1 and TIR1 among others, involved in the assimilation and deficiency of both nutrients. The morphological responses to nutritional limitation were different between populations: 1) Biomass and height of PA seedlings were similar between nutritional treatments, unlike PM. 2) The CRs formation in PA was negatively correlated with the availability of both P and N, contrary to PM that was constant. We conclude that the reaction to nutritional treatments varies according to the population, and we expect that this research allow us to understand the molecular mechanisms associated with the differential morphological responses.

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PS 63

STUDY OF THE ROLE OF THE UDP-RHAMNOSE/GALACTOSE TRANSPORTERS IN THE SYNTHESIS OF RHAMNOGALACTURONAN I IN *ARABIDOPSIS* SEED COAT MUCILAGE

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The cell wall consists in a complex extracellular matrix composed mainly of polysaccharides. Pectins are important component of the cell wall. Pectins are a family of covalently linked galacturonic acid-rich polysaccharides subdivided in Homogalacturonan domains (HG), Rhamnogalacturonan I (RG-I) and Rhamnogalacturonan II (RG-II). Pectin synthesis occurs in the lumen of the Golgi apparatus by type II membrane glycosyltransferases (GTs), these enzymes use as substrate

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activated sugars in form of nucleotide sugar to transfer it onto specific acceptors. UDP-rhamnose is a key substrate for the synthesis of the RG-I and RG-II, since the synthesis of UDP-rhamnose occurs in the cytosol; it is essential this molecule get into the lumen of the Golgi where rhamnose containing polysaccharides synthesis occurs. Recently we have identified and characterized a family of six Golgi localized UDP-rhamnose/galactose transporters (URGT1→6) in *Arabidopsis thaliana*. To study the role of these transporters in pectin biosynthesis we took advantage of *Arabidopsis* seed coat mucilage, since it is a structure mainly composed of the unbranched pectin RG-I. We have analyzed the expression of different members of *URGT* family in developing seeds, and we found that *URGT2*, *URGT4* and *URGT6* have a peak of expression during the stage when massive synthesis and accumulation of RG-I occurs. Monosaccharides composition analysis and immunolabeling experiments show that *urgt2*, *urgt4* and *urgt6* mutants contain decreased amounts of the pectin RG-I on seed coat mucilage. Results suggest that UDP-rhamnose transporters are important players during RG-I synthesis in seed coat mucilage.

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PS 64

EFFECT OF WARMING ON THERMIC ACCLIMATION OF LEAF RESPIRATION IN ANTARCTIC PLANTS

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Warming is an important characteristic of climate change and the Antarctic Peninsula is one of the most affected regions. It has been predicted that night temperatures will increase rapidly than day temperatures. Antarctic plants have developed a series of mechanisms that allow them to cope with the hard Antarctic conditions. Plant respiration is a physiological process highly sensitive to temperature and for that will be the most affected by nocturnal warming. To test this hypothesis, plants of *D. antarctica* and *C. quitensis* from King George Island, were cultured at 5/2°C and 5/5 °C. Temperature response curves of dark Respiration (Rd) during day and night were performed. Response curves were modeled using a modified Arrhenius equation to determine the sensitivity of respiration under each treatment. Total soluble sugars and starch were evaluated. Additionally, some important proteins in respiration process, as Cytochrome oxidase (COXII) and Phosphoenolpyruvate carboxylase (PEPc) were analyzed. We observed that under night warming, increases the Rd in *D. antarctica*, however, this change is observed mainly during day without effect on soluble sugars and starch concentrations. COX-II was higher at night warming, but PEPc decreased its content. *C. quitensis* doesn't show significant differences in Rd, sugars and starch content but also in this species COX-II was higher and PEPc decreased this content under night warming. Our results indicate that night warming conditions in the Antarctic probably will increase the respiration in *D. antarctica* but *C. quitensis* seems to be less influenced. For both species, the effect of warming would be related with an increase on respiration capacity at electron transport chain level.

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PS65

MANIPULATION OF AUXIN LEVELS IN POLLEN LEADS TO ABNORMAL FLOWER DEVELOPMENT IN *ARABIDOPSIS THALIANA*

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The phytohormone auxin was the first hormone to be described in plants and is one of the most important molecules involved in plant development. 3-indole acetic acid (IAA) is the most important auxin, with greater preponderance in the

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whole plant. The role of this hormone has been largely described during vegetative development (cell elongation, cell division and cell differentiation) but also have an important role in reproductive tissues, particularly flower development. For example, *Arabidopsis thaliana* mutants defective in auxin biosynthesis and/or perception display abnormal phenotypes affecting flower morphology, stamen filament elongation, anther maturation and the correct development of pollen grains. Strikingly, several male sterile mutant plants display similar phenotypes to the ones described for auxin mutants, as lack of stamen, shorter stamen filaments and defects in anther development and maturation. Altogether, the existing bibliographical evidence suggest that pollen grains could be involved in flower development and/or maturation through an unknown mechanism that involves auxin signaling. To evaluate this, auxin levels in pollen grains were manipulated by using the bacterial gene *iaaL* under the transcriptional control of a pollen specific promoter (pPOLLEN:iaaL). The *iaaL* protein catalyzes the conjugation of auxin with lysin, rendering the hormone inactive. Transgenic plants expressing this construction present phenotypes in the flowers, including shorter stamen filaments, loss of short stamens and abnormal nectar glands. These results suggest that auxin present in pollen grain would be important to regulate flower development and maturation, suggesting a novel role for pollen in reproductive development.

PS 66

EFFECT OF THINNING ON POLAR METABOLITE PROFILE IN FRUITS OF 'BUEN LINDO' PEACH VARIETY

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Thinning is an agronomical practice that consists in the removal of fruits from the tree to improve the growth of the remaining ones. The reduction in the number of fruit leads to an increase of sugar assimilates that are translocated towards the remaining fruit improving its size and soluble solid content. Although it was observed an increase in soluble solids in fruits from thinned trees, still which metabolites are altered and any impact on the organoleptic properties remain to be elucidated. The purpose of this work was to compare the polar metabolic profile of fruit from thinned and unthinned trees during different developmental stages including a postharvest period of an early harvest peach variety. The aforementioned analysis was carried out through the identification and quantification of sugars, sugars alcohols, aminoacids, and organic acids by gas chromatography coupled to a mass spectrometry detector (GC-MS). Multivariate analysis (partial least square regression - discriminant analysis) revealed differences between fruits from unthinned and thinned trees related to relative abundance of sugars such as fructose, glucose and sorbitol and also the aminoacids such as asparagine, leucine, phenylalanine, and threonine. Furthermore, early developmental stages displayed a clear separation from the postharvest evaluated stage due to differences in the relative amount of quinic and oxalic acids and aminoacids such as valine, serine, alanine and aspartic acid. Our results suggest that tree thinning affects different physiological aspects impacting not only fruit size but also fruit flavor. Some of the identified metabolites could be used as markers for early fruit quality segregation.

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PS 67

FcSYP24-like, A PUTATIVE SYNTAXIN FROM THE CHILEAN STRAWBERRY (*FRAGARIA CHILOENSIS*)

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The Chilean strawberry, *Fragaria chiloensis*, has a fruit with unique organoleptic characteristics. *F. chiloensis* fruits are comprised of numerous achenes (the true fruits) which are embedded in a fleshy structure called the receptacle. Communication between achenes and receptacles is mediated by vascular tissue that allows the flow of nutrients and hormones. Therefore, during *F. chiloensis* fruit growth, vascular biogenesis is essential for fruit development. In our

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laboratory, we determined that the gene *FcSYP24-like* is related to group 2 Arabidopsis syntaxins (AtSYP24) and is expressed differentially during strawberry fruit development (Espinoza *et al*, 2016). The group 2 Arabidopsis syntaxins are required for correct vascular tissue development. Our goal is to evaluate whether the molecular function of FcSYP24-like is to act as a group 2 syntaxin, with the longer-term aim of evaluating its role in vascular tissue development. Hydrophobicity analysis indicates that FcSYP24-like has a single transmembrane domain. Consistently, transient FcSYP24-like expression in *Nicotiana tabacum* leaves reveals plasma membrane localization, due to co-distribution with the protein PIP2a-mCherry and the lipid FM4-64, both plasma membrane markers. *In silico* analyses show that the homology between AtSYP24 and FcSYP24-like is given by a Late Embryogenesis Abundant (LEA) domain sharing 44% amino acid identity. To evaluate the molecular functionality of the strawberry protein, we are currently performing stable transformation of $\Delta pep12$, a loss of function syntaxin mutant of yeast. FcSYP24-like-EGFP localises in endosome-like structures in $\Delta pep12$ and wild-type yeast. The rescue of specific growth and developmental phenotypes in $\Delta pep12$ expressing FcSYP24-like are under study.

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PS 68

EFFECT OF ROOTSTOCK ON GROWTH AND MINERAL CONTENT IN OLD LIMACHINO TOMATO UNDER GREENHOUSE CONDITIONS IN THE REGION OF VALPARAISO

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Research on the effects of tomato-rootstock on nutrition and fertility of has been poorly developed in Chile, particularly in local varieties. In order to fill this gap, our proposal considers the implementation of grafting management in the Old Limachino Tomato, local specie cultivated in the Valley of Limache, in the region of Valparaíso. Our objective is to determine the effect of the INIA-rootstock on growth, productivity, nutrient content and uptake of the Old Limachino Tomato cultivated under cold greenhouse conditions. To this end, two treatments were made: T1 (self-grafted Old Limachino Tomato) and T2 (Old Limachino Tomato grafted onto INIA-rootstock), with a statistical design of six completely randomized block. Growth, mineral content and uptake were measured across five harvests during five months at INIA-La Cruz, in the región of Valparaíso. No effect on fresh and dry biomass growth and in mineral content in fruit, leaf, or stem was reported. On the other hand, the effect of the rootstock on nutrient uptake showed a significant increase in N, P, and K in fruit, leaf, and stem, being the increase in K uptake in the fruit the most remarkable. A greater uptake of Ca and Mg was reported in leaf and stem than in fruit. In short, we conclude that nutrient uptake levels in grafted plants on INIA-rootstock are different from and superior to those in auto-grafted plants, which suggests a need for different fertilizer dosing management.

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PS 69

IDENTIFICATION OF STAGE-SPECIFIC CYTOKININ RESPONSIVE GENES DURING PEACH FRUIT DEVELOPMENT REVEALS A NOVEL SET OF CONSERVED CYTOKININ-RESPONSIVE GENES BETWEEN PRUNUS PERSICA AND ARABIDOPSIS THALIANA

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Cytokinin plays a very important role in plant growth and development. The ancient hormone, cytokinin, has been diversified during land plant evolution performing different functions, including cell division, meristem maintenance, shoot initiation and growth, vascular development, nutrient uptake, chloroplast differentiation, light perception, leaf senescence and fruit ripening. Through a transcriptomic and qPCR analyses of peach fruits treated exogenously with trans-zeatin at different stages of fruits development, we have reported a set of cytokinin responsive genes expressed in peach fruits at three stages of fruit development: Pre-Lignification, Lignification and Post-Lignification of the endocarp. Comparison analyses of these peach cytokinin-responsive genes with published Arabidopsis meta-analyses reveal a novel set of 68 cytokinin-responsive genes conserved between these two species.

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PS 70

EFFECT OF THINNING ON SUGAR PRODUCTION AND TRANSPORT IN PEACH (*Prunus persica* (L). Bastch)

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Peach is a worldwide demanded fruit, being Chile the main exporter in counter season. The properly peach fruit development and ripening depends on the production and translocation of sugars from adult leaves (source organs) and the partitioning among all sink organs as fruit, meristem, stem, and roots. The source-sink balance is currently manipulated through agronomic practices as thinning, which consists on the removal of some fruits favoring the development of the remaining ones. The sugar partitioning in a tree is determined by the ratio of photosynthesis, sugar production, phloem loading and unloading and finally its storage in fruits. We postulated that changing source-sink balance thorough thinning may affect photosynthesis, hence influencing sugar production and translocation. In this work we evaluated non-destructive physiological parameters in the early harvest peach variety 'Buen Lindo' during the whole season of fruit development. Moreover, samples of leaves, petiole, fruit and pedicel were histological evaluated and polar sugars from these same organs were quantified by HPLC. The results showed that unthinned trees have a higher photosynthetic rate than the thinned trees and that these decrease is related to stomatal limitation. Leaf sugar quantification showed an increment of sorbitol in leaves from thinned trees compared with the unthinned ones. On the other hand, fruit from the thinned trees showed significant difference in sucrose levels at the end stage of fruit development (S3) and glucose and fructose in early stages (S1, S2) compared with the one from unthinned trees. There was no difference in the number cells in fruit from thinned and unthinned trees. We concluded that thinning affects sugars levels in different organs of the tree through effects in photosynthetic activity and sugar translocation throughout the phloem.

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CLATHRIN-MEDIATED TRAFFICKING IS REQUIRED FOR CENTRAL VACUOLE CONFIGURATION IN *ARABIDOPSIS THALIANA*

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In differentiated plant cells, the Central Vacuole (CV) occupies about 90% of the volume. This compartment is essential for homeostasis, cell growth and development. In roots, the configuration of the CV begins in the meristematic growth zone where the immature vacuole is expanding progressively by increasing its content and membrane to reach the state of a CV in the cell differentiation zone. In order to study the contribution of cellular trafficking in CV configuration, we observed the vacuoles across the cell growth gradient in *Arabidopsis thaliana* roots. We observed that sucrose promotes an early vacuole configuration at the root tip respect to a sucrose-free growth condition. Interestingly, we found that the presence of sucrose in the growth media positively stimulates plasma membrane (PM)-internalization and Clathrin-mediated trafficking. Chemical inhibition of PM-internalization leads to vacuolar configuration defects mimicking sucrose-

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free growth condition. Congruently, impairment of Clathrin light and heavy chains function resulting in lower PM-internalization leads vacuolar configuration defect mimicking sucrose free growth condition. Overall our evidences show that the Clathrin-mediated trafficking is required for CV configuration process. Since the internalization of PM drives membrane trafficking to the vacuole our results strongly point to PM as a lipid-membrane contributor for vacuole configuration.

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PS 72

ESTIMATING AGRONOMIC AND PHYSIOLOGICAL TRAITS IN WHEAT USING SPECTRAL REFLECTANCE INDICES, REGRESSION AND CLASSIFICATION METHODS

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The projected increase in global demand of wheat and the current effects of climate change makes necessary to accelerate the breeding process and releasing of wheat varieties tolerant to water deficit. In this study, 384 genotypes of wheat (*Triticum aestivum* L.) weretested under fully irrigated (FI) and water stress (WS) conditions. Grain yield (GY), spikes per square meter (SM2), kernels per spike (KPS), thousand kernel weight (TKW), chlorophyll content (SPAD), stem water soluble carbohydrate concentration and content (WSC and WSCC), carbon isotope discrimination ($\Delta^{13}\text{C}$) and leaf area index (LAI) were evaluated and assessed trough spectral reflectance. The performance of spectral reflectance indices (SRI), four regression (PCR, PLSR, Ridge, and SVR) and three classification (PCA-LDA, kNN and PLS-DA) methods were assessed for the prediction of each trait. For classification two classes were established for each trait, lowest 80% of trait variability (Class1) and highest 20% (Class 2). Both, SRI and regression methods performed better when data of FI and WS were combined. The traits with higher SRI-based prediction were GY and $\Delta^{13}\text{C}$ with $r^2=0.82$ and $r^2=0.92$. Ridge and SVR regression methods showed high prediction power and similar performance. Similar to SRI-based prediction, the higher predicted traits were GY ($R^2=0.90$ and $R^2=0.93$) and $\Delta^{13}\text{C}$ ($R^2=0.92$ and $R^2=0.94$). The PLS-DA showed the best performance among categorical methods. Unlike SRI and regression models, most traits were relatively well classified in a specific hydric condition (FI or WS); therefore, this method is an alternative for wheat genotype evaluation under these conditions.

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PS 73

LATERAL ROOT INITIATION IS REGULATED BY PHOSPHATIDYLINOSITOL 4-KINASE THROUGH THE ENDOCYTIC TRAFFICKING TO THE VACUOLE IN *ARABIDOPSIS THALIANA*

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Lateral roots (LR) increase contact area with the rhizosphere to absorb water and nutrients from the soil. The transcriptional activation led through the auxin complex receptor SCF^{TIR1/AFBs} has been proposed as a key component of LR initiation. However, we had described to the endocytic trafficking toward the vacuole as a positive regulator of SCF^{TIR1/AFBs}-independent LR initiation in *Arabidopsis thaliana* by means of the biomodulator Sortin2. We propose that this process impacts on founder cell specification. In order to deepen the cellular mechanism leading LR initiation, we have studied the role of phosphatidylinositols in this process. We have found that phosphatidylinositol 4-kinase (PI4K) activity

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and coherently the enrichment of its product, phosphatidylinositol 4-phosphate, modulate LR initiation triggered by Sortin2. Consistently, PI4K is required for endocytic trafficking and it participates in the acceleration of endocytic trafficking to the vacuole induced by Sortin2. Particularly, the PI4KIIIb protein family is essential to promote LR initiation mediated by endocytic trafficking toward the vacuole induced by Sortin2. Based in our evidences, we propose that PI4KIIIbs impact on LR initiation as negative regulators on the endocytic trafficking flow to the vacuole. Furthermore, Sortin2-induced LR initiation also requires extracellular calcium uptake as a downstream event of PI4KIIIb function suggesting a signaling pathway resulting on cell specification. Overall, our work supports that endocytic trafficking to the vacuole regulated by PI4K function is involved on the LR initiation promoted by a distinctive SCF^{TIR1/AFBs}-independent mechanism in *Arabidopsis thaliana*.

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FLUORESCENCE PHENOTYPING IN BLUEBERRY BREEDING PROGRAMS

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In Chile, especially in the Maule Region, climate change has led to an increase in temperature and a decrease in precipitation rates. These factors would affect the physiology and development of plants, including blueberry plants (*Vaccinium* spp.). Thus, physiological traits can be used to select tolerant cultivars to environmental stress conditions. Six cultivars of highbush (*Vaccinium corymbosum* L.) (three Northern and three Southern) and two rabbiteye (*Vaccinium ashei* R.) blueberry were subjected to combinations of watering and temperature treatments under greenhouse conditions. Water treatments were: continuous irrigation (Full irrigation–FI); and water deficit (one third of FI water volume, water deficit (WD) and temperature treatments were: ambient conditions (At) and heat stress conditions (At+10°C). Measurements of modulated chlorophyll “a” fluorescence were done in blueberry cultivars under four combinations of both environmental conditions. A principal components analysis was made using sixteen fluorescence parameters and two physiological traits (stem water potential and chlorophyll a/b relation). PC1 and PC2 was capable to differentiate cultivars under hydric conditions and PC2 and PC4 to discriminate heat stress conditions. Chlorophyll “a” fluorescence could be used in a blueberry plant breeding program focused to select cultivars of well performance under hydric or heat conditions.

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PS 75

INTRODUCING C2PE, A NEW QPCR ALGORITHM AND WEB INTERFACE FOR RAW DATA ANALYSIS

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The determination of transcript levels via quantitative polymerase chain reaction (qPCR) is now widespread and instrumental in research, medicine and a broad range of other areas. The standard method of analysis is delta Ct, that is simple to use, but has a high probability of deviating from the true value. Several alternative approaches that give more consistent results have been presented but they are all complex to use. The C2Pe method we have developed can improve on the delta Ct method by 51%, using the PCR curve to estimate the efficiency of each reaction. The main innovations are that the embedded equations use the second phase of the curve to add a quality value to the data and to correct the information given by the exponential phase. We have also incorporated revised statistics to improve the robustness of the analysis and constructed a web-based interface to give a straightforward, streamlined qPCR experience.

PS 76

VARIABILITY STUDY OF GRAIN YIELD, PHENOLOGY AND SAPONIN CONTENT IN QUINOA (*CHENOPODIUM QUINOA* WILLD.)

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Quinoa (*Chenopodium quinoa* Willd.) is an Andean crop, which has been cultivated for over 7,000 years by pre-Incan cultures, mainly in Peru and Bolivia, but also in Chile. It is allotetraploid ($2n = 4x = 36$) species, mainly autogamous with a percentage of cross-pollination ranging between 0.5 and 17.4%, and therefore it presents a high phenotypic and genotypic variability. In this work we evaluated number of days from the emergency to flowering (DEF) and harvest (DEH), seed yield per plant, weight of 1000 seed and saponin grain content of 96 genotype of quinoa from INIA germplasm bank collection, under fully irrigated conditions. DEF ranged from 65 to 110 days, but the majority of the genotypes (87) flowered between 75 and 90 days after emergence. Plant maturity ranged from 135 to 185 days after emergence, but the highest frequency (46 genotypes) presented 145 days. Seed yield per plant was lower than 0.03 kg/plant in 45 genotypes, but 11 genotypes yielded more than 0.1 kg/plant. The weight of 1000 seeds ranged between 0.2 and 3.2 g, with the highest frequency (18 genotypes) with 2.6 g. The saponin content (Koziol method), which gives a bitter taste, showed also a wide range of variation, with the highest frequency (26 genotypes) presenting 5.5 mg saponin/ g fresh weight, using. This is a preliminary study and is part of a PhD thesis on GxE interaction and variability of morpho-physiological traits in a diverse panel of quinoa genotypes.

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PS 77

ANTIOXIDANT PROPERTIES IN FRUITS OF *BERBERIS MICROPHYLLA* AND *ARISTOTELIA CHILENSIS* FROM DIFFERENT GEOGRAPHIC AREAS

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Calafate (*Berberis microphylla*) is a native species from Argentina and Chile, being known due to its medicinal properties such as high antioxidant concentrations in fruits. Maqui (*Aristotelia chilensis*), endemic species of Chile, has also high

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antioxidants. Thus, the aim of this work was to compare the antioxidant features of calafate and maqui fruits from different Chilean areas. The antioxidant activity (AA) was assessed by DPPH method, total phenols (TP) by Folin-Ciocalteu method and total anthocyanins (TA) by a differential pH method. The results showed that calafate TP from Faja Maisan were 37% higher than in Lonquimay, while in maqui, from Temuco TP were 20% greater than in Carahue. AA in calafate was 43% in Mañihuales and Coyhaique areas respect to Lonquimay. However, AA of maqui was 33% higher in Temuco respect to Pucón. Calafate TA was 49% higher in Mañihuales area than in Lonquimay, while in maqui from Temuco was smaller than from Pucón and Carahue. Comparing both species, TP of maqui was 29% higher than calafate, while maqui AA was 18% higher than calafate. In conclusion, due to the high antioxidant properties, both species could be interesting raw material for advanced studies and later use for human health, especially maqui species.

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PS 78

ASSESSMENT OF GENETIC DIVERSITY AND POPULATION STRUCTURE IN QUINOA (*Chenopodium quinoa* WILLD.) GERMPLASM COLLECTION USING SIMPLE SEQUENCE REPEAT MARKERS (SSR)

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Quinoa (*Chenopodium quinoa* Willd.) is an important seed crop domesticated in the Andean region of South America. The genetic variability of quinoa might explain its wide adaptation to different ecological environmental constraints (salinity, drought, frost and high radiation). Nevertheless, there are few cultivars available in the country for intensive agriculture. For this reason, quinoa-breeding programs are being carried out in Chile and other South American countries. The aim of this work was to analyse the genetic diversity and population structure of quinoa selected lines from the breeding program at INIA Intihuasi. Twenty-three microsatellites from public databases were analysed for genotyping 96 selected lines using capillary electrophoresis. Genetic diversity was determined through phylogenetic cluster and population structure analysis. We identified between 2 and 15 alleles with a mean of 4.75 alleles in this genotypes. The average heterozygosity was 0.24 and 0.40 was the mean PIC value. Using Structure software we identified three sub-populations in our genotypes, related to Salares and lowland/coastal ecotypes and another putative 'south-lowland' ecotype exclusive from Chile. This information will be important to assist selection program for combining superior traits in the breeding pipeline by means of NGS tools.

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PS 79

CHARACTERIZATION OF ANTIOXIDANT METABOLISM IN TWO WILD TYPES OF MAQUI *ARISTOTELIA CHILENSIS* (MOL.) STUNTZ

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At the present time the native species of Chilean berries have a great development in the identification and characterization of several secondary metabolites for its antioxidant role beneficial to human health, thus becoming a highly attractive functional food. *A. chilensis* is a native woody species of our country, its fruit is a berry color black, characterized by containing high concentrations of antioxidant compounds, also has been found in a white variant in some natural populations of this species. We studied the antioxidant metabolism of these two types of maqui in fruits and

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leaves, through the determining of antioxidant activity (DPPH), total phenols (Folin-Coicalteau) and flavonoids (aluminum trichloride method). The results show higher antioxidant activity in leaves than fruits where white maqui was 7-fold higher and 21-fold in black maqui. Similar trends for total phenols are also obtained. Otherwise, flavonoids showed a minor difference between these organs obtaining about 2.5 and 1.3-fold in leaves than fruit of white and black maqui respectively. Our results show that the maqui leaves exhibit greater antioxidant activity, phenol concentration and total flavonoids compared with fruits. Regarding the white maqui fruit, they contain a high antioxidant activity and total phenolic content, different to the determined for flavonoids where it is observed a lower concentration. This study constitutes an advance in the understanding of these types of wild maqui regarding their antioxidant metabolism and its potential uses.

PS 80

FUNCTIONAL CHARACTERIZATION OF THE TRANSCRIPTIONAL CO-FACTOR *PAR1* BY OVER-EXPRESSION IN CARROT

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Carotenoids are pigments that provide color to flowers, fruits, and some roots. In plants, it has been described that are precursors of phytohormones, play a role in photosynthesis, and provide protection against photo-oxidative damage. During plant development, light induces the transcription of carotenogenic genes and carotenoid synthesis in leaves, flowers and fruits. On the other hand, in *Arabidopsis* plant the transcriptional cofactor PAR1 promotes the carotenogenic genes expression, thereby inducing carotenoid synthesis during photomorphogenic development. Orange *Daucus carota* (carrot) variety produces a large amount of carotenoids in its modified root grown in darkness (RD). Surprisingly, light impairs carrot root development and carotenoid synthesis. In order to identify non-carotenogenic genes involved in carotenoid synthesis in RD, a *de novo* RNAseq analysis was carried out comparing RD and roots grown in light (RL). Genes involved in light signaling, photomorphogenic development and plastid differentiation were overexpressed in RD than in RL. We found that *DcPar1* gene is almost 2,000 fold over expressed in RD than in RL. This result was confirmed with a qPCR and new RNAseq analysis using the recently published carrot genome. Here we show that *DcPar1* has a higher expression in RD than in RL when carrot root starts to develop. The over-expression of *Arabidopsis Par1* gene in carrot was achieved to determine if it promotes carotenoid synthesis. We observed that transformed somatic embryos present an orange phenotype even in light and mature transgenic lines have changes in carotenoid levels respect to wild-types. The expression of key carotenogenic genes will be presented. Our results suggest that *Par1* participates in carotenoid synthesis in carrot storage root.

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PS 81

DCPSY1 AND *DCPSY2* PROMOTE THE SYNTHESIS OF CAROTENOIDS AND ABIOTIC STRESS TOLERANCE IN CARROT AND PARTICIPATE IN CARROT STORAGE ROOT DEVELOPMENT IN A DARK-INDEPENDENT MANNER

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In plants, carotenoids are isoprenoid compounds synthesized in plastids where they act as accessory pigments during photosynthesis and protect cells against photooxidative damage. They are precursors of hormones such as abscisic acid and provide yellow, orange and red colors to flowers and fruits. In humans, carotenoids act as powerful antioxidants and provitamin A precursors.

Daucus carota is one of the few plants that synthesizes and accumulates high amounts of carotenoids in its storage root that grows only in darkness. Within the carotenoid biosynthetic pathway, PSY enzyme is a rate-limiting step. In *Daucus carota* the two paralogs, *DcPSY1* and *DcPSY2* are differentially expressed during plant development being *DcPSY1*

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preferably expressed in mature leaves while *DcPSY2* is mostly expressed in roots. Moreover, *DcPSY2*, and not *DcPSY1*, is induced during abiotic stress treatment. In the current work, using PSY1:YFP and PSY2:GFP fusion proteins we prove that they present plastidial subcellular localization. By means of overexpression of *DcPSYs* genes in *D. carota* we demonstrated the functionality of both genes, as they promote an increment in carotenoids in carrot leaves and storage root. Additionally, we determined that the expression of *DcPSY1* and *DcPSY2* in transgenic lines induce salt stress tolerance by a lesser presence of reactive oxygen species. Surprisingly, transgenic embryos and seedlings present an orange-enriched-carotenoid phenotype and develop a normal storage root *in vitro* in the presence of light, on the contrary than wild-type seedlings, where light impairs storage root development. These results suggest that *DcPSY1* and *DcPSY2* are required for carotenoid synthesis in leaves and storage roots and play a key role in carrot storage root development in a dark-independent manner.

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PS 82

IDENTIFICATION OF MICROSATELLITE MARKERS IN *ATRIPLEX DESERTICOLA* USING NEXT GENERATION SEQUENCING (NGS)

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Species of the genus *Atriplex* (Chenopodiaceae) are halophytes and able to photosynthesize under low soil water availability and high temperatures, thus having a C4 photosynthetic pathway. Several *Atriplex* species are known for their high biomass generation, which made them excellent candidates for solid biofuels production. Besides, *Atriplex* sp. also can be used as animal forages, especially in drought periods. In Chile, 21 native species of *Atriplex* have been recognized. Most of the native Chilean species from *Atriplex* genus are endemic. They grow in arid areas of Chile's north, except a species that grow until the Estrecho de Magallanes. In this study we work with *Atriplex deserticola*, which is found in the Atacama Desert, one of the driest deserts of the world. Here the soil is sandy and has thick salt layers on the surface. Precipitations are almost absent and most of the humidity comes from coastal fogs.

The objective of this work is to develop microsatellite or simple sequence repeat (SSR) markers from genome sequencing of *A. deserticola*. We have generated and characterized genome sequences using Illumina technology, HiSeq2500 paired-end, specifically. Previously, the library preparation was performed with Truseq DNA PCR free 350bp library preparation kit. Once obtained the reads, a quality control with FastQC software was realized. Then, a pre-processing of the sequences including trimming and filtering was realized with PRINSEQ software. Finally, the ribosomal, mitochondrial and chloroplastic sequences were eliminated. Assembly of the obtained nucleotide sequence reads was performed using the SOAPdenovo software. Finally, the software MISA was used to found microsatellite markers of *Atriplex deserticola*. In this work, we provided evidence of generating levels of diverse microsatellite markers from high throughput next generation sequencing of the *Atriplex deserticola* genomic DNA. The markers could be used in germplasm analysis, accessing genetic diversity and linkage mapping of *Atriplex deserticola*.

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PS 83

DETERMINATION OF POLYPHENOL CONTENTS AND HPLC- MS ANALYSIS OF *NERTERA GRANADENSIS* (MUTIS EX LF.) AND *EMPETRUM RUBRUM* (VAHL EX WILLD)

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The specie *Empetrum rubrum* is a subshrub, which grows in Patagonia, Chile Malvinas/Falklan Islands, which is characterized to tolerate Andean conditions, dryland environments, temperatures as low as -15° C and direct sun exposure. *Nertera granadensis* is a creeping plant, distributes mainly around the Pacific Ocean. Polyphenols or phenolic compounds are secondary natural metabolites synthesized in plants and are produced in response to biotic and abiotic stresses. Because of their antioxidant activity, plant phenols play a role in the maintenance of the pro/antioxidant balance by neutralizing the reactive oxygen species (ROS). In this study total polyphenol contents, expressed as gallic acid equivalents (GAE), were determined in *Nertera granadensis* and *Empetrum rubrum* by the spectrophotometricFolin - Ciocalteu method. The phenolic composition of these vascular plants were studies with HPLC-DAD-ESI-MS. Total polyphenol contents was 32,40 ± 0,02 mg GAE/g and 29,66 ± 0,03 mg GAE/g in aqueous extract and in methanol extract of *Nertera granadensis*, respectively. In aqueous extract and methanol of *Empetrum rubrum*, total polyphenol contents was 173,5 ± 10,5 mg GAE/g and 240,5 ± 3,4 mg GAE/g, respectively. The qualitative HPLC-DAD-ESI-MS analysis of the methanol and aqueous extract of *Empetrum rubrum* (leaves and stems) showed the presence of the following phenols: chlorogenic acid, coumaroylquinic acid, laricitin hexoside, quercetin hexoside and isorhamnetin hexoside. The same method showed the presence of chlorogenic acid in methanol extract of *Nertera granadenis* (fruits, leaves and stems). Acknowledgements: VRID214.418.007-1.0 Proyect Career Engineering Vegetal Biotechnology. Mrs. Claudia Flores For Her Technical Support.

PS 84

BIOTECHNOLOGICAL TOOLS APPLIED TO *VASCONCELLEA SPP*: HAPLOIDS GENERATION AND GENETIC VARIABILITY USING GENOTYPING BY SEQUENCING (GBS)

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A study has been conducted to obtain haploid plant form *Vasconcellea pubescens* (Lenne' et C. Koch) Badillo. Preliminary results showed differences in microspore developmental state after CuSO₄ treatments of flowers, favoring the prevalence of mid and late uninucleated state. Then, microspores were isolated from anthers and were supplemented with different combination of 2,4-dichlorophenoxyacetic acid (2,4-D) and naphthaleneacetic acid (NAA). Microspores cultured in liquid medium formed small cell clusters after 15 days of culture. This is typically the first sign of embryo formation in liquid medium. On the other hand, anthers were isolated and placed on MS medium supplemented with 2,4-D and ANA. After 21 days, the first calli appears on the surface of the anther. Additionally we used GBS as a biotechnological tool to study the genetic structure of *Vasconcellea* species present in Chile. In this regard, we have analyzed the organization of genetic variability of four natural populations of *V. chilensis* and four cultivated populations of *V. pubescens*. The GBS allowed the identification of 4,280 and 2,814SNPs for 95 individuals of *V. chilensis* and 95 individuals of *V. pubescens*, respectively. Here we discuss the level and organization of SNPs variability for both species.

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PS 85

PUTATIVE MITOCHONDRIAL IRON TRANSPORTER IN *Arabidopsis*

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Iron is an essential plant micronutrient because it acts as a cofactor in metalloproteins containing iron-sulfur clusters, hemes or bimetallic iron. Plant mitochondria have a crucial role in the metabolism of iron cofactors; nevertheless the mechanisms that govern mitochondrial iron sensing and uptake are poorly studied. Recently, the first mitochondrial iron transporter in plants, named Mitochondrial Iron Transporter (MIT), has been described in *Oryza sativa*. *OsMIT* is an essential gene, and *Osmit* heterozygous mutant plants have decreased mitochondrial iron content and show whole plant iron imbalance. We identified two *MIT* homologous genes in *Arabidopsis thaliana* genome, At1g07030 (*AtMIT1*) and At2g30160 (*AtMIT2*). In this work, T-DNA mutant lines for *AtMIT1* were analyzed. Preliminary results indicate that heterozygous *Atmit1* mutant plants are hypersensitive to iron excess with an increase in reactive oxygen species in leaves. Analysis of segregation of the mutated locus for different *Atmit* mutant alleles will be shown. Our results suggest that *AtMIT1* might participate in mitochondrial iron transport.

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PS 86

MORPHOLOGICAL AND MOLECULAR STUDIES OF RUNNER BEAN LINES (*PHASEOLUS COCCINEUS*. L)

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Runner bean (*Phaseolus coccineus* L.) originated in Mexico, Guatemala and Honduras, and is a perennial species that involves three botanical varieties based on the color of the flower. In this research, a characterization of ten lines of *P. coccineus* from different locations of Chile was made, including morphological and molecular studies, using morphological analysis of the most representative traits based upon UPOV descriptors. Emergency, germination, v2, v4, flower bud, flower color, pod characteristics, branching height, and type of growth were evaluated. Regarding seed traits, their weight, color, width, length, shape and color of the seed hilum were assessed. Concerning roots, their color, type and presence or absence of nodules were investigated. In parallel, molecular analyses with ISSR (Inter-Simple Sequence Repeat) markers were conducted, being the first time that this is studied in Chile using *P. coccineus*. Also, four lines of *P. vulgaris* and one line of *P. lunatus* were analyzed, to discard hybrids between these species. The analyses of the *P. coccineus* lines originated two main groups. The first showed tuberous root lines with cross-pollination, and displayed long-beak and short type pods, and these lines tended to produce both colored flowers and colored seeds. The second group exhibited fibrous root lines, self-pollination, long- beak pods, and long type of white flowers associated to white seeds.

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PS 87

EFFECT OF PHOSPHORUS ON THE PRODUCTION OF BIOMASS AND PHENOLICS COMPOUNDS IN VARIETIES OF WHEAT GROWN IN HYDROPONIC SYSTEMS

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Phosphorus (P) is an essential element for plant growth. This element is one of the main components of fertilizers required to support modern agriculture. Plants differ widely in their sensitivity and tolerance to nutritional deficit, including P

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deficiency, which could influence the production of phenolic compounds and plant growth. Wheat varieties (Púrpura, Maxi and BTP-314) were cultivated hydroponically at increasing P supply levels (with 0, 0,01, 0,1 or 0,4 mM P) with the aim of studying the effect of different P doses on the plant growth and accumulation of phenolic compounds. The assay was performed for 21 days under greenhouse conditions, and the pH of nutrient solution was adjusted to 6.0 daily. In leaves the dry weight, P content, total phenols concentration and lipid peroxidation were quantified. Difference was observed in dry weight, which was dependent on the concentration of P added. Plants grown under P deficiency (0 or 0,01 mM P) showed a reduced P concentration in leaves as well as increased formation of malondialdehyde (due to oxidative damage) and enhanced production of total phenols. Plants with optimal or exacerbated P nutrition exhibited adequate content of P in leaves, whereas a reduction of total phenols content and formation of malondialdehyde was found. Acknowledgements: FONDECYT Project 1161326 And Dirección De Investigación De La Universidad De La Frontera.

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EXPRESSION QTL ANALYSES REVEAL CANDIDATE GENES ASSOCIATED WITH FRUIT SOFTENING RATE IN PEACH

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Melting flesh (MF) and non-melting flesh (NMF) are the two main flesh types in peaches and nectarines. MF varieties show a higher softening loss in postharvest than NMF. However, there are significant differences in the MF class on softening speed. In some populations derived from crosses between MF varieties, it is possible to observe a normal distribution for this trait indicating a polygenic control. The aim of this work was to identify candidate genes involved in flesh softening through QTL and expression QTLs (eQTL) analysis. An F2 population (n= 152) derived by selfing 'Venus' nectarine was phenotyped at harvest + 3 days at room temperature during three consecutive seasons. Eight individuals showing contrasting softening rate were submitted to total RNA isolation, and they were sequenced using RNA-seq. Based on a previous genetic map a conventional QTL analysis was performed. From the RNA-Seq analysis we found 2,822 differentially expressed genes between high and low softening rate groups. Three co-localized QTLs were detected on linkage group 4 (mean LOD score equal to 9.7 and 58% of variation explained) using phenotypic data from three seasons. Eight eQTLs were detected co-localizing on LG4 (7 trans-eQTL and cis-eQTL) with a LOD score between 3.2 and 6.9. These genes (eQTL) are related to remodeling cell wall, sensing and ethylene biosynthesis and auxin synthesis. This work contributes to unravel the molecular mechanisms responsible for softening rate in nectarines.

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CAN BRASSINOSTEROIDS IMPROVE BERRY COLOR IN TABLE GRAPE CV. 'RED GLOBE'?

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Skin color is a limiting factor for quality of red table grapes. Under certain environmental conditions, proper development of color is not possible and precise technical managements such as the application of growth regulators are required. In this respect, little is known about the effect of brassinosteroids on ripening of grapevine berries and their potential as a viticultural tool. For this reason, a trial was carried out where three brassinosteroid analogues (24-epibrassinolide, Analog 1 and Analog 2) and a commercial formulation of brassinosteroids (B-2000®, IONA, Chile) at concentrations of 0.0 (control treatment), 0.4, 0.8 mg·L⁻¹ for analogues and 60 mg·ha⁻¹ for the commercial formulation were applied to cv. 'Red Globe' clusters at véraison. The 24-epibrassinolide, Analog 1 and B-2000® treatments increased berry skin color (measured as

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Color Index for Red Grapes, CIRG) and total anthocyanin concentrations. Furthermore, anthocyanin's profile changed compared to the control treatment. There were no changes in other berry quality or yield parameters. These results indicate that the different forms of brassinosteroids have a consistent effect on color development, showing that they can play an important role in the ripening of the grapevine berries and they have potential as viticultural tool. Nevertheless, further studies are required to understand how these changes are achieved.

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PS 88

EXPRESSION OF SWEET PROTEINS THAUMATIN AND BRAZZEIN IN TOMATO (*SOLANUM LYCOPERSICUM* VAR. *MICROTOM*) FRUITS

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Sweet proteins like Thaumatin (TAU) and Brazzein (BRA) are non-toxic proteins that have 2000 to 3000 fold more sweetness than sucrose and 10 times more sweetness than stevia. At present, they have been used as sweeteners and flavor enhancers in different meals and unlike stevia, they have a taste similar to sucrose but without providing calories. For these reasons the expression of TAU and BRA could be a useful strategy to improve the sweet taste to fruits without adding calories and carbohydrates. To express these proteins in tomato fruits, we used a eukaryotic bicistronic expression system, which allowed us to express both proteins in a single open reading frame, under the control of a unique fruit specific promoter. We also generated vectors, which let us to express each protein in an independent way.

The functionality of these vectors was achieved through transient transformation of tomato fruits in which the expression of TAU and BRA was successfully obtained. Thus, tomato explants were stable transformed with the TAU-BRA, TAU and BRA vectors. During this work we successfully standardized the transformation of tomato using leaves as explants, and transformation efficiency regard cotyledon explants will be presented. Transformation procedure takes approximately 16 weeks, after which transformed seedlings were transferred to soil and then the correct transformation and expression of TAU and BRA genes were evaluated by PCR and RT-PCR, respectively.

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PS 89

ANTIOXIDANT PROPERTIES AND DETERMINATION OF TOTAL PHENOLS IN FRUITS OF *RHAPHITHAMNUS SPINOSUS*

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Rhaphithamnus spinosus or also known as Arrayan Macho is a specie with a violet blue fruit, belonging to the family Verbenaceae, endemic to Chile and it is distributed from the IV to XI region in this country. There is no information about the antioxidant activity of *Rhaphithamnus spinosus* and the fruits of this specie are toxic. The objective of this research was to evaluate the antioxidant capacity and phenolic compounds content in methanol extract of *Rhaphithamnus spinosus* fruits. The antioxidant activity was determined by spectrophotometric measurements with the free radical 2,2-diphenyl-2-picryl-hydrazyl (DPPH) and the cation radical 2,2'-azino-bis (3 ethylbenzothiazoline-6- sulphonic acid) (ABTS) in presence of *Rhaphithamnus spinosus* fruit extract. Antioxidant capacity was determined by calculating the percentage inhibition of DPPH and ABTS absorbance. For the determination of total polyphenols in this fruits, Folin-Ciocalteu assay was performed. The percentage inhibition for DPPH was 69,75% with an extract concentration of 5,0 mg/ml, and 75.58% for ABTS with an extract concentration of 0,47 mg/ml. The total polyphenol content expressed in gallic acid equivalents was 29,19 ± 1,51

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mg/g of metanol extract. Phytochemical screening of *Rhaphithamnus spinosus* fruits showed the presence of flavonoids and saponins.

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PS 90

TRANSCRIPTOME CHARACTERIZATION OF *V. PUBESCENS* AND *V. CHILENSIS*: TWO PHENOTYPICALLY CONTRASTING PAPAYA SPECIES.

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Papaya (*Carica papaya*) is the fourth economically most important tropical species and the current tendencies indicate that the papaya industry will continue growing. However, the papaya suffers some problems related with tolerances to abiotic and biotic stress. In Chile we can find two papaya species, one of them, *Vasconcellea pubescens*, botanically similar to *C. papaya* and the other one, *Vasconcellea chilensis* that lives under extreme environmental conditions. Due to these properties, it is important to start new studies for these two species in order to obtain important biological information that will increase the knowledge about them and supporting conservation strategies as well as breeding program for the *Vasconcellea* and *Carica* genus. In this work, we obtained the transcriptome for *V. pubescens* and *V. chilensis* using the Illumina platform. The RNA sequenced generated 303,927,496 paired-end reads that correspond to libraries of fruit (small, medium and large size) from both species. *De novo* assembly using the CLC Genomic Workbench version 9.0.1 produced 132,007 contigs with an average of 549 bp and a total of 30,375 full-length cDNA genes. Additionally, based on similarity search with known proteins, those genes were annotated with B2G and InterProScan. The differential expression of selected genes like papain, among others, will be confirmed by qPCR. Thus, transcriptome information for this species is a good resource that will greatly enrich molecular information and help future studies.

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WRKY7, -11 AND -17 TRANSCRIPTION FACTORS, ARE REPRESSORS OF UNFOLDED PROTEIN RESPONSE GENES DURING PAMP-TRIGGERED IMMUNITY AGAINST BACTERIAL PATHOGENS IN *ARABIDOPSIS THALIANA*

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Plants have evolved sophisticated mechanisms to protect themselves from that enable them to avoid pathogens. The recognition of pathogens triggers a signaling cascade, which leads to the biosynthesis of salicylic acid, reactive oxygen species, callose and the transcriptional activation of pathogenesis-related proteins (PRs). The accumulation of PRs generates endoplasmic reticulum stress and triggers the unfolded protein response (UPR). However, failure to attenuate the UPR in response to pathogens may have detrimental effects on plants. In this context, WRKY7, 11 and 17 transcription factors play a key role in the regulation of the defense response since mutant plants lacking these factors are more resistant to pathogenic bacteria infection. We show that double-mutant plants (*wrky7/wrky11* and *wrky11/wrky17*) are more effective at establishing a defense response against bacterial infections (*Pst* DC3000). Additionally, triple *wrky*

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mutant plants (*wrky7/wrky11/wrky17*) are more resistant than double-mutant plants to pathogenic bacteria and exhibited a larger number of callose deposits in response to Flg22. In order to get insights about the molecular mechanisms involved in WRKYs mutant resistance phenotype, we analyze the expression of *CalS12* and ER chaperones genes. Our results indicate that *wrky7/wrky11/wrky17* mutant accumulates more transcripts of *CalS12* and ER chaperones. In addition, an expression analysis of the main components of UPR signaling pathways in plants suggest that bZIP28 transcription factor plays a key role in the regulation of ER chaperones upon plant exposure to Flg22. Also, *wrky7/wrky11/wrky17* mutant accumulates more transcript of *bZIP28* suggesting that WRKY7, 11 and 17 act as transcriptional repressors of this gene. Based on these observations, we postulate a fine-tuning model of basal defense response regulation in Arabidopsis, including the negative control of gene expression associated with UPR and other key-defense response genes such as *CalS12* that together control the physiological response of plant-pathogen interaction.

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PS 92

MOLECULAR CHARACTERIZATION OF *PRUNUS* ROOTSTOCKS GERMPLASM BASED ON A GENOTYPING-BY-SEQUENCING (GBS) APPROACH

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In modern plant breeding, a high number of molecular markers are currently required for segregation analysis, gene mapping and marker discovery for marker-assisted selection (MAS). Genotyping-by-sequencing (GBS), an SNP genotyping approach based on next-generation sequencing (NGS) technology, is highly convenient compared with previous molecular methods. It enables the discovery of a great number of markers and the rapid processing of large populations. CEAF (Centro de Estudios Avanzados en Fruticultura) located in Rengo, Región de O'Higgins, Chile, started a breeding program for *Prunus* rootstocks in 2010. Consequently, different interspecific crosses have been carried out based on the *Prunus* rootstock germplasm collection established at CEAF and the available pollen obtained from the *Prunus* rootstocks germplasm of the Spanish EEAD-CSIC (Estación Experimental de Aula Dei-Consejo Superior de Investigaciones Científicas). In the present study, a GBS approach with diploid *Prunus* rootstocks is performed for SNP identification and to assess the genetic diversity of both Chilean and Spanish germplasm collections. GBS analysis has been performed based on 59 genotypes, among them 34 from CEAF and 25 from EEAD-CSIC. Double-digest GBS libraries were constructed and analysed at Clemson University Genomics Computational Laboratory (CUGCL, Clemson, South Carolina, USA). Sequence reads were aligned to the *Prunus persica* reference genome (Peach v2.1). A total of 18,274 high quality SNPs (minor allele frequency, MAF>0.05; missing data < 5%), were identified. They are distributed over the eight pseudomolecules representing the 8 chromosomes of peach. The number of identified SNPs ranged from 1,736 for the pseudomolecule 8 to 4,403 for the pseudomolecule 1. These SNPs were used for cluster and population structure analysis and accordingly the studied *Prunus* genotypes were grouped into four major clusters (peach, cherry, almond and plum rootstocks). Relationships between *Prunus* genomes and comparative genomics, as well as phylogenetic and population structure analysis, will be discussed. Acknowledgments: CONICYT-REGIONAL/GORE O'HIGGINS/CEAF/R0811001; FONDECYT 3160316; FONDECYT 1160706; And Spanish Ministry Of Science And Innovation (MICINN) Grant RFP2012-00020.

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EFFECT OF SALINE STRESS ON ANTIOXIDANT CAPACITY IN FRUITS OF TWO TOMATO GENOTYPES: WILD TYPE AND CHERRY CULTIVAR

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Salt stress (or salinity) in plants induces excessive generation of reactive oxygen species (ROS intermediates) such as superoxide, hydrogen peroxide and hydroxyl radicals. According to the FAO, approximately 20 % of the current 230 million ha of irrigated land is salt-affected. Over the last two decades, human activities and global climate change have accelerated soil salinization with a broad impact on vegetable cropping. In this context, the study of wild relatives of tomato has become a modern tool to improve the genetic variability of traditional cultivated species. The trial was conducted to determine the effect of salinity stress (NaCl) on antioxidant capacity (FRAP and DPPH), total polyphenols, reduced (GSH) and oxidized glutathione (GSSG), reduced (AsA) and oxidized ascorbate (DHA), in fruits of two tomato genotypes viz. wild type (*Solanum chilense* Dun.) and cherry (*Solanum lycopersicum* var. *cerasiforme* L.). Both tomato species were grown in a greenhouse under a hydroponic system at two NaCl concentrations: 40 and 80 mM, representing two different saline stress treatments, and compared to the control at 0 mM NaCl. FRAP and DPPH assay were established by Benzie and Strain (1996) and by Brand-Williams, Cuvelier, and Berset (1995) respectively. GSH, GSSG, AsA and DHA were determined by a spectrophotometer. The data were processed using a multi-variates analysis (PCA). Results reported that the wild tomato presented a higher antioxidant capacity (FRAP) and total polyphenols content than cherry tomato. The PCA showed the antioxidant capacity were more elevated in wild than cultivated tomato. Total polyphenol content would account for this difference. On the other hand, results suggest that the antioxidant capacity in wild tomato genotype is different from the cherry genotype's one, which opens interesting opportunities for plant breeding and in turn for obtaining new commercial varieties.

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PS 94

IDENTIFICATION OF YIELD RELATED QTLs IN TABLE GRAPE

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Among the characteristics that determine the success of a new table grape variety, yield is probably the most important one but has received very little attention due to its complex nature. To understand the genetic determinism of yield, several related traits were evaluated through association analysis conducted over the 2015/16 growing season. With an experimental F1 progeny of more than 600 individuals derived from a cross between Crimson Seedless and Muscat of Alexandria and up to 4,000 SNPs, we conducted a fine QTL mapping analysis for days to harvest, number of inflorescences, number of flowers, number of berries, berry weight, berry shatter and *millerandage*. This high-resolution mapping allowed us to identify QTLs and to propose candidate genes. More than a dozen of QTLs were identified for these complex traits. Most of them with minor effects that individually explain less than 10% of the phenotypic variation and one large effect QTL that explained above 20% of berry weight variation. The most important Candidate Genes were associated to floral identity, flowering time and phytohormones. Finally, the combination of the most significant and with large effect QTLs (up to six SNPs segregating independently) allowed the capture of a largest phenotypic variation, between 15-76%, for these traits. The results of this study revealed that complex traits like several independent genes and each gene control yield has cumulative effect. These results are the basis for the development of a model to understand yield in table grapes, validation in additional seasons and different genetic backgrounds is required to develop assisted breeding.

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PS 95

MOLECULAR AND MICROBIOLOGICAL STUDY OF CHILEAN ISOLATES OF *PSEUDOMONAS SYRINGAE* PV *ACTINIDIAE*

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Pseudomonas syringae pv *actinidiae* (*Psa*) is a gram negative bacteria which produces the bacterial canker disease in kiwifruit plants, the main cause of the economic losses in the kiwifruit industry worldwide. *Psa* has being classified into 5 different biovars, being the biovar 3 the most virulent one. Chile is one of the main exporter countries of fresh kiwifruit and only *Psa* belonging to biovar 3 has been identified so far in the infected orchards. In this work we have performed a molecular characterization of fourteen *Psa* isolated obtained from Chilean orchards. We have sequenced 3 conserved genes (*cts*, *gyrB* and *rpoD*) and the sequences were used to build a phylogenetic tree. Interestingly, we identified 3 isolates with significant differences in comparison to the others Chilean *Psa* isolate. Furthermore, we used the *Psa* isolated to perform a hypersensitivity (HR) assay in tobacco plants; in this model *Psa* biovar 3 produces a HR response. We observed that all the Chilean isolated produce HR responses in tobacco but at different levels, suggesting a different degree of recognition of *Psa*. We previously determined that all the *Psa* isolated were able to develop swimming and swarming movements in specific agar plates, now we are studying whether kiwifruit extracts are able to attract *Psa*, changing the pattern of these movements.

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WHOLE GENOME SEQUENCING AND RNA-SEQ ANALYSES FOR FRUIT POSTHARVEST DISORDERS IN A SEGREGATING POPULATION OF PEACH [*Prunus persica* (L.) BATSCH]

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Chile is an important fruit exporter, and its peach breeding initiatives have been focused on postharvest and fruit quality in order to satisfy consumers located in distant markets. Flesh mealiness is a relevant postharvest disorder in peach and nectarine, and its phenotype shows lack of juice after long cold storage (0-4 °C), reducing significantly quality and consumer acceptance. Thus, the aim of this research was to identify some candidate genes associated with fruit quality traits using a genetic linkage map, the whole genome sequencing (WGS), and RNA-seq analysis. Fruits of the F1 population formed by 194 individuals (O'Henry X NR-053) were evaluated in four periods: Immediately after harvest (E1), After harvest + shelf life (E2), After 21 days at 0 °C (E3) and After 21 days at 0 °C + shelf life (E4). The correlation between QTLs for mealiness and the identification of SNP, INDEL and structural variations of 30 individuals showing a contrasting expression of flesh mealiness allowed to identification of candidate genes. Further, RNA-seq was carried out to obtain a better understanding of flesh mealiness and its physiological regulations involved. For this purpose, a subset formed by 5 high sensitive and 5 tolerant individuals were used for studying the correlations between the transcriptome and the genomic variations, in order to reach a deeper knowledge of this phenotype.

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TGA CLASS II TRANSCRIPTION FACTORS REGULATE THE BIOSYNTHESIS OF SALICYLIC ACID THROUGH TRANSCRIPTIONAL REPRESSION OF *SARD1* GENE IN ARABIDOPSIS

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Salicylic acid (SA) is a key hormone in the plant defense responses to biotic and some abiotic stress conditions. In *Arabidopsis thaliana*, the main source of SA is the chloroplastic isochorismate (IC) pathway in which, isochorismate synthase 1 (ICS1) is the only known enzyme involved. It has been described that the accumulation of *ICS1* transcript is correlated with an increase in SA levels, which in turn triggers transcriptional reprogramming of defense genes. Transcription factors from the TGA family have been identified in this response. The TGA family in *A. thaliana* is composed by 10 members grouped in 5 classes, being the class II (TGA2, TGA5, TGA6) essential for SA-regulated expression of defense genes. Through a transcriptomic analysis of WT and *tga2/5/6* triple mutant plants in response to UV-B treatments, we found that *ICS1* gene, together with a group of genes involved in SA biosynthesis, were up-regulated in *tga256* mutant plants. To evaluate whether TGA2/5/6 factors directly repress SA biosynthetic genes, we measured SA levels in *tga256* plants and evaluated the recruitment of TGA2 to the *SARD1* promoter by ChIP assays. *SARD1* is a regulator of *ICS1* expression. We also evaluated the functionality of the TGA box in *SARD1* promoter (pSARD1) by analyzing plants carrying the wild type or a mutant version of pSARD1 in the TGA box fused to the *GUS* reporter gene. Results from this work indicate that TGA2 is able to regulate the SA biosynthesis through the transcriptional repression of *SARD1*.

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HIGH DENSITY QTL MAPPING TOWARDS GENOMIC SELECTION FOR QUALITY RELATED TRAITS IN TABLE GRAPE

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Grapevine (*Vitis vinifera* L.) is one of the first crops domesticated worldwide and it was present all along human history over centuries in forms of fresh fruit. Chile is one of the main fresh table grape exporters; this achievement is supported by an industry focused in the production of high quality that is principally determined by visual and organoleptic attributes such as berry size, skin elasticity, flesh texture and seedlessness. Genotyping based in next generation sequencing and improved statistics mixed models are improving plant breeding built over the traditional phenotype-based selection. Breeding is moving towards marker-assisted selection that uses genotype-phenotype associations to establish predictive methodologies. Based on one of the largest F1 biparental progenies derived from the cross between Muscat of Alexandria and Crimson Seedless, 615 segregating plants were genotyped with the 20K Illumina SNP chip resulting in 6,441 polymorphic markers, and were phenotypically evaluated over two seasons (2014-2015 and 2015-2016). Finally, a fine QTL mapping and a Genomic Selection (GS) based strategy were compared to test their accuracy for selection purposes. Regardless of the limitations of our experimental design, our results suggest that both, QTL analysis and GS, have advantages and disadvantages related to identification of candidate genes and most favorable alleles. However, GS tends to have greater accuracy for very complex traits; nevertheless a significant correlation between results of both approaches was detected. Our case study shows that both QTL haplotype based selection and Genomic Selection have the power to improve the bases and efficiency of selection of seedlings for the next breeding cycle and enhancing the cost benefits of a breeding program and additionally provide novel genes involved in grape-quality traits that generate unique variety release.

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FUNCTIONAL CHARACTERIZATION OF AN ANTIFUNGAL PEPTIDE ISOLATED FROM TABLE GRAPES

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Most cultivars of *Vitis vinifera* are highly susceptible to several fungal diseases that result in quality drop at harvest and postharvest, generating economic losses around the world. Introgression of resistance genes, that occur naturally in other *Vitis* species, to table grapes through conventional breeding would require several cycles to recover the table grape genetic background. Alternatively, development of new varieties based on friendly genetic engineering approaches requires the identification and characterization of genes suitable for resistance development. Defensins are small cationic peptides with a conserved cysteine-rich motif found in both vertebrates and invertebrates that have also been reported in plants, these peptides kill microorganisms inserting them into membrane bilayers and forming pores and could be promising targets to develop fungal disease resistance in table grape and grapevine. These small peptides play a role in the innate defense system of plants and are suitable for agrobiotechnological applications. A defensin peptide of 50 amino acid residues was isolated from table grapes and expressed in *E. coli* and transgenic tobacco lines to evaluate its antipatogenic potential. *In vitro* co-cultivation of *E. coli* expressing the plant defensin and *Botrytis cinerea* showed a significant antimicrobial activity. *In vitro* established transgenic tobaccos showed resistance levels that were correlated to the accumulation of defensin transcripts measured by RT-qPCR. Greenhouse transgenic tobacco lines that express ectopically the defensin under control of the strong CaMV 35S promoter revealed a significative tolerance to fungal disease, affecting both establishment of infection and severity measured as the surface of affected leaf area at 12 days post infection. Both, *in vitro* and greenhouse results showed that the isolated peptide is a suitable candidate for future development of genetically modified crops with resistance to fungal pathogens or the development of biocontrol agents. Acknowledgments: FONDEF Grant G09i1007 And Biofrutales Consortium.

ALKALOID QTL IDENTIFICATION IN YELLOW LUPIN (*LUPINUS LUTEUS* L.)

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Lupin low alkaloid varieties has facilitated their inclusion in human and animal nutrition and satisfied food industry standards. However, it has also increased susceptibility to herbivores and transmission of aphid-borne viruses and bacteria. Few alkaloid quantitative genetic studies had been conducted in yellow lupin, pointing out the need of generating breeding tools to aid the efficient manipulation of these secondary metabolites. To genetically dissect these traits, we analyzed 164 diverse *L. luteus* accessions from several origins. The accessions were assessed for lupinine, sparteine and gramine content in seeds over two seasons. Association analyses were carried out in 315 co-dominant molecular markers (genomic SSRs, EST-SSRs, INDELs, and SNPs). Analyses were conducted using mixed models (principal component analysis (PCA) + kinship matrix (K)). Although there was a strong genotype x environment interaction for all evaluated alkaloids, an important number of significant markers were observed in both seasons. For instance, nine and eight markers were associated with lupinine and sparteine, respectively, and gramine was associated with 11 markers. Three markers were associated with both lupinine and sparteine, suggesting one or more common QTLs for quinolizidine seed alkaloids. Currently, backcross populations are being used to validate significant alkaloid associated markers.

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EFFECT OF THE USE OF TOMATO INIA ROOTSTOCK ON THE SYNTHESIS OF POLYAMINE PUTRESCINE, SPERMIDINE AND SPERMINE IN LIMACHINO GRAFTED PLANT DURING INFECTION PHYTOPHOTOGENIC *PSEUDOMONAS SYRINGAE* PV TOMATO

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Pseudomonas syringae pv *tomato* (*Pst.*) is one of the most harmful bacteria for tomato production, causing significant economic losses due to diseases produced both in fruit and leaf tissues. The use of rootstocks is an effective solution for disease control, especially in sensitive tomato varieties like the local high-quality old Limachino tomato, which is highly affected by deleterious environmental conditions such as salinity, drought and pathogens. Polyamines (PAs) constitute a group of low molecular weight aliphatic amines present in all living organisms. The most widespread forms in living in plants are putrescine (Put), spermidine (Spd) and spermine (Spm). Polyamines have been implicated as key players in growth and development processes, and in response to biotic and abiotic stresses. Pathogens may strongly impair plant growth and development producing major changes in the polyamine (PA) metabolism of the host. It has been well documented that the levels of both free and conjugated PAs undergo profound changes in plant tissue during the interaction with pathogens like *Pst.* These metabolic pathways depend on the nature of the microorganism, a concept that stems from the fact that these amines mediate the activation of plant defense mechanisms. The aim of this study is to determine the effect of tomato rootstock INIA on defense response of the grafted plant Limachino to *Pst* by synthesis of polyamines by HPLC. We probe if polyamine plays a role in the plant response and in the defense against pathogens and if this synthesis would be related with H₂O₂ synthesis.

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EVALUATING ROOT VARIABILITY AND METABOLITE CONTENT IN YELLOW CONTENT (*LUPINUS LUTEUS* L.)

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Plant breeders have continuously generated new better yielding varieties more adapted to local conditions and specialized to specific industry needs. However, this breeding effort has been mostly dedicated to increase shoot biomass and seed yields, leaving the study of roots, and their influence upon grain yield, in the rear seat of crop breeding. Recent efforts have shown that by better understanding root physiology, morphology and genetics, significantly increases on seed yield could be achieved. Thus, breeding lupins with strong and deep roots should increase and stabilize seed yields, one of the hardest traits to breed in lupin crops. The main goal of this research is to genetically analyze root natural variation, including morphology and metabolite content, in a diverse set of *L. luteus*, to facilitate the manipulation and introgression of favorable root traits into cultivated types. Lupin accessions were genotyped using a set of molecular markers including SSRs, EST-SSRs, SNPs, and INDELs. Association analyses were conducted using MIXED models and including Population Structure and Kinship to find out the fittest model. Several genomic regions were associated to root morphology and secondary metabolite content. Currently, we are carrying out bioinformatic analyses to uncover candidate genes responsible of root variability.

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CLONAL IDENTIFICATION OF *Vitis vinifera* CV PINOT NOIR USING WHOLE GENOME SEQUENCING

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Grapevine is one of the most economically important fruit crops and Chile is the fourth world wine exporter. There are many grape collections; this large diversity is mostly due to the long history of grapevine cultivation and vegetative propagation, which has enabled the conservation of cultivars over centuries. Molecular markers have been used to study grapevine diversity. For instance, microsatellites are a powerful tool for cultivars identification. However, clones identification remains a problem due to the minimum genetic differences between them. Our aim is to characterize the most important cultivars and clones currently used for Chilean wineries. For this, we developed molecular markers and we expect to implement high-throughput genotyping methodologies. We sequenced four 'Pinot noir' clones from two Chilean wineries. Raw data sequences were mapped against the reference genome 'PN40024'. We detected an average of 156,200 homozygous variants between different clones. The SNP frequency was around 0.3 SNP per Kb, whereas for InDel was 1 per 23 Kb. We selected as candidate markers InDel higher than 10 bp on coding regions. We expect to develop PCR-based detection protocols to identify clones used for Chilean wine industry based on molecular marker fingerprint. The identification of these stable molecular markers will be useful in clonal diversity studies.

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PROTOCOLS TO INTRODUCTION OF *COLOBANTHUS QUITENSIS* AT *IN VITRO* CULTURE

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Colobanthus quitensis (Caryophyllaceae) is a vascular native plant of Antarctica, which also has a wide distribution from maritime Antarctica to Mexico and from 0 to 4.200 m.a.s.l. All their habitats stand out for extreme edaphoclimatic conditions, which has led to *C. quitensis* to develop adaptive mechanisms, getting to form environmental ecotypes. Germplasm conservation of the species populations is imperative to constitute it as a potential model in studies of plant stress adaptation. The establishment of this species *in vitro* has become a challenge due to contamination by endophyte microorganisms. The microbicide and phytotoxic effect of calcium hypochlorite, silver nitrate and silver nanoparticles was evaluated to introducing explants from Arctowski (Antarctica), Laredo (Patagonia) and Conguillio (Andean) populations to *in vitro* culture. The percentage of contamination, oxidation and survival of the explants were considered and then number of shoots and roots was evaluated for the plantlets establishment *in vitro*. Treatments with calcium hypochlorite or silver nitrate prevented explants contamination in both Arctowski and Laredo populations, but not Conguillio because the silver nitrate caused tissue oxidation delaying the establishment and sometimes death of tissue. Treatment with calcium hypochlorite 10% for 20 minutes proved to be the best for Arctowski and Laredo populations being necessary to assess other times exposure and/or concentrations to Conguillio or evaluate other protocols.

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CONTRIBUTION OF FLOWER TRAITS IN THE DIFFERENTIATION OF TOMATO LANDRACES

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To the end of the XIX century multiple cultivars of different colors and shapes of tomatoes were available in America. Nowadays considered as landraces produced by the early breeding. Limache is one of the main tomato grower communes in Chile since to 1955. A local variety of this territory, the Limachino tomato has been dated back to the 1960's. Local varieties often lack of a proper characterization, making it hard to identify. Tomato plants characterization is traditionally carried out using fruit descriptors. Many vegetative descriptors from IPGRI and UPOV show no variation in the field, making the differentiation by vegetative characters of little use for close related tomato landraces. IPGRI flower descriptors have shown a better differentiation approach. The flower and inflorescence architecture has been associated with the tomato plants productivity and correlated with fruit size. A high-throughput flower description was made of 18 tomato accessions conserved at INIA's germplasm bank network, which included 11 Limachino type tomatoes, a local pink variety and six red commercial varieties. PCA showed that flower characters were useful for differentiating very close related varieties, in which vegetative descriptors did not, showing great use of a high-throughput flower description, for identifying tomato landraces and commercial varieties.

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CHARACTERIZATION OF TRADITIONAL YELLOW MAIZE VARIETIES FROM COIHUECO, ÑUBLE PROVINCE

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In the commune of Coihueco, Chillan province, traditional farmers still cultivate yellow maize landraces with a wide diversity of morphological characteristics that have been preserved from generation to generation. The gene reservoir maintained in these populations has not been studied and it is being lost due to the replacement or contamination with hybrid commercial varieties. An evaluation the genetic diversity of some of the maize populations cultivated by farmers could contribute to the implementation of an effective in situ conservation and utilization. Eleven accessions collected from Coihueco were morphological characterized for plant, ear and kernel trait. Additionally, these accession plus some other representative landraces of Chilean maize races cultivated in Chillan province before the 1990s are being genotyped by SSR markers. Results showed the existence of significant morphologic differences among accessions for all evaluated traits. PCA revealed that accession is separated mainly by plant vigor and ear length (PC1) and kernel trait (PC2). At least three morphotype were described: flint type and semi-flint type. Qualitative traits showed the existence of varietal admixture. Morphological data allowed us to determine that one accession is an Ocho Corridas landrace that is clearly differentiated from the others, which correspond to semi flint and flint accession, this last probably close to Camelia landrace.

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EVALUATION OF ANTIOXIDANT ACTIVITY AND TOTAL POLYPHENOL CONTENT IN THE AQUEOUS EXTRACT OF *KAGENECKIA OBLONGA* RUIZ ET PAV

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Free radicals cause oxidative damage and are responsible for causing health problems. The antioxidant activity of an aqueous extract of *Kageneckia oblonga* was evaluated by analyzing DPPH (1,1-diphenyl-2-picryl-hydrazyl) free radical scavenging and ABTS+ [2,2'-azino-bis (3 ethylbenzothiazoline-6- sulphonic acid)] radical cation scavenging activity. The total phenolic content of the aqueous extract was determined by the Folin-Ciocalteu spectrophotometric method. The types of Secondary Metabolites were investigated according to the common phytochemicals methods. In the assay using DPPH, an inhibition of 93,1 % with a concentration of 1,5 mg/ml was observed and using the ABTS+ assay an inhibition of 72,8% with a concentration of 0,27 mg/ml was detected. The IC₅₀ (concentration of aqueous extract to produce 50% of decrease of the absorbance) values were 0.31 mg/ml and 0,176 mg/ml with DPPH and ABTS+ assay, respectively. One gram (g) of aqueous extract is equivalent to 0,129 ± 0,004 g of gallic acid (DPPH assay) and to 0,267 g ± 0,002 of Trolox (ABTS+ assay) and the polyphenol content in gallic acid equivalents was 0,204±0,017 g/g extract. Phytochemical screening of *Kageneckia oblonga* showed the presence of tannins and saponins. Our results revealed antioxidant activity in the aqueous extract of *Kageneckia oblonga*.

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OPEN SOURCE TOOLS AND RESOURCES FOR COMMUNITY-BASED PLANT ENGINEERING

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Community-based practices are changing science, technology and engineering across academic institutions, community labs, hackspaces, industries and NGOs. The use of crowd-sourced technologies and the adoption of open source frameworks have already fuelled a revolution in software and hardware engineering, from DIY computing to advanced machine learning endeavours. Repositories of data and resources, such as Github, are facilitating standardisation and curation of tools and protocols through distributed and collaborative user-developer ecosystems. At the OpenPlant Synthetic Biology Centre and SynBio Lab UC, we promote the development and adoption of open source technologies, repositories of IP-free resources and better practices for bioengineering.

Here, we present a set of computational and genetic tools that aim to engage the plant biology community. First, we will describe a new set of IP-free genetic resources and methods for multiplex, efficient and low cost DNA fabrication that allows the assembly of up to 16 genes routinely from a broad range of basic elements (e.g. promoters, tags, repressors, etc). Second, we will present computational tools that allows the compilation of genomic data into gene-centric oriented DNA repositories, allowing for automatic annotation, community based curation and streamlined sequence visualisation and retrieval, implemented in *Marchantia polymorpha* through an open source database framework and available through Github. Third, we will describe work in process related to Open MTA legal frameworks aimed to lubricate user-user interactions by optimising distribution and sharing of resources. Finally, we will highlight how these efforts are aligned

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within wider narratives such as the OpenPlant Project and UNESCO-supported TECNOx competition, which seek to engage citizens into open source technologies for problem-solving in an era of pressing global challenges.

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IDENTIFYING GENETIC FACTORS UNDERLYING SEED OIL AND MUCILAGE CONTENT IN FLAXSEED (*LINUM USITATISSIMUM* L.) BY ASSOCIATION MAPPING

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Flaxseed (*Linum usitatissimum* L.) is well-known for the content of functional compounds with specific biological activity and health-related benefits. Flaxseed oil is highly rich in polyunsaturated fatty acids, specifically α -linolenic acid, and its hull is an importance source of soluble dietary fiber (mucilage). With the aim of identifying genomic regions associated to seed oil and mucilage content we performed an association mapping study among 100 accessions from the Canadian flax core collection assessed across two seasons in Chile and genotyped with 391 genome-wide microsatellite markers. The mean seed oil and mucilage content ranged from 28.2% – 43.9% and 25 – 87.9 mg/g of seed, respectively, and a non-significant correlation between the traits was observed in the population. A mixed linear model adjusted by population and family structures (PCA + K) identified three and two candidate QTL, which explained 35.6% and 5.8% of the phenotypic variation (R^2) for seed oil and mucilage content, respectively. Several promising functional candidate genes were identified near the QTL regions. For example, for seed oil content, genes involved in cell wall and fatty acid biosynthesis pathway were identified. Similarly, for mucilage content an enzyme with a critical role in the translocation of nucleotide sugars from the cytosol into the lumen was found. The candidate QTL identified herein provides a valuable foundation for future marker-assisted breeding, which could contribute to further diversify the food and feed market for flaxseed.

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METHODOLOGY TO USE CRISPR/CAS9 IN LONG SPAM LIFE PLANT SPECIES, USING FLOWERING STIMULATION AND PRECISION LIGHTING

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As a renewable resource, the demand for wood products is expected to continue to increase into the future. Compared to annual crop plants, direct genetic modification of trees species has gained little attention, partially because trees have much longer lifecycles and tight regulations opposing transgenic use in the field. The newly developed gene editing technologies, such CRISPR/Cas9 increase the potential for the modification of species. CRISPR/Cas9 has several major advantages over previous transgenic-based approaches and can work alongside conventional breeding programs by directly improving known yield-related loci or genes. We have a modified CRISPR/Cas9 system that promotes early flowering in plants, by ectopic expression of genes related with flowering time. Together with precision lighting with

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different ratios of Blue, Red and Far Red light we have managed to regulate this accelerates sexual development obtaining viable flowers. The CRISPR/Cas9 mutated plants flower earlier than the wild type plants, resulting in fast recovery of the second generation (T2) in *Arabidopsis*. We will use this technology to accelerate breeding in arboreous species.

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CHARACTERIZATION OF CHILEAN *SOLANUM MURICATUM* (AITON) POPULATIONS BY MEANS OF SSR MARKERS

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In Chile, *Solanum muricatum* (Aiton) is mainly cultivated in north-central regions of Coquimbo and Valparaíso. This species native to the Andean region was probably introduced in pre-Columbian times as a domesticated fruit plant, and little is known about its genetic variability. Nowadays, the water deficit caused by climate change is a serious threat to this crop. In order to avoid genetic losses, INIA is collecting and characterizing the most representative material cultivated by farmers in the north-central regions of Chile. More than 150 accessions from 21 populations, belonging to different farmers from regions IV, V and XV of Chile, respectively, have been collected. The *ex situ* collection is being maintained at Pan de Azúcar Experimental Station (INIA-Intihuasi, La Serena). A genetic characterization, using robust and friendly molecular markers such as SSR, is desirable to optimize its conservation. To accomplish this goal, available genomic platform from potato and tomato genomes, plus a transcriptome of *S. muricatum* were used to design high interspecific transferable SSR among these species. A panel of 12 SSR was selected to perform the genetic characterization of the entire collection. Analysis of identity, genetic variability and genetic structure intra- and interpopulations, will be useful information to optimize the conservation of this valuable genetic resource of *S. muricatum*, including breeding purposes.

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A CODOMINANT DIAGNOSTIC MARKER FOR THE SLOW RIPENING TRAIT IN PEACH

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Chile is the main peach exporter in the South Hemisphere. Currently, postharvest performance and fruit quality are essential for selection of new cultivars in breeding programs. However, breeding is a time consuming and costly process. In peach, slow ripening (SR) trait is a recessive mutation consisting of fruits that are unable to ripe. For example, flesh-softening rate tends zero and SR fruits do not produce ethylene. SR individuals are discarded from breeding programs. Through QTLs analysis and whole genome sequencing, we detected a deletion of 26 kb in the region associated with the SR phenotype. In this region, we identified a NAC transcription factor as the best candidate responsible for the SR phenotype. Thus, the aim of this work was to develop a co-dominant molecular marker to early determination for the SR phenotype. Two pair of primers were designed (PSR3) to genotype this structural variant on the progeny of 'Venus' F2 (N=141) and commercial cultivars. Finally, the PSR3 marker co-segregated with the SR phenotype in all cases, allowing the clear and reliable discrimination of the *sr* allele. Moreover, we characterize the expression profile of NAC gene (*PpNAC72*) in fruits from a normal ripening sibling of 'Venus' F2 population. Furthermore, we identified more and smaller cells in fruit flesh between SR and normal ripening siblings during development. This work contributes to unravel the molecular mechanisms responsible for the SR phenotype.

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GENETIC DETERMINANTS THAT CONTROL DEVELOPMENT AND OVERALL BERRY QUALITY IN GRAPEVINE REVEAL UNIQUE AND COMMON ROLES

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Discovery of genetic determinants to implement Marker Assisted Breeding was hampered for complex traits due to the lack of significant and reliable genotype-phenotype associations, in its turn caused by the absence of large populations characterized both at genetic and phenotypic level. On the other hand, factors influencing overall berry quality in table grape like seedlessness, berry size, skin elasticity and flesh texture, are intrinsic to its developmental process and yet were never analyzed, at genetic level, in an integrative approach. Quantitative trait loci (QTL) analysis was performed over two seasons in a F1 biparental cross of more than 500 individuals genetically characterized with up to 4,000 SNP markers. The genetic architecture describes the complex nature of quality-related traits: 23 QTLs were detected for seed palatability traits, 15 for berry size, 16 for skin elasticity and 38 for flesh texture, most significative QTLs were reproducible among seasons. These QTLs explain a very low portion of phenotypic variation, reflecting the complex or very complex nature of these traits, making difficult the feasibility of assisted selection with one or very few markers. However, the combined use of most significant associated markers, up to six SNPs by trait, captures the largest proportion of phenotypic variations (up to 50 %) enabling the possibility, in the near future, to apply assisted selection with a panel of validated markers. Holistic QTL analysis of berry quality subtraits resulted in the discovery of genetic determinants that contribute to the simultaneous control of up to three traits, in the same or opposite directions in relation to quality. Additionally, genetic interactions between QTLs and the major loci that controls seedlessness were discovered. Validation of these results in different genetic backgrounds and development on markers for assisted selection could improve significantly breeding practices.

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ANALYSIS OF GENETIC DIVERSITY, STRUCTURAL POPULATION AND IDENTIFICATION OF SNP ASSOCIATED WITH FRUIT TRAIT IN PEACH

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The peach-tree (*Prunus persica* [L.] Batsch) stands as one of the most important temperate fruit. It's a model species for his family (*Rosaceae*) where multiple genetic and genomic studies have been done to the date. Because of the history of domestication of this specie, the genetic variability has been decreased greatly, raising also the linkage disequilibrium (LD) of the actual domesticated germplasm. For this reason, actual breeding programs have problems due to the low level of genetic diversity available to develop new varieties. The use of genetic markers such as single nucleotide polymorphism (SNP) are useful to determinate the actual degree of variability between populations or parent collections. This work consisted in the sequencing of 95 individuals of a local germplasm collection through genotyping by sequencing (GBS). After the sequencing, 5,890 SNP were selected with an average depth of 7 and a minor allele frequency (MAF) of 1.0% or higher. Using this set of data, genetic variability, phylogenetic relationship and genetic structure of the germplasm were tested. Using association genetic strategy, 3 traits were tested (flesh color, skin pubescence and harvest date), with markers associated to regions in the genome corresponding to chromosome 1, 5 and 4, respectively. This work continues to unravel the genetic basis of major traits in peach-tree, giving also a robust set of markers to test more traits in the near future.

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GENOME SIZE COMPARISON IN *COLOBANTHUS QUITENSIS* POPULATIONS SHOW DIFFERENCES IN SPECIES PLOIDY

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Colobanthus quitensis is the only native dicotyledoneae in the Antarctic. This species also represents a wide geographic distribution, from 68°S to 17°N and from 0 m a.s.l. in the south to 4,200 m a.s.l. in the north of its distribution area. As the described habitats for different populations coincide in their extreme abiotic characteristics, there has been an increasing interest in studying different populations, as well as the existence of phenotypic or genetic variability among them. In contrast, very little is known about its genome; knowledge of genome size and ploidy levels allows the development of strategies to generate information in population studies related to structure, gene flow and genetic diversity to describe phenotypic characteristics. Several studies have related genome size to the ecologic requirements of the species distributed through a wide environmental gradient. For several years now, flow cytometry has become a simple method to determine genome size in a large list of species. In this work, we determined genome size for three *C. quitensis* populations. The populations of Arctowski (Antarctica) and La Marisma (Punta Arenas) have 2C= 1.95 pg, while the Conguillio (South-Central Chile) population reported 2C= 0.84 pg, approximately half as much. This might evidence different ploidy levels between the populations, which creates new questions regarding the number of chromosomes and the possible existence of endopolyploidy related to the distribution and adaptive mechanisms of this species throughout its wide distribution.

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GENETIC TRANSFORMATION OF *DESCHAMPSIA ANTARCTICA* DESV., MEDIATED BY *AGROBACTERIUM TUMEFACIENS*

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Antarctic is one of the most extreme environment around the world; very cold temperatures, high UV radiation, low nutrients availability in the soil and sea spray are some of the abiotic stressors that must endure the species living there. The native species have developed mechanisms that allow them their establishment in the ecosystem. *Deschampsia antarctica* is one of them, some tolerance mechanisms and gene have been described for the specie. *D. antarctica* belong to the Poaceae family where there are several plants of agricultural interest. Therefore, genomic studies are required to facilitate the use of the genes of *D. antarctica* in other species of the same family. The development of genetic transformation protocols is a necessary tool for these gene studies. In this work an *Agrobacterium tumefaciens*-mediated protocol from explants of seedlings established *in vitro* is developed. Two strains of *A. tumefaciens*, three bacterial concentration (0.5, 0.7 and 1) equivalent to the absorbance of the bacterial suspension at OD = 600_{nm} and three times of co-culture (10, 20 and 30 min) were evaluated. All treatments applied produced a high percentage of transient expression (98%) without significant differences ($\alpha=0.05$) for transient percentage nor to the percentage of tissue staining between treatments. Results about selection of transformed plants will be shown. This is the first report about genetic transformation in the specie.

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GENETIC TRANSFORMATION OF *COLOBANTHUS QUITENSIS* (KUNTH) BARTL MEDIATED BY *AGROBACTERIUM TUMEFACIENS*

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Genetic transformation allows the introduction of genes of interest in the plant genome or modifies its own; being *Agrobacterium* the most used methods for introducing genes into plant cells and its subsequent regeneration of transgenic plants. *Colobanthus quitensis* better known as Antarctic pearlwort, it is the only native dicot of Antarctica. Its ability to adapt to extreme abiotic conditions, does regard it as a plant model for studies about ecophysiological and molecular mechanisms of plant adaptation to stress. Preliminarily, two *Agrobacterium* strains (EHA105 and LBA4404), inoculation times of 30 and 50 minutes and absorbance of 0.4, 0.7 and 0.9 at OD of 600 nm were evaluated. The first results showed that the greater transient expression was obtained with LBA4404 strain, 30 minutes of inoculation and in 0.7 and 0.9 absorbance without significant differences between them. From these results, callus and plantlets from *in vitro* plants from three *C. quitensis* populations were tested. The effect of acetosyringone addition at liquid and solid co-culture medium was also evaluated. The highest percentage of transient was obtained in the treatment with acetosyringone added only at solid co-culture medium in plantlets from Conguillio and Arctowski populations, similar results were obtained for callus from Conguillio and Laredo populations. Acetosyringone application in solid co-culture medium increased the inoculation of explants by the bacterium, increasing efficiency transformation. This constitutes the first report about genetic transformation of species, opening a door to the use of this species in functional genomics studies. Acknowledgments: VRID 213.418.004-1.0 Project And The Departamento De Ciencias Y Tecnología Vegetal For Funding This Research.

QTL IDENTIFICATION FOR AGRONOMIC TRAITS IN *PRUNUS SALICINA* THROUGH GENOTYPE BY SEQUENCING (GBS)

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Assisted selection by molecular markers for fruit plants breeding is today a difficult challenge to achieve due to polygenic nature of the most agronomic traits. In many cases resulting in several QTLs for the same trait located in different chromosomes. Therefore it becomes increasingly necessary to use more efficient technologies, such as genotyping by sequencing (GBS), which allows generating saturated genetic maps and facilitate more accurate QTLs identification. The F1 Japanese plum population '98-99' × 'Angeleno' of 153 seedlings was genotyped by GBS, using peach v1 as a reference genome, and resulting in a filtered data set of 42,909 SNPs. Genotyping errors, homozygotes and heterozygotes under-calling as well as SNPs with over 10% of missing data were eliminated. A total of 955 SNPs were mapped in '98-99' × 'Angeleno' family. Parental maps were constructed with 454 SNPs for '98-99' and 501 SNPs for 'Angeleno' covering a genomic region of 673.56 and 643.01cM respectively. Several phenological and agronomic traits were measured during 2016 season, finding major QTLs for ripening time, skin color and fruit weight in LG4, LG3 and LG7, respectively. These preliminary results represent a promising beginning for attempt molecular assisted selection as a tool in the new breeding programs of Japanese plum.

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THE TRANSCRIPTIONAL DYNAMICS OF TWO RESURRECTION FILMY FERNS FROM HYMENOPHYLLACEAE UNRAVEL KEY ASPECTS OF THEIR RESURRECTION STRATEGY ASSOCIATED TO ITS VERTICAL DISTRIBUTION IN WILD.

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Ferns from the Hymenophyllaceae family are one of the main components of the epiphytic species diversity in the Chilean temperate rain forest. These species are called filmy ferns because they possess membranous fronds of a single layer of cells, lack of cuticles, present no differentiated epidermis, and have no stomata, showing a poikilohydric strategy most typical of bryophytes. From an ecophysiological approach, light intensity and the vapor pressure deficit increases whereas the relative humidity decreases significantly vertically along host trees. These conditions act as a selective pressure for filmy ferns to deal with high irradiance and high evaporative demand, conditioning their vertical distribution. RNA-seq on the Illumina Hi-seq platform was used to study the transcriptional responses of *Hymenophyllum caudiculatum* and *Hymenophyllum dentatum* (Hymenophyllaceae), which contrast in their vertical microhabitat preferences and in their rates of water loss. Specifically, we look at the dynamics differential gene expression of fronds subjected to experimental desiccation-rehydration cycles. Our analysis identified commonalities and differences in gene regulation, and key genes correlated with the fronds hydration state, providing a broad view of the patterns of gene expression responding to microenvironmental signals and behind the physiology of their resurrection strategy.

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IDENTIFICATION AND MOLECULAR CHARACTERIZATION OF CONSTANS-LIKE GENES IN STONE FRUIT TREE SPECIES (*PRUNUS L.*)

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The *CONSTANS* (CO) family is an important regulator of flowering and dormancy in photoperiod sensitive plants. But information regarding their role in stone fruit trees (*Prunus L.*) is limited. Through bioinformatics analysis, we identified nine *CONSTANS-like* (COL) genes in the peach (*P. persica*) genome. To establish a relationship between the putative peach CO-like proteins and those from the Arabidopsis, a phylogenetic tree was developed. The tree showed that the peach CO-like proteins can be subdivided into three subfamilies as in Arabidopsis. Genome mapping analysis revealed that peach COL genes were distributed on several chromosomes, especially on chromosome 1 (4 genes) and 3 (3 genes) but also in chromosomes 5 and 8. The peach COL TFs from each subfamily were shown to share similar amino acid motif compositions. Analysis of the exon-intron structure of *PpCOL* genes showed that they have 2-4 exons and suggests that exon gain and loss occurred during the evolution of this gene family. Based on the peach COL gene family information, we studied the expression patterns of 9 COL genes in leaves and floral buds of sweet cherry (*P. avium*) trees. The *Prunus* CO-like genes were differentially regulated in leaves and floral buds suggesting roles in the perception of light signals and sexual reproductive development in this species. Our results will provide a platform for functional identification and molecular evolution studies of CO-like TFs in *Prunus*, which can be valuable for understanding photoperiod-dependent development processes in stone fruit trees.

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A PAIRWISE PROBABILISTIC FRAMEWORK TO INFER FUNCTIONAL GENE NETWORKS AND IDENTIFY KEY GENES IN RESPONSE TO PERTURBATIONS

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It is second nature nowadays to use changes in gene expression to identify relevant genes in response to a perturbation or in a developmental transition. However, many key genes for an organism's response are not regulated at the gene expression level (e.g. early genes in signaling pathways). These genes are hidden to molecular profiling approaches such as transcriptome analysis. Here we sought to address the problem of finding functionally relevant genes for responding to a perturbation regardless of whether they change at the gene expression level under contrasting experimental conditions to evaluate the perturbation.

In order to identify these genes, we first model transcriptome states and boundaries using large public expression databases currently available for *Arabidopsis thaliana* and *Saccharomyces cerevisiae*. Using a novel entropy-based framework we uncovered inherent restrictions in gene expression at the genome-wide level, that reveal novel functional relationships for genes that are not obtained by widely used methods such as correlation or mutual information. Moreover, our approach allowed us to identify key genes involved in response to perturbations, some of which are and some of which are not regulated in response to the perturbation. Our novel framework to analyze transcriptome data provides insights into gene regulatory networks that cannot be attained with existing bioinformatics methods. This approach can be easily applicable to any organism with large transcriptome databases.

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PS123

KIWIFRUIT PLANTS VARIETIES GROWN IN CHILE SHOW DIFFERENTIAL SUCEPTIBILITY TO INFECTION WITH *PSEUDOMONAS SYRINGAE* PV. *ACTINIDIAE* (PSA)

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The kiwifruit plant species (*Actinidia spp.*) are native from China and have been recently introduced and commercially exploited in several countries, including Chile. Since 2008 the kiwifruit industry has been severely jeopardized by the kiwifruit bacterial canker disease, caused by the bacteria *Pseudomonas syringae* pv. *actinidiae* (Psa). This bacteria moves systemically through the plant producing the progressive death of all plant tissues. Among the 5 different Psa biovars, biovar 3 is the most virulent one, which according to sequencing data would be the biovar present in Chile. On the other hand, the most cultivated varieties of kiwifruit are from the species *A. chinensis* and *A. deliciosa*. Although both species are susceptible to Psa biovar3 infection, it is still unclear whether the Psa 3 causes the same damage in the different varieties of kiwifruit. To gain insight in these issues we: 1) evaluated whether 4 different Chilean isolated Psa 3 produce the same severity of disease in one kiwifruit variety, and 2) determined the proliferation of one Psa 3 isolated in several varieties of kiwifruit (male and female plants). Our results suggest different levels of susceptibility among the varieties and species, being the KC8 cultivar more susceptible and the cultivar KA2 more resistant to Psa. Furthermore, we evaluated the expression of SA-defense genes and the SA levels in mock and Psa-infected kiwifruit plants, in order to associate this defense pathway to the different levels of susceptibility found in different varieties.

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PERFORMANCE OF NATURALIZED *VITIS* GENOTYPES AS ROOTSTOCKS FOR DROUGHT TOLERANCE IN CABERNET SAUVIGNON AND SYRAH

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Water availability for irrigation has been progressively declining in grapevine production areas due to climate change in Chile. A compelling strategy for increasing the water use efficiency under these conditions is selecting proper scion-rootstock combinations. With this aim, we studied contrasting Cabernet Sauvignon (isohydric) and Syrah (anisohydric) cultivars grafted on different rootstocks: G25 G32 (Copiapó); G57, G65, G70 (Huasco), from our collection "GermoVidNor", Ruggeri140 (commercial, drought tolerant), and self-grafted controls. Vines were established in 35 L pots and drip irrigated 100% and 30% (water deficit) in random block design (4 replicates) at Coquimbo. Morphological, physiological traits and gene expression (hormone, aquaporins, stress and development) were assessed during growth season. Stomatal conductance and photosynthesis were reduced by deficit irrigation but unaffected by scion and rootstock. Conversely, significant differences in rootstock diameter, leaf area and leaf number were determined and positively correlated to root area and volume. For both scions, G32 exhibited the best performance under drought, significantly higher than commercial rootstock. Moreover, up-regulation of NCED1 & NCED2, AP2/EREBP, TIP2.1 & PIP2.2, PRP1, GDH & VvNAC1 were displayed in Cabernet Sauvignon grafted on G32. Morphometric and functional parameters resulted in improved performance of G32 under stress for both vines, pointing G32 as most promising rootstock for both scions, enhancing their adaptive responses.

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GETTING CHILEAN TOMATO ROOTSTOCK USING INTERSPECIFIC CROSS BETWEEN WILD (*SOLANUM CHILENSE*) AND CULTIVATED (*SOLANUM LYCOPERSICUM*) TOMATO TOLERANT TO ENVIRONMENTAL STRESSES

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One of the consequences of climate change for world agriculture is a steady decline of arable land for vegetables production, which has led to a drastic decline in supply of products in some areas. In Chile, this problem has become important for the fresh tomato market, especially in the region of Arica and Parinacota. These areas are indeed encountering numerous problems such as salinity, drought and boron excesses, which have a direct impact on plant productivity and fruit quality. A possible strategy to solve these problems consists in the selection of Chilean inter-specific rootstocks adapted to each of these stresses. The wild tomato (*Solanum chilense*) has been extensively studied and is recognized as having a broad spectrum of resistance to biotic and abiotic diseases, which makes it a promising material for stress-resistant rootstocks identification after inter-specific crosses with commercial tomato (*Solanum lycopersicum*) cultivars sensitive to these stresses. In this work hand pollinations were performed for the production of interspecific hybrids from crosses between wild tomato (*S. chilense*) and a local variety of tomato (*S. lycopersicum*). Identification of

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interspecific rootstock (F1) was performed using molecular markers (CAPS) C2At4g04955, At1g28530, C2At3g08760 and T0386A on DNA extracted from leaf tissues. The obtained results confirm that the harvested material was a hybrid issued from the two species. To the best of our knowledge, this is the first report mentioning such an hybrid between *S. chilense* and *S. lycopersicum*.

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CHARACTERIZATION OF CHILEAN SWEET CHERRY (*PRUNUS AVIUM* L.) GERMPLASM BY MEANS OF SSR ASSOCIATED TO COLOR, FRUIT SIZE, MATURITY TIME AND CROSS COMPATIBILITY

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Sweet cherry (*P. avium* L.) production in Chile presents the greatest growing and profitability in the last decade. Fruit quality is one of the aspects that will define our competitiveness in future scenarios, albeit the increasingly limited access to new varieties can be a serious constraint. The Chilean industry, supported by the state, implemented its own breeding programs for sweet cherries. Long generation time and larger plant size of cherry trees severely limit the breeding based on traditional practices of cross and selection. The INIA sweet cherry breeding program (INIA-SCBP) is developing molecular breeding methods (MBM) to improve the cost effectiveness of breeding process to obtain new varieties. Useful markers can help to identify the best genotypes (progenitors and progenies) carrying favorable alleles associated to desirable traits. Nowadays there are available markers to identify specific alleles associated to important traits such as color, fruit size, maturity time and cross compatibility. The germplasm of INIA-SCBP consisting of 68 genotypes, including varieties and advanced clones, were characterized by means of markers Pav-Rf-SSR, BPPCT034, CPSCT038, Pav-G4Mat-SSR and S-universal, linked to loci involved in fruit color, fruit size, maturity time and cross compatibility, respectively. Frequency of desirable haplotypes in the germplasm collection and their expected genotypes within different segregant populations of the INIA-SCBP will be analyzed. It is expected that identification genotypes carrying the best allele combinations for these traits will increase the likelihood of better progeny with the desired characters within the breeding population of INIA-SCBP.

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