CHILEAN SOCIETY OF PLANT BIOLOGISTS

XII REUNIÓN DE BIOLOGÍA VEGETAL

4 al 7 de Diciembre del 2017

Hotel Enjoy Park Lake
Villarrica, Chile

PROGRAM AND ABSTRACTS

CHILEAN SOCIETY OF PLANT BIOLOGISTS

XII CHILEAN SOCIETY OF PLANT BIOLOGY MEETING

December 4th – 7th, 2017

Hotel Enjoy Park Lake, Villarrica. Chile

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Michael Handford, Universidad de Chile

SCIENTIFIC PROGRAM

MONDAY, DECEMBER 4TH

12:00 – 15:00 REGISTRATION

15:00 – 16:00 OPENING WELCOME
Chair: Rodrigo A. Gutiérrez

Keynote Speaker
Jorge Casal- Instituto Leloir, IFEVA, Argentina.
DYNAMIC SIGNALLING NETWORK IN PLANT RESPONSES TO SHADE.

16:00 – 18:30 PLENARY SESSION 1 – GENES AND DEVELOPMENT
Chairs: Rodrigo A. Gutiérrez & Alejandra Moya

16:00 – 16:30 **Christian Fankhauser**/ University of Lausanne, Switzerland.
PLANT STRATEGIES FOR ENHANCING ACCESS TO SUNLIGHT.

16:30 – 17:00 **Pablo Cerdán**/ IIBBA-CONICET, Universidad de Buenos Aires, Argentina.
IDENTIFICATION OF NEW PLANT GROWTH INHIBITORS.

17:00 – 17:30 Coffee Break

17:30 – 18:00 **Markus Schmid**/ Umea University, Sweden.
INTEGRATION OF FLOWERING TIME SIGNALS IN Arabidopsis thaliana.

18:00 – 18:15 **Pablo Figueroa**/ Universidad de Talca, Chile.
STRUCTURAL AND INTERACTION STUDIES ON THE COI1-JAZ CO-RECEPTOR FOR JASMONOYL-ISOLEUCINE IN Fragaria x Ananassa REVEAL A NEW FUNCTIONAL JAZ DEGRON IN PLANTS.

18:15 – 18:30 **Susana Saez-Aguayo**/ Universidad Andrés Bello, Chile.

IDENTIFICATION OF PECTIN METHYLESTERASES (PME) AND PECTIN METHYLESTERASES INHIBITORS (PMEI) USING ARABIDOPSIS SEED COAT MUCILAGE.

18:30 – 18:45 **Flash Talks**
(PS1, PS17, PS21, PS37, PS43, PS49, PS63, PS67, PS87, PS93)

18:45 – 20:30 **Welcome Reception & Poster Session I (Odd Numbers)**

TUESDAY, DECEMBER 5TH

09:00 – 11:00 **PLENARY SESSION 2 – PLANT ABIOTIC INTERACTIONS**
Chairs: Paula Pimentel & Michael Hanford

09:00 – 09:30 **Miguel Blázquez**/ CSIC-Universidad Politécnica de Valencia, Spain.
AN ANCESTRAL ROLE FOR DELLA PROTEINS IN THE COORDINATION BETWEEN GROWTH AND STRESS RESPONSES.

09:30 – 10:00 **David Alabadí**/ Universidad Politécnica de Valencia, Spain.
THE COP1/SPA COMPLEX RELAYS LIGHT AND TEMPERATURE INFORMATION ON DELLA PROTEINS IN ARABIDOPSIS.

10:00 – 10:15 **Braulio Soto-Cerda**/ Centro de Genómica Nutricional Agroacuícola, Chile.
GENOME-WIDE ASSOCIATION STUDY REVEALS FIRST INSIGHTS INTO THE GENETIC FACTORS UNDERLYING POST-FLOWERING DROUGHT TOLERANCE IN FLAXSEED (*Linum usitatissimun* L.).

10:15 – 10:30 **Ema Olate**/ Pontificia Universidad Católica, Chile; CSIC Madrid, España.
THE MASTER REGULATOR OF IMMUNITY RESPONSES, NPR1, MEDIATES A NOVEL REGULATORY PATHWAY IN COLD ACCLIMATION BY INTERACTING WITH HSFA1 FACTORS.

10:30 – 10:45 **Paula Pimentel**/ Centro de Estudios Avanzados en Fruticultura, Chile.
MEMBRANE INTRINSIC PROTEINS AND ADAPTATION TO ABIOTIC STRESS: AQUAPORIN NIP1;1 AND ITS ROLE IN WATERLOGGING RESPONSES IN PRUNUS ROOTSTOCKS.

10:45 – 11:00	**Luis Villalobos**/ Universidad de Chile, Chile. *MORPHO-ANATOMICAL AND HYDRAULIC TRAITS RELATIONSHIPS BETWEEN TWO GRAPEVINE VARIETIES FROM A COMMERCIAL VINEYARD IN CHILE.*
11:00 – 11:30	**Coffee Break**
11:30 – 13:30	**Plenary Session 3 - Natural Variation & Breeding** **Chairs: Raúl Herrera & Reinaldo Campos**
11:30 – 12:00	**Pere Arús**/ IRTA, CSIC-IRTA-UAB, Spain. *NEW STRATEGIES FOR MARKER-ASSISTED PEACH BREEDING.*
12:00 – 12:30	**Patricio Hinrichsen**/ INIA-La Platina, Chile. *GRAPEVINE GENETICS AT INIA-CHILE: FROM GENETIC DIVERSITY TO BREEDING TOOLKITS.*
12:30 – 13:00	**Ignazio Verde**/ CREA, Rome, Italy. *HIGH THROUGHPUT LINKAGE MAPPING IN PEACH FOR ASSISTING GENOME ASSEMBLY AND FOR ADVANCED QTL ANALYSES AND GENE TARGETING.*
13:00 – 13:15	**Verónica Guajardo**/ Centro de Estudios Avanzados en Fruticultura, Chile. *GENOME-WIDE SNP IDENTIFICATION IN PRUNUS ROOTSTOCKS GERMPLASM COLLECTION USING GENOTYPING-BY-SEQUENCING (GBS): DISTRIBUTION OF SNPS AND PREDICTION OF THEIR EFFECT ON GENE FUNCTION.*
13:15 – 13:30	**A. Donoso**/ INIA- La Platina, Chile. *CHARACTERIZATION AND GROUPING OF LOCAL VARIETIES OF TOMATO CULTIVATED IN CHILE.*
13:30 – 15:30	**Lunch poster installation (Even Numbers)** **Town Hall Session (CSPB members only)**
15:30 – 18:00	**Plenary Session 4 – Natural Variation & Breeding II** **Chairs: Claudio Meneses & Andrés Schwember**

15:30 – 16:00	**Conxita Royo**/ IRTA Lleida, Spain. *CONTRIBUTION TO BREEDING OF DURUM WHEAT LANDRACES FROM THE MEDITERRANEAN BASIN.*
16:00 – 16:30	**Fabrice Roux**/ Université de ToulouseCastanet-Tolosan, France *THE GENETICS UNDERLYING NATURAL VARIATION OF PLANT-PLANT INTERACTIONS IN Arabidopsis thaliana.*
16:30 – 17:00	**Coffee Break**
17:00 – 17:30	**Javier Botto**/ IFEVA, CONICET, Universidad de Buenos Aires, Argentina. *GENOTYPING AND PHENOTYPING ARABIDOPSIS POPULATIONS COLLECTED IN PATAGONIA.*
17:30 – 18:00	**Claus Schwechheimer**/ Technische Universität München, Germany. *PIN-NING DOWN THE FUNCTION OF D6PK PROTEIN KINASES IN AUXIN TRANSPORT REGULATION.*
18:00 – 18:15	**Flash Talks** **(PS10, PS16, PS22, PS24, PS30, PS40, PS46, PS58, PS78, PS82)**
18:15 – 20:00	**Poster Session II (Even Numbers)**
20:00 – 22:00	**Dinner**

WEDNESDAY, DECEMBER 6TH

09:00 – 11:00	**Plenary Session 5- Genome and System Biology** **Chairs: Ingo Dreyer & Javier Canales**
09:00 – 09:30	**Karen Halliday**/ University of Edinburgh, UK. *PHYTOCHROMES, RESOURCE MANAGEMENT AND GROWTH.*
09:30 – 10:00	**Ignacio Poblete**/ Universidad Andrés Bello, Chile. *SYSTEMS BIOLOGY OF PLANT-PATHOGEN INTERACTION.*

10:00 – 10:15	**Isabel Fredes**/ Pontificia Universidad Católica, Chile. *IDENTIFYING THE ROLE OF ARGONAUTE1 PHOSPHORYLATION IN THE NITRATE RESPONSE IN ARABIDOPSIS THALIANA.*
10:15 – 10:30	**Andrea Vega**/ Pontificia Universidad Católica, Chile. *UNCOVERING PLANT HORMONE SIGNALING IN NITRATE-DEFENSE RESPONSE INTERACTION IN TOMATO.*
10:30 – 10:45	**Ricardo Nilo**/ FONDAP-CRG, Universidad Andrés Bello, Chile. *BLAST-KNN - A BLAST MACHINE-LEARNING ENSEMBLE THAT RELIES ON INTERPRO EXTRACTED FEATURES TO IMPROVE ENZYMES FUNCTIONAL ANNOTATION.*
10:45 – 11:30	**Coffee Break**
11:30 – 13:00	**Plenary Session 6 – Genome Regulation and Epigenetics** **Chairs: Loreto Holuigue & Hannetz Roschzttardtz**
11:30 – 12:00	**Christian Dubos**/ INRA, Versalles, France. *INTEGRATION OF THE RESPONSES TO IRON AVAILABILITY FLUCTUATIONS* IN *Arabidopsis thaliana.*
12:00 – 12:30	**Robert Schaffer**/ Institute for Plant and Food Research, New Zealand. *THE MANUAL ANNOTATION OF THE A. chinesis (KIWIFRUIT) GENOME.*
12:30 – 12:45	**Karin Rothkegel**/ UNAB, Chile. *SINGLE-BASE RESOLUTION OF THE METHYLOME IN THE HIGH CHILL REQUIREMENT VARIETY OF SWEET CHERRY (Prunus avium L.) 'KORDIA' DURING DORMANCY.*
12:45 – 13:00	**Gabriela Madrid**/ INIA La Platina, Chile. *IMPROVING GENOME ENGINEERING EFFICIENCY IN VITIS VINIFERA USING DNA REPLICONS.*
13:00 – 15:00	**Lunch**

15:00 – 17:00	**Plenary Session 7- Plant Biotic Interactions** **Chairs: Francisca Blanco & Herman Silva**
15:00 – 15:30	**Uwe Conrath**/ Aachen University, Germany. *PRIMING PLANTS FOR ENHANCED DEFENSE.*
15:30 – 16:00	**Bernardo González**/ Universidad Adolfo Ibáñez, Chile. *MOLECULAR BASIS OF ARABIDOPSIS-BURKHOLDERIALES BACTERIAL STRAINS INTERACTIONS.*
16:00 – 16:30	**Stephan Pollman**/ CBGP, Spain. *AMI1, A NOVEL MOLECULAR NEXUS CONTROLLING GROWTH-DEFENCE TRADE-OFFS.*
16:30 – 17:00	**Coffee Break**
17:00 – 17:30	**Ingo Dreyer**/ Universidad de Talca, Chile. *THE BATTLE OF THE FUNGAL UMSRT1 AND MAIZE ZMSUT1 SUCROSE TRANSPORTERS FOR PLANT SUGAR RESOURCES.*
17:30 – 17:45	**Nicolás Cecchini**/ Universidad Nacional de Córdoba, Argentina. *A NEW PLASTID TARGETING MECHANISM REVEALED BY THE SYSTEMIC DEFENSE-ASSOCIATED LIPID TRANSFER PROTEIN AZI1.*
17:45 – 18:00	**Ariel Herrera-Vásquez**/ Pontificia Universidad Católica, Chile. *TGA CLASS II TRANSCRIPTION FACTORS NEGATIVELY REGULATE THE SALICYLIC ACID PRODUCTION UNDER STRESS.*
18:00 – 20:00	**FREE TIME**
20:00 – 22:00	**AWARD CEREMONY & CONFERENCE DINNER**
22:00	**CONFERENCE PARTY**

ABSTRACTS

KEYNOTE LECTURE

Keynote Opening

DYNAMIC SIGNALLING NETWORK IN PLANT RESPONSES TO SHADE

Jorge J. Casal [1,2]

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To take advantage of the resources provided by the environment, agricultural crops are cultivated at a high density of plants per unit soil surface. As a result of this condition, plants become exposed to mutual shading, which reduces yield per plant. Photo-sensory receptors such as phytochrome B and cryptochrome perceive the modifications of the light environment caused by the presence of neighbouring vegetation and initiate molecular modifications that generate growth responses. In turn, these reactions tend to mitigate the degree of mutual shading among plants. The early steps of these responses involve elevated levels of the growth hormone auxin. However, a more detailed analysis of the network reveals that, particularly under prolonged shade, the photosensory receptors have multiple points of action on auxin perception and signalling and on the action of other growth hormones. The latter involves organ-specific modifications of the dynamics of signalling components. This system-level modification generates a commitment that reinforces shade-avoidance responses.

Acknowledgements. We thank research grants from Agencia Nacional de Promoción Científica y Tecnológica and Universidad de Buenos Aires (Argentina) and financial support by SIGNAT (MSCA-RISE-2014, European Union).

PLENARY LECTURES

PLENARY SESSION 1 – GENES AND DEVELOPMENT

PLANT STRATEGIES FOR ENHANCING ACCESS TO SUNLIGHT

Markus Kohnen[1], Emanuel Schmid-Segert[2], Anupama Goyal[1], Olivier Michaud[1], Anne-Sophie Fiorucci[1], Ioannis Xenarios[2], **Christian Fankhauser**[1]

[1] Center for Integrative Genomics, University of Lausanne, CH-1015 Lausanne, Switzerland

[2] Swiss Institute of Bioinformatics, University of Lausanne, CH-1015 Lausanne, Switzerland
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Light is a vital resource for plants, which compete for its availability particularly in dense communities. Plants possess multiple photosensory receptors to detect the presence of competitors and thereby adjust their growth and developmental strategies accordingly. I will discuss the photoperception mechanisms and growth responses elicited by the neighboring vegetation in Arabidopsis a typical shade-avoiding species. These responses include rapid shade-induced organ-specific transcriptional reprogramming mediated by Phytochrome Interacting Factors (1). This leads to a rapid burst of auxin production in cotyledons that is then transported to the hypocotyl where it promotes elongation. Shade-enhanced auxin production also sensitizes the phototropic response favoring reorientation of photosynthetic organs towards canopy gaps (2). Finally, in leaves shade-induced auxin production leads to petiole elongation and upward movement (hyponasty) that is restricted to the shaded leaf (3).

(1) Kohnen, M.V., et al., Neighbor Detection Induces Organ-Specific Transcriptomes, Revealing Patterns Underlying Hypocotyl-Specific Growth. Plant Cell, 2016. **28**:2889-2904.
(2) Goyal, A., et al., Shade Promotes Phototropism through Phytochrome B-Controlled Auxin Production. Curr Biol, 2016. **26**:3280-3287.
(3) Michaud, O., et al., Local auxin production underlies a spatially restricted neighbor-detection response in Arabidopsis. PNAS, 2017. **114**:7444-7449.
The authors acknowledge funding from the Swiss National Science Foundation.

IDENTIFICATION OF NEW PLANT GROWTH INHIBITORS

Mariana Antonietti,[1], Maximiliano Sánchez-Lamas[1], Gabriel Gola[2], Javier Ramirez[2], David Alabadí[3], Miguel Blázquez[3], **Pablo Cerdán**[1]
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We have isolated compounds that inhibit germination during a chemical screening. These compounds comprised sulfonamides that inhibited germination in the presence of gibberellic acid. We observed a synergistic interaction with Abscisic acid (ABA) to inhibit germination; addition of fluoridone (an inhibitor of carotenoid and ABA biosynthesis) restored germination, suggesting that these compounds could be acting in the ABA pathway. Seedlings overexpressing enzymes involved in ABA catabolism were less sensitive

to these compounds. However, ABA levels were lower in seeds exposed to these compounds and *PYR/PYL* (ABA receptor) deficient plants were also sensitive to the compounds, ruling out that they could act as agonists of ABA. We performed an RNAseq assay to try to understand the mode of action of these compounds. A significant subset of genes was activated by both ABA and the compounds, suggesting a mechanistic connection. However, this interaction was restricted to a specific subset of genes, including UV response genes, ruling out a general effect of these compounds in the ABA signaling or metabolic pathways that could explain their effects. Further analysis at the seedling stage indicated that these compounds inhibit plant growth, probably affecting cell division. The inhibitory action occurs both in dark and light conditions, but weak light protects seedlings from compound effects, whereas high light produces plant death. This is consistent with the similar transcriptome profiles of seedlings treated with these sulfonamides compared to seedlings treated with the herbicide norfluorazon. Now we expect to identify the potential targets through a genetic screening.

Acknowledgements: ANCPCyT for funding

INTEGRATION OF FLOWERING TIME SIGNALS IN *Arabidopsis thaliana*

Markus Schmid[1]

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The induction of flowering is a central event in the life cycle of plants. When timed correctly, it helps ensure reproductive success, and therefore has adaptive and economic value. Because of its importance, flowering is under the control of a complex genetic circuitry that integrates endogenous signals such as hormonal and carbohydrate status, and environmental signals such as temperature and light. Genetic analyses had initially suggested the existence of distinct, genetically defined pathways that regulate flowering in response to specific inputs. Over the last several years, however, it has become apparent that many important flowering time genes are not regulated by single inputs, but rather integrate multiple, often contradictory signals to control the induction of flowering. Importantly, these flowering time signals are usually perceived and act in specific tissues or even cells.

We have established INTACT for the shoot apical meristem and phloem companion cells to analyze changes in histone modifications and gene expression during flowering in a tissue- and cell type-specific manner. Using these lines, we have identified unusual chromatin states that are not easily detectable in complex tissues, demonstrating the power of tissue-specific epigenomics. I will discuss how such tissue-specific changes of

epigenomic modifications might contribute to the regulation of integrator genes to ensure that flowering commences under optimal conditions.

Acknowledgements.

We acknowledge funding from DFG (SCHM 1560/10–1) and the Wallenberg Foundations (KWA; 2016.0025).

PLENARY SESSION 2 – PLANT ABIOTIC INTERACTIONS

AN ANCESTRAL ROLE FOR DELLA PROTEINS IN THE COORDINATION BETWEEN GROWTH AND STRESS RESPONSES

Jorge Hernández-García, Asier Briones-Moreno, David Alabadí, **Miguel A. Blázquez**

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The plant hormones gibberellins (GAs) have been described to regulate multiple developmental processes throughout the whole life cycle, and also to modulate the response to abiotic stress factors and plant pathogens. The diversification of GA functions is based on the promiscuity of DELLA proteins, a family of transcriptional regulators reported to interact with over 60 DNA binding transcription factors. Given that DELLA stability is reduced when GA levels increase, DELLAs are considered negative GA signaling elements. However, *DELLA* genes are found also in the genomes of early-diverging land plants, like mosses and liverworts, which do not synthesize the GA molecules known to be active in vascular plants, nor do they have recognizable GA receptors. Therefore, we have investigated the possible ancestral role of DELLA proteins with two approaches. First, comparative analysis of Gene Coexpression Networks of *A. thaliana*, *S. lycopersicum*, *P. patens* and *C. reinhardtii* has shown that the landscape of putative DELLA targets became more coordinated after the appearance of DELLAs, and even more after their recruitment as GA signaling elements. Moreover, gene ontology categories related to 'stress response' were over-represented among the putative DELLA targets common to all land plants, but absent in the examined chlorophyte. Second, overexpression in the liverwort *Marchantia polymorpha* of its own Mp*DELLA* gene caused dwarfism (equivalent to the phenotype of *DELLA* overexpressors in vascular plants), and also the misregulation of stress-related genes, such as those involved in flavonoid metabolism. These results suggest that the role in the coordination between growth and stress responses is ancestral to DELLAs in all land plants and has been actively maintained.

THE COP1/SPA COMPLEX RELAYS LIGHT AND TEMPERATURE INFORMATION ON DELLA PROTEINS IN ARABIDOPSIS

Eugenio G. Minguet[a], Martina Legris[b], Noel Blanco-Touriñán[a], Manuel Pacín[c], Elisa Iniesto[d], Antonella Locascio[a], Martin Černý[e], Břetislav Brzobohatý[e], Henning Frerigmann[f], Vicente Rubio[d], Miguel A. Blázquez[a], Jorge J. Casal[b,c], **David Alabadí[a]**. [a]IBMCP, Spain. [b]Fundación Instituto Leloir, Argentina. [c]IFEVA, Argentina. [d] CNB, Spain. [e]Mendel University, Czech Republic. [f]Max Planck Institute for Plant Breeding Research, Germany
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The correct integration of environmental information into growth and developmental outputs is an extraordinary ability of plants that allows them to adapt and survive. DELLA proteins are transcriptional regulators that restrain growth and adjust development in response to environmental signals. Two characteristics of DELLAs sustain this role: (i) they are degraded in response to the hormone gibberellin (GA), whose metabolism is highly responsive to the environment; and (ii) they interact with multitude of transcription factors. Our results show that DELLAs are also regulated by COP1/SPA, a complex that destabilizes negative regulators of growth, owing to the E3 ubiquitin ligase activity of COP1, and that is inactivated by light and low/moderate temperature. COP1 ubiquitinates the DELLA protein GAI in vitro. Remarkably, SPA1 facilitates the recruitment of DELLAs GAI and RGA to nuclear bodies and their interaction with COP1. We provide evidences that the destabilization of DELLAs by COP1/SPA is relevant to respond to light and temperature. The steady disappearance of RGA from hypocotyls of wild type seedlings exposed to shade or warm temperature is delayed in *cop1*. In agreement, GA-treatment or genetic inactivation of GAI and RGA restore the ability of *cop1* to respond to darkness, shade and temperature. We propose that the destabilization of DELLAs by the COP1/SPA complex defines a novel entry point to relay information about light and temperature into the growth transcriptional network.

PLENARY SESSION 3 - NATURAL VARIATION & BREEDING I

NEW STRATEGIES FOR MARKER-ASSISTED PEACH BREEDING

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The important challenges faced by peach breeding require the development and use of innovative tools and approaches to achieve key goals such as the improvement of taste, disease resistance, shelf life, and adaptation to climate change. The availability of molecular markers with complete coverage of the genome facilitates their use for selection of individual genes, and the design of new breeding schemes potentially more efficient that the traditional ones. Introducing novel variability in the peach gene pool coming either from exotic sources or from cultivated or wild compatible *Prunus* is urgently needed to meet new breeding goals. For that purpose, we developed marker-assisted introgression

(MAI), allowing the integration of a DNA fragment coming from a donor species (almond) in the background of a peach cultivar only two backcross generations after the hybrid. A first survey of the map position of certain major genes coming from the donor species is also achieved in MAI, using a small subset of BC1 plants with a low number of introgressions. As a side result we are also developing a first introgression line collection of almond fragments in the peach genome background. Another strategy, resynthesis, consists of producing sets of lines having slightly different genetic compositions than a cultivar of already known outstanding performance. A large selfed offspring from this cultivar is screened with markers and individuals having most of its genome like this cultivar and another part different from it are selected. MAI and resynthesis can be combined to generate lines nearly identical to a given cultivar and with a single chromosomal fragment containing a gene/QTL of interest from a wild or exotic donor.

GRAPEVINE GENETICS AT INIA-CHILE: FROM GENETIC DIVERSITY TO BREEDING TOOLKITS

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During the last two decades, we have been exploring the grapevine genome with different purposes, always having in mind the main one: to provide support to the breeding of this precious fruit crop. In this route, we have characterized the germplasm of this exotic species of European origin (so nicely adapted to our local environment), focused on the criolla genotypes originated locally. At the same time, we were part of the International Vitis Microsatellite Consortium in which framework the first series of SSR markers were developed, being exhaustively used to build genetic maps of the species as well as dimensioning the genetic diversity of the Vitaceae family as a whole. Also, these markers were the pioneer tools to develop a reliable fingerprinting platform still worldwide used. Then, having the skeleton (linkage maps) it was of interest to decipher what were the individual pieces behind the performance of particular traits. In the case of table grape, we have been working since then in the search for QTLs and genes related to stenospermocarpy, berry size, responsiveness to gibberellic acid, sugar and acids contents, berry drop, among others. In this presentation, I will summarize our efforts to identify markers that could be useful as selection tools in our breeding program at INIA La Platina, based on the combination of phenotyping and different platforms including the use of various marker types (SSRs, SNPs mainly), transcriptomics, genome sequencing and qPCR of specific genes.
Financed by INIA and FONDECYT + FONDEF grants of CONICYT-Chile.

HIGH THROUGHPUT LINKAGE MAPPING IN PEACH FOR ASSISTING GENOME ASSEMBLY AND FOR ADVANCED QTL ANALYSES AND GENE TARGETING

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The availability of the genome sequence of many crops has fostered genetic studies allowing the identification of causal genes controlling important agronomic traits. Since its release in 2010 the peach genome sequence has promoted the construction of genomic tools such as the IPSC 9K SNP array, the adoption of emerging SNP analysis technologies such as Genotyping by Sequencing (GBS) and the individuation of important genes controlling agronomic traits (nectarine, flesh color, tree architecture, phenology). The IPSC 9K SNP array was used to saturate the PxF linkage map. This map was employed to assist the refinements and improve the peach genome sequence. The availability of a high density and resolution linkage map with about 2000 loci helped the anchoring and orientation of the peach genome sequence: 99.2% of the sequences are now mapped onto chromosomes and 98.4% are correctly oriented. The availability of saturated linkage maps was also helpful in QTL analyses and gene tagging. Using the PxF SNP map for advanced QTL analyses we were able to restrict the confidence interval of some known QTLs, to detect new ones and to individuate candidate genes underpinning the trait. In particular, two regions involved in the control of powdery mildew were identified in LG7 and LG8. In LG7 an interval of about 50 kb underlying the region controlling the leaf glands was identified and candidate genes were proposed. Further analyses are ongoing aimed at confirming the role of these genes.

PLENARY SESSION 4 - NATURAL VARIATION & BREEDING II

CONTRIBUTION TO BREEDING OF DURUM WHEAT LANDRACES FROM THE MEDITERRANEAN BASIN

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The Mediterranean Basin is the largest producing area and the largest consumer of durum wheat products. From its domestication in the Fertile Crescent (10,000 BP) to its arrival to the Iberian Peninsula (7,000 years BP), natural and human selection resulted in the establishment of local landraces, which were largely grown until the advent of the homogeneous and more productive semi-dwarf cultivars from the early 1970s. Landraces are a valuable source of genetic diversity for the improvement of commercially valuable traits. A collection of 172 durum wheat landraces from 21 Mediterranean countries was genotyped with SSR and DArT markers and phenotyped in six environments. Electrophoretic analysis of high (HMW-) and low (LMW-) molecular weight glutenin subunit composition at 5 loci revealed 131 different allelic/banding pattern combinations. The frequencies for Phytoene synthase allelic variants at *Psy1* loci indicated large variability, with *Psy1-A1* showing significant differences in semolina yellowness. Landraces useful in

breeding programs to improve gluten strength, grain weight and grain colour were identified. Climatic data of the collecting zones affected the agronomic performance of landraces: the collected in the warmest and driest zone had earlier flowering, more spikes and grains per unit area, lighter grains and lower yields than the collected in colder and wetter zones. The genetic and phenotypic population structures were strongly related, and connected with the geographic origin of the landraces. Association mapping identified 245 significant marker trait associations (MTAs): 86 corresponding with yield and yield component traits, 70 to phenology and 89 to biomass production.

THE GENETICS UNDERLYING NATURAL VARIATION OF PLANT-PLANT INTERACTIONS IN *ARABIDOPSIS THALIANA*

Cyril Libourel[1], Harihar Jaishree Subrahmaniama[1], Dominique Roby[1], **Fabrice Roux**[1]

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Studying the mechanisms underlying plant-plant interactions is essential to understand the structure and functioning of communities, which may in turn help to predict ecosystem responses to global change. It is also of primary importance for the optimization of breeding programs based on crop mixtures. While this exciting challenge calls for a multidisciplinary approach at the frontiers between evolutionary ecology and functional genomics, our understanding of the genetic and molecular bases underlying natural variation of plant-plant interactions is largely limited in comparison to other types of biotic interactions. Our work contributes to understanding the genetic and molecular bases of plant-plant interactions at the intraspecific and interspecific levels.

By using 195 whole-genome sequenced local accessions of *Arabidopsis thaliana*, we identified different types of interactions at the intraspecific level, in particular cooperation. To identify the kinship relationships between cooperative accessions, we tested three hypotheses, namely kin recognition, Greenbeard effect and compatibility genes.

At the interspecific level, 96 local accessions were grown in monospecific and multispecific competition treatments (based on the combinations of three competitor species, *i.e. Poa annua*, *Stellaria media* and *Veronica arvensis*). We identified strong genotype-by-environment interactions for competitive ability. Most of the significant SNPs identified by GWA mapping were located in a complex QTL region containing three independent major association peaks whose levels of statistical significance were highly dependent on the competition treatment. The remaining significant SNPs were mainly organized in four QTL regions, each being detected for a specific competition treatment. The functional validation of one of these specific QTLs revealed a receptor-like kinase underlying response to the presence of *P. annua*.

GENOTYPING AND PHENOTYPING ARABIDOPSIS POPULATIONS COLLECTED IN PATAGONIA

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The growing collection of sequenced or genotyped Arabidopsis thaliana accessions includes mostly individuals from the native Eurasian and North African range and introduced North American populations. I will describe the genetic and phenotypic diversity, along with habitats and life history, of *A. thaliana* plants collected in Patagonia, the southernmost end of its worldwide distribution. Seed samples of Patagonia accession represent the first germplasm collected in South America for this species. Whole-genome resequencing revealed that plants from four sites of collection and a Patagonia herbarium specimen collected in 1967 formed a single haplogroup. ADMIXTURE and principal components analyses suggest that the ancestor of the Patagonia haplogroup either came from Italy or the Balkan/Caucasus regions of Eurasia. In the laboratory, plants from the Patagonia haplogroup were hyposensitive to red and shade light, with corresponding changes in the expression of phytochrome signaling genes. Patagonia had higher *PIF3* and *PIF5* and lower *HY5* expression under red light; and lower expression of *PIL1, ATHB2* and *HFR1* under shade compared to Col-0. In addition, Patagonia plants had a strong vernalization requirement associated with high levels of *FLC* expression. In this talk, I will show advances in this line of work.

PIN-NING DOWN THE FUNCTION OF D6PK PROTEIN KINASES IN AUXIN TRANSPORT REGULATION

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The biosynthesis and proper distribution of the phytohormone auxin within the plant influences almost every aspect of plant growth and development. To the largest extent, differences in the morphology between plants are the results of differential auxin distribution and auxin actions at the level of individual plants cells. Whereas auxin transport from cell to cell and within a plant had for a long time been inferred solely based on the polar distribution of PIN auxin exporters, we have recently shown that PINs require activation by protein kinases, such as the D6 PROTEIN KINASE, to become active auxin transporters. I will describe the biochemistry of D6PK and mechanisms that are required for targeting D6PK to the plasma membrane and the PINs. I will also present data that challenge the current view of how PIN polarity is controlled by phosphorylation. Finally, I will highlight some other regulatory functions of D6PK that are independent of PIN-dependent auxin transport control.

This work is funded through grants from the Deutsche Forschungsgemeinschaft.

PLENARY SESSION 5 - GENOME AND SYSTEM BIOLOGY

PHYTOCHROMES, RESOURCE MANAGEMENT AND GROWTH

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The phytochromes are important information-transducing photoreceptors that drive developmental transitions and essential adaptive responses to a changing growth environment. This growth plasticity requires an ability to refactor molecular-signalling and resource management. Our knowledge of the molecular signalling events pre- and post-phytochrome activation is now quite detailed, but we know much less about how signalling impacts carbon metabolism.
Recently we have used genetic approaches to show that phytochromes control carbon allocation and biomass production in the developing plant (Yang et al. PNAS 2016). *phy* mutants exhibit reduced growth, reduced CO_2 uptake, but unexpectedly, higher daytime levels of sucrose and starch. This implies that the elevated carbon resource levels either cause or arise from the *phy* mutant growth defects. To address this question, we extended our analysis to measure time-resolved plant biomass accumulation and metabolite levels. We also quantified $^{13}CO_2$ labelling enrichment in free amino acids, in protein, and in cell wall glucose, in order to estimate the absolute rates of protein and cell wall synthesis. This analysis indicated that during early development (~ 2.5 weeks), the relative growth rate of *phy* mutants is slower than WT, but more mature *phy* and WT plants grow at the same rate. Dynamical growth imaging, gas exchange and mathematical modelling support this finding and show that the delayed development in *phy* seedlings results solely from reduced cotyledon size that limits the area of photosynthetic green tissue. Our study illustrates that inactivating phys (e.g. by vegetation shade) during seedling de-etiolation slows early growth, which in turn has a profound impact on final plant biomass.
Acknowledgements, BBSRC, ERA-CAPs, University of Edinburgh Darwin Trust, DFG: German Research Foundation.

SYSTEMS BIOLOGY OF PLANT-PATHOGEN INTERACTION

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Bacterial pathogenesis of plants is a complex interaction process of molecular signaling that governs all activities of the cells. To decipher these connections at a systems level, two different approaches can be applied in practice: the top down and the bottom up. The first one deals with the analysis of gene expression, proteins, metabolites, and flux carbon distribution within the network and their crosstalk. The bottom up starts by building a mathematical model based on genomic data, aiming at predicting the resulting phenotype under define environmental conditions, which can be fed with *omics* data and further be refined. In this talk, I give an overview of the use of both systems biology approaches on bacteria-plant interaction with special focus on *Pseudomonas syringae* infection. This pathogen is a versatile bacterium that can rapidly change its metabolism when infecting various host plants. It possesses a vast array of virulence factors that deceive the immune systems of the plant. In addition, *P. syringae* pv. tomato DC3000 uses the nutrient of the host cells to thrive, secreting various by-products, which certainly alter the metabolic state of the host. As the final aim of host-pathogen systems biology is to predict the resulting phenotype of each organism during infection, I will present genome-scale metabolic models of *P. syringae* and *A. thaliana*, and how they can be used to get more insight into the metabolic response of the bacterial strain and the host plant.
FONDECYT Regular: 1170259.

PLENARY SESSION 6 – GENOME REGULATION AND EPIGENETICS

INTEGRATION OF THE RESPONSES TO IRON AVAILABILITY FLUCTUATIONS IN *Arabidopsis thaliana*

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Iron (Fe) homeostasis is crucial for all living organisms. Perturbations of Fe uptake, circulation, metabolism or storage are responsible of neurodegenerative diseases and cancer in humans, and alter productivity and product quality of plants. In mammals, an integrated post-transcriptional mechanism couples the regulation of both Fe deficiency and excess responses. Whether an integrated pathway involving common players controls these responses in plants is still to be determined. Using a combination of molecular, genetic and biochemical approaches, we found that bHLH105/ILR3, a transcriptional activator of *Arabidopsis thaliana* responses to Fe shortage negatively regulates ferritin gene expression, the main markers of the plant responses to Fe excess. We demonstrated that various facets of plant development in response to Fe deficiency or excess rely on ILR3. We thus showed that ILR3 repressed the expression of several structural genes involved in the control of Fe homeostasis by directly interacting with their promoter, and that ILR3 repressive activity was likely conferred by its dimerization with bHLH47/PYE. Altogether, we found that ILR3 is at the center of the transcriptional regulatory network that controls Fe homeostasis in Arabidopsis, where it acts as both transcriptional activator and repressor.

THE MANUAL ANNOTATION OF THE *A. CHINENSIS* (KIWIFRUIT) GENOME

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With the advent of large numbers of low quality "draft" genomes the research communities in non-model organisms rely heavily on computationally annotated genes. The huge variation in the quality of these draft genomes and the predicted gene lists affects research and development. The draft *Actinidia* (Kiwifruit) genome (Huang et al. 2013) was a big step forward in our understanding of this important horticultural crop. Typical of draft genomes, a large proportion of the sequence was not assigned to chromosomes, and the gene list missed key published genes. To address this, we developed an international consortium firstly to improve the genome construction and secondly to manually annotate the whole genome. Manual annotation was performed using the WebApollo software and employed tracks of computationally predicted genes, EST sequences and mRNA-seq data from a variety of different tissues. In total 93 researchers from around the world produced evidence-based gene models for 33,318 genes. Our subsequent analysis showed that the majority of computational gene predictions (96%) in the published kiwifruit genome do not align to the manually edited genes. In particular, the computationally generated genes did not accurately predict intron-exon structures or translation start and stop regions. Non-canonical splice sites were particularly poorly annotated. The accuracy of the new models was tested by single molecular sequencing of 812 cloned cDNAs, it was found that approximately half were fully represented in the original computer gene models, while from this exercise we now have a second generation genome to start to understand the biological processes associated with this plant and a method for the scientific community to improve the accuracy and utility of draft genomes.
Keywords: Kiwifruit, Genome, Annotation

PLENARY SESSION 7- PLANT BIOTIC INTERACTIONS

PRIMING PLANTS FOR ENHANCED DEFENSE

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When locally infected by pathogens, plants activate a systemic immune response, called systemic acquired resistance (SAR). In this process, distal leaves become primed to activate a more robust defense response upon further infection. Defense priming is associated with

an elevated level of receptors for microbial patterns (e.g. flagellin-sensing [FLS] 2), accumulation of dormant signaling enzymes (e.g. mitogen-activated protein kinases [MPKs]) and transcriptional coactivators (e.g. WRKY transcription factors), and with modifications to chromatin. The latter comprise the covalent modification of histones (e.g. histone H3 and H4 acetylation and/or methylation) and the formation of open chromatin indicative of regulatory DNA sites with a role in defense priming. Together, these events provide a memory to the initial infection, which enables the boosted recall immune response of plants. I will disclose the impact of these fascinating discoveries on sustainable agriculture by introducing smart tools and approaches for the identification of priming-inducing chemistry. I will also elaborate on the so-called Green Release technology that allows the controlled release of agrochemicals from plant surface-stuck micro gels, thus allowing the smart management of plant performance.

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MOLECULAR BASIS OF Arabidopsis-*Burkholderiales* BACTERIAL STRAINS INTERACTIONS

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The interaction between plants and bacteria is a fascinating world where negative presumably "neutral" and positive (mainly plant growth promoting rhizobacteria-PGPR) effects are part of a continuum based on complex and not yet fully explored molecular mechanisms. We have studied the interaction of the plant model *Arabidopsis thaliana* with four closely related β-proteobacteria belonging to the *Burkholderiales* order: the well-known PGPR *Paraburkholderia phytofirmans* and *Cupriavidus taiwanensis*, and the non-PGPR (but quite versatile aromatic compounds degrader model) *C. pinatubonensis*, and (multimetal resistant bacterium) *C. metallidurans*. These bacteria establish rhizospheric and (under some conditions) endophytic associations with *A. thaliana*. Studies on molecular mechanisms explaining plant growth promotion and protection by PGPR indicated that plants face hydric and saline stress activating expression of specific plant genes: related to production of osmolality protecting molecules, transcriptional regulators and transporters. Complex plant hormone signaling networks are also playing a role in bacterial mediated plant responses. In addition, *P. phytofirmans* allowed us to make a detailed description of the auxin phytohormone turnover, the complex quorum sensing signaling regulatory

network, the induction of the induced systemic resistance response to phytopathogen, and the role of new volatile compounds in plant protection to salt stress effects. *A. thaliana* root exudates, whose composition changes depending on the life cycle, the presence of abiotic (organic pollutants, metals) or biotic stresses, allow (differential) growth levels for these four *Burkholderiales* strains which under some conditions compete each other for these carbon and energy resources. Plant protection to phytopathogen, nutrient limitation, and herbicide and metal stress, performed for some of these strains, is therefore controlled by specific bacterial genes, the particular plant root exudates composition, and a complex array of molecular signaling and transcriptional responses.

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AMI1, A NOVEL MOLECULAR NEXUS CONTROLLING GROWTH-DEFENCE TRADE-OFFS

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Plants are highly prone to injury by pathogens, herbivores, and mechanical stresses jeopardizing their tissue integrity. In order to maintain fitness, plants have to adequately respond to these threads. In this regard, they largely rely on plant hormone crosstalk and a complex signal transduction network that connects damage-associated signals with appropriate adjustments of metabolic processes in the short-term and changes in plant growth and development in the long-term. These wounds induced adaptive responses are nearly exclusively triggered by *de novo*-biosynthesis of the plant hormone jasmonic acid (JA). However, recently, we were able to demonstrate that auxin biosynthesis, and therewith plant growth responses, are seemingly tightly linked to this process. Here, we present the functional characterization of AMI1, an *Arabidopsis thaliana* IAM amidohydrolase contributing to cellular auxin homeostasis, that apparently acts as a novel molecular hub connecting the energy status of the plant with auxin levels and defence fitness. We were able to detect that *AMI1* expression levels are controlled by glucose and sucrose, but most intriguingly we found that the *ami1* knockout line contains significantly increased JA contents and shows a higher resistance towards biotic predators.

PLENARY SESSIONS

PLENARY SESSION 1 – GENES AND DEVELOPMENT

STRUCTURAL AND INTERACTION STUDIES ON THE COI1-JAZ CO-RECEPTOR FOR JASMONOYL-ISOLEUCINE IN *Fragaria* X *ananassa* REVEAL A NEW FUNCTIONAL JAZ DEGRON IN PLANTS

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Jasmonoyl-isoleucine (JA-Ile) is an important phytohormone regulating developmental and defense responses. JA-Ile mediates the interaction between the F-box protein COI1 (part of the SCF^{COI1} E3 ubiquitin ligase) and a JAZ repressor leading to early jasmonate responses. Most of Arabidopsis JAZs contain a degron sequence responsible for the stabilization of the COI1-JA-Ile-JAZ complex. However, information about this complex in other species such as strawberry (*Fragaria* x *ananassa*) is still scarce. To gain insight into the strawberry JA-Ile perception complex at the structural level, protein models were built and analyzed for FaCOI1 and FaJAZ1/10. The interaction between FaCOI1 and FaJAZ1/10 were explored using several ligands, through molecular docking and molecular dynamics simulations (MDS), finding the strongest interaction with (+)-7-*iso*-JA-Ile than other ligands. Then, we tested interactions between FaCOI1 and FaJAZs by yeast-two hybrid assay in the presence of coronatine (COR, a JA-Ile mimic). We detected strong COR-dependent interactions between FaCOI1 and FaJAZ1/10, which have a new non-canonical (IPMQRK) and canonical (LPIARR) degron sequences, respectively. Phylogenetic analysis showed that the new IPMQRK degron is only present in orthologs belonging to the Rosoideae but not in other Rosaceae subfamilies. Together, this study uncovers a new degron sequence in plants, which could be required to make an alternative and functional JA-Ile perception complex in strawberry.

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IDENTIFICATION OF PECTIN METHYLESTERASES (PME) AND PECTIN METHYLESTERASES INHIBITORS (PMEI) USING Arabidopsis SEED COAT MUCILAGE

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Pectin is one of the major components of the plant cell wall. Methylation of homogalacturonan (HG), the most abundant pectin domain, is essential to confer the cell wall its biochemical and biomechanical properties. The degree of methylation (DM) of HG is tuned after secretion into the cell wall, thanks to the activity of two family of specialized enzymes: pectin methylesterases (PMEs) and its inhibitors (PMEIs). In Arabidopsis, there are 67 putative genes encoding for PMEs and 69 for PMEIs. Given the presence of a large numbers of PMEs and PMEIs, we can expect a fine regulation of HG methylesterification. Arabidopsis seeds accumulate a large amount of mucilage, composed of the pectin domain Rhamnogalacturonan-1 (RG-1) and HG. Thus, in this study, the Arabidopsis seed mucilage will be used as a model to help us understanding how PMEs and PMEIs regulate pectin methylesterification. *In silico* data analyses revealed that 11 *PMEs* and 16 *PMEIs* present a high level of expression in the seed coat during the developmental stages when mucilage

is produced in epidermal cells, suggesting their participation in HG methylation. In our laboratory, it was carried out a mutant screen based on biochemical analysis, immunolabeling and PME activity measurement of T-DNA mutant lines. To date this screening led us to select 5 mutant lines affected in 3 *PMEIs* that have not characterized yet. Preliminary experiments show that mucilage in these mutants presents changes in the global PME activities and different HG methylation patterns.
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PLENARY SESSION 2 – PLANT ABIOTIC INTERACTIONS

GENOME-WIDE ASSOCIATION STUDY REVEALS FIRST INSIGHTS INTO THE GENETIC FACTORS UNDERLYING POST-FLOWERING DROUGHT TOLERANCE IN FLAXSEED (*Linum usitatissimum* L.)

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Drought stress acts simultaneously on many traits and developmental stages which ultimately affects seed yield of crops worldwide. In particular, drought stress at the reproductive stage (flowering and seed development) can result in the most significant reductions in crop production. In this study, yield and yield-related drought tolerance indices were assessed on 120 flaxseed accessions under mild drought and irrigated conditions at flowering time. A set of ~700,000 single nucleotide polymorphisms (SNPs) was screened for marker-trait associations using general models. In average, drought stress reduced seed yield by 18% and start of flowering was brought forward by 5 days. Based on the stress tolerance index (STI), three genomic regions on linkage groups 2, 7 and 9 were identified which explained 68.2% (R^2) of the phenotypic variation. Ten candidate genes were located nearby peak SNPs (~50 kb either side) where a clathrin heavy chain 1 (CHC1), a mitogen-activated protein kinase (MAPK), a peptide chain release factor and a CCCH-type zinc finger protein genes, which have previously been involved in drought response in other crops were the most promising candidates for further studies. This information provides important genetic insights into the natural variation of flaxseed drought tolerance. The identified SNPs or candidate genes could serve as direct targets for both genetic engineering and selection for flaxseed trait improvement.
This research was supported by Fondo Nacional para el Desarrollo Científico y Tecnológico (FONDECYT) Chile, project N° 1161133.

THE MASTER REGULATOR OF INMUNITY RESPONSES, NPR1, MEDIATES A NOVEL REGULATORY PATHWAY IN COLD ACCLIMATION BY INTERACTING WITH HSFA1 FACTORS

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NPR1 is a master coactivator of Systemic Acquired Resistance that confers immunity against pathogens through a transcriptional cascade mediated by salicylic acid (SA) and the TGA transcription factors. Several lines of evidence suggest interaction between low temperature and biotic stress signaling, however, little is known about NPR1 implication in plant response to cold. Here, we demonstrate that Arabidopsis NPR1 is a positive regulator of cold acclimation by regulating cold-induced gene expression independently of SA and TGA factors. Our results demonstrate that cold promotes the oligomer-to-monomer conversion of NPR1, and as a consequence its nuclear import and interaction with HSFA1s transcription factors triggers the induction of HSFA1-regulated genes and cold acclimation. Concordantly, our results show that Arabidopsis mutants deficient in HSFA1 factors display reduced capacity to cold acclimate and that cold induction of heat stress-responsive genes is required for correct development of cold acclimation. All these findings unveil an unexpected function for NPR1 in plant response to low temperature, reveal a new regulatory pathway for cold acclimation mediated by NPR1 and HSFA1 factors, and place NPR1 as a central hub integrating cold and pathogen signaling for a better adaptation of plants to their ever-changing environment.
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MEMBRANE INTRINSIC PROTEINS AND ADAPTATION TO ABIOTIC STRESS: AQUAPORIN NIP1;1 AND ITS ROLE IN WATERLOGGING RESPONSES IN *Prunus* ROOTSTOCKS

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Under field conditions waterlogging events occur due to problems of soil compaction, heavy soils with poor drainage or irrigation problems. The stone fruit trees (*Prunus sp.* L.) are grafted onto rootstocks which determine their tolerance to different stresses, e.g. root hypoxia. Although most *Prunus* rootstocks have been classified as sensitive to hypoxia, different tolerance responses have been found among genotypes. Aquaporins are structural membrane proteins that have been characterized as carriers of water and/or solutes and involved in plant responses to abiotic stresses. NIPs (Nodulin 26-like intrinsic proteins) represent a large and diverse family of aquaglyceroporins, with multiple members found in every sequenced plant genome. Based on structure–function studies, the NIP family can be subdivided into three subgroups (I, II and III) based on the identity of the

amino acids in the selectivity-determining filter (ar/R region) of the transport pore. These subgroups contain multifunctional transporters with low to no-water permeability and the ability to flux multiple uncharged solutes of diverse sizes depending of residues composition of the ar/R filter. In this work, we characterized a NIP gene, orthologous to *AtNIP2;1*, a lactic acid transporter. Gene expression was evaluated in two contrasting *Prunus* genotypes to root hypoxia, 'Mazzard F12/1' (sensitive) and 'Mariana 2624' (tolerant). qPCR analysis revealed either its root specific expression and differential expression patterns between both genotypes under waterlogging treatment. Molecular simulation analyses of PruavNIP1;1 and PrucxmNIP1;1 proteins showed potential substrates and identified structural differences between genotypes. These results suggest that this NIP aquaporin is part of the mechanism to cope the root waterlogging stress in tolerant species of *Prunus*.

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MORPHO-ANATOMICAL AND HYDRAULIC TRAITS RELATIONSHIPS BETWEEN TWO GRAPEVINE VARIETIES FROM A COMMERCIAL VINEYARD IN CHILE.

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Climate change has become a threat to the wine industry due to increases in temperature and rainfall reductions in Mediterranean climates. Therefore, it is necessary to improve our knowledge about the mechanisms conferring resistance to water shortages in grapevines varieties. Due to leaves are the most important, although not exclusive, evaporating organs in plants and they develop the highest water tension through their hydraulic systems, we evaluated morphoanatomical and hydraulic traits in Carménère (**C**) and Syrah (**S**) leaves. Two irrigation levels were imposed (I: irrigated and NI: non-irrigated) in a vineyard from the Cachapoal Valley during the 2016-17 growing season. Our results shown that C have a more sensitive stomatal conductance (g_s) in response to dehydration than S, probably by the more positive osmotic potential at full turgor (π_0) and higher relative water content at turgor loss point (RWC_{TLP}) in their leaves. Also, both varieties showed a similar non-linear negative trend in leaf hydraulic conductance (K_{leaf}) during dehydration, but K_{leaf} was highest in S than C when stem water potential was higher than -1.2 MPa. This trait could be related to the bigger value in major veins density (**MVD**) showed in S. Finally, because of the higher Leaf Dry Matter Content (**LDMC**) and MVD, it is suggested that S leaves are more tolerant to dehydration than C, although C leaves could be capable to avoid water stress closing their stomata upon less negative water potential, and finally, loosing less water.

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PLENARY SESSION 3 - NATURAL VARIATION & BREEDING

GENOME-WIDE SNP IDENTIFICATION IN *Prunus* ROOTSTOCKS GERMPLASM COLLECTION USING GENOTYPING-BY-SEQUENCING (GBS): DISTRIBUTION OF SNPs AND PREDICTION OF THEIR EFFECT ON GENE FUNCTION

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Modern plant breeding utilizes a high number of molecular markers for segregation analysis, gene mapping and marker discovery to facilitate marker-assisted selection. We initiated a *Prunus* rootstocks breeding program in 2010 and since then, different interspecific crosses have been carried out utilizing *Prunus* rootstock germplasm collection established at CEAF and available pollen obtained from the *Prunus* rootstocks germplasm collection at EEAD-CSIC. In order to contribute to the development of molecular markers, we genotyped 53 diploid *Prunus* rootstocks and five cultivars, which belong to subgenus *Amygdalus*, *Prunus* and *Cerasus*, using Genotyping-by-sequencing (GBS). Sequence reads were mapped to the peach genome sequence v2.0. In addition to the assessment of the genetic diversity of both Chilean and Spanish germplasm collections, the distribution and putative effect of SNPs discovered was analyzed. Of 45,382 high-quality SNPs obtained, 41,080 SNPs (90.3%) were located in genic sequences. Based on their putative effect on annotated genes, 76.0% of the SNPs could have a modifier effect, 14.0% a low impact, 9.9% a moderate impact and 0.1% (128 SNPs) could have a high impact on gene function and phenotype of the plant material analyzed. Our results provide valuable information which could be important for rootstock breeding programs and to facilitate comparative genomics and the study of adaptive variation across the *Prunus* genus.

CONICYT-REGIONAL/GORE O´HIGGINS/CEAF/R08I1001; FONDECYT 3160316; FONDECYT 1160706; and Spanish Ministry of Science and Innovation (MICINN) grant RFP2012-00020.

CHARACTERIZATION AND GROUPING OF LOCAL VARIETIES OF TOMATO CULTIVATED IN CHILE

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Local tomato varieties are a historical genetic resource, from which elite commercial varieties have been generated. The replacement of local varieties by commercial varieties has generated a loss of diversity. In Chile, the town of Limache has historically been the tomato producing area by excellence. In the present work we evaluated the morphological and molecular diversity of 24 tomato accessions present in Chile in the last 80 years and that have been collected in different periods. The morphological characters were stable and of high heritability, being useful for the characterization and distinction of nearby tomato varieties. A loss of variability and a tendency to homogeneity over time were observed. The Limachino type varieties can be considered as a group differentiated from the rest of the local and commercial varieties. The molecular characterization with 15 SSR supported the morphological differentiation of this traditional variety. A hypothesis of its origin is proposed.

Proyecto FIA PYT-2014-0227; Proyecto Fontagro FTG/RF-15460-RG; Proyecto INIA/MINAGRI Conservación de Recursos Genéticos 501453-70

PLENARY SESSION 5 - GENOME AND SYSTEM BIOLOGY

IDENTIFYING THE ROLE OF ARGONAUTE1 PHOSPHORYLATION IN THE NITRATE RESPONSE IN *Arabidopsis thaliana*

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Nitrate is the major source of N available to plants in agricultural soils. Nitrate activates a signaling pathway that modulate expression of a wide range of genes with impact in metabolism, growth and plant development. Although the gene expression response induced by nitrate has been characterized in great detail, our understanding of the nitrate signaling pathway is still limited. Signaling pathways commonly regulate protein activity, localization or interaction through posttranslational protein modifications such as phosphorylation. In this work, we analyzed the impact of nitrate in the global dynamics of protein phosphorylation in Arabidopsis roots using quantitative time-course analysis by mass spectrometry (MS/MS) combined with liquid chromatography. We identified ARGONAUTE1 as a molecular factor which changes its phosphorylation status under nitrate treatment. Our preliminary results show that AGO1 phosphorylation may act as a key component to coordinate the balance between plant development and environmental clues such as nitrogen availability at the post-transcriptional level. Our data provides new insights into early events triggered by nitrate in plants articulating transcriptional and post-transcriptional mechanisms of regulation of gene expression.

Collaborators: Dr. Steve Briggs And Dr. Shen Zhouxin, Division Of Biological Sciences, UCSD. Dr. Xuemei Chen, Botany And Plant Sciences, UCR

Beca Doctorado Nacional CONICYT 21140874 and FONDECYT Regular 1141097.

UNCOVERING PLANT HORMONE SIGNALING IN NITRATE-DEFENSE RESPONSE INTERACTION IN TOMATO

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Nitrogen (N) is an essential macronutrient whose availability significantly impacts plant growth and crop yield. Despite its role as a nutrient, N acts as a signaling molecule that modulates gene expression of a wide range of plant processes. Nitrate availability, the main N source found in agricultural soils, influences different developmental programs and plant ability to cope with pathogen attacks. Since plant defense is complex biological process and energetically costly response mechanism, it is expected that the metabolic state of the plant plays a fundamental role in the outcome of the plant-pathogen interaction. Although significant progress has been made in the characterization of disease severity under different N availability, the interaction between the plant N status and its defense responses are poorly understood. In this work, we analyzed the global gene expression response of *Solanum lycopersicum* against infection by the necrotrophic fungus *Botrytis cinerea*, under contrasting nitrate conditions. Our results indicate that defense responses to *B. cinerea* infection are affected by N availability, showing more susceptibility in nitrate-limiting conditions, in both leaves and fruits. Using a systems biology approach, we identified ethylene (ET) and jasmonic acid (JA) transcriptional regulatory networks implicated in plant response to the fungus infection under contrasting nitrate conditions. Moreover, we characterize expression patterns of genes for the biosynthesis, modification and signal transduction of ET, JA, salicylic acid (SA) and abscisic acid (ABA) to infer the potential link between hormones and plant N status in plant–pathogen interactions. We integrated these results with susceptibility phenotypes of plants compromised in hormone synthesis and perception, to provide a model describing how nitrate influence the susceptibility of tomato to *B. cinerea*.

FONDECYT-Chile 1171631 and 11140678, Millennium Nucleus Center for Plant Systems and Synthetic Biology (NC130030) and Millennium Nucleus for Fungal Integrative and Synthetic Biology (NC120043).

BLAST-KNN - A BLAST MACHINE-LEARNING ENSEMBLE THAT RELIES ON INTERPRO EXTRACTED FEATURES TO IMPROVE ENZYMES FUNCTIONAL ANNOTATION

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Rapid advances in DNA sequencing technologies will enhance our understanding of genotype-phenotype relationships with functional annotation of enzyme-coding genes being crucial to achieve this goal. Enzymes experimental annotation validation is cost and time expensive, leading to differences of two orders of magnitude between validated and available data. This gap has driven the development of *in silico* tools that assigns functionality to unannotated proteins using homology-based inference approaches. The most popular of these tools is BLAST, given its performance and ease of use. Albeit the homology-based inference approach has proven effective, homologous proteins not always share the same function. In this sense, a Machine Learning standpoint enables us to develop self-adjusting algorithms for automatically extracting relevant information from training data and then extrapolate this knowledge to unseen data. The present work proposes a novel approach to improve enzymes functional classification that combines the strength of BLAST with a Machine Learning tool for nonparametric classification called *K-nearest neighbors* (KNN). The proposed approach, *BLAST-KNN*, relies on assigning EC classes to proteins using BLAST, and re-assessing those proteins assigned to classes without perfect scores for BLAST using KNN. BLAST-KNN relies on extracting features from InterPro and selecting using mutual information, training using a Nested Cross Validation and annotating using KNN. Using SWISSPROT data, it was possible to improve an average of 13.4% the F1 score of 835 classes, representing 56% of those classes without perfect scores for BLAST, with a particular improvement for classes with more than one assigned EC. FONDECYT_INICIACION 11150107

PLENARY SESSION 6 – GENOME REGULATION AND EPIGENETICS

SINGLE-BASE RESOLUTION OF THE METHYLOME IN THE HIGH CHILL REQUIREMENT VARIETY OF SWEET CHERRY (*Prunus avium* L.) 'KORDIA' DURING DORMANCY

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Epigenetic modifications can provide information about the connection between genotype and phenotype variation due to environmental conditions. In temperate perennial fruit species like sweet cherry, prolonged exposition to cold temperatures is required for dormancy release and flowering. Besides genetic diversity, epigenetic variation is believed to contribute to different chilling requirements and phenotypic plasticity among varieties. DNA methylation is a heritable modification that in plants occurs in tree different contexts (CpG, CHG and CHH; H= non-guanine residue), and plays a key role in gene expression regulation. With the objective to identify regions with differential methylation, we performed whole genome sequencing of bisulfite-treated DNA from floral buds of 'Kordia'

at four time points of cold accumulation during dormancy. In average, 75.6% of total reads mapped to the 'Kordia' reference genome and from these, 50% corresponded to unique alignments. On the other hand 23.5% of the reads did not align under any condition and a 0.6% of the reads did not correspond to a genomic sequence. We obtained global methylation levels, gene body methylation in MADS-box genes associated to dormancy (Dormancy Associated MADS-box genes like), and methylation-demethylation patterns at 0, 443, 1295 and 1637 chilling hours. Approximately 25-30% of total cytosines were methylated in all the conditions, corresponding to 10-12%, 9-10% and 7-8% of specific methylations at the CpG, CHG and CHH sites, respectively. Finally, annotation of Differentially Methylated Regions (DMRs) is under development, in an attempt to describe epigenetic marks that may be contributing to contrasting chilling requirement.
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IMPROVING GENOME ENGINEERING EFFICIENCY IN *Vitis vinifera* USING DNA REPLICONS

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Genome engineering is a rapidly emerging discipline that seeks to develop strategies and methods for the efficient, targeted modification of DNA in living cells. In plant sciences, gene editing has enormous potential for basic and applied research allowing for both the study of individual genes and crop improvement. Current genetic engineering techniques are mostly based on sequence-specific nucleases (SSNs), such as clustered regularly interspaced short palindromic repeats (CRISPR)/Cas9, that create a targeted DNA double-strand break (DSB) in a genome. These breaks are most frequently repaired by non-homologous DNA end joining, which creates insertion/deletion (indel) mutations at the break site that knock-out gene function. The CRISPR/Cas9 system is composed of Cas9 endonuclease and a synthetic guide RNA (gRNA), which is complementary to a specific target site. gRNAs can be designed and led to form editing complexes with Cas9 under *in vivo* conditions generating indels. In *Vitis vinifera*, a limiting step in genome editing is the low expression of reagents achieved by T-DNA vectors. To improve efficiency, we developed a system based on DNA replicons from viruses that increased the amount of Cas9 and gRNAs available for gene editing in the cell nucleus. Results showed a fourfold increase in the editing efficiency of a target gene, compared to T-DNA vectors. This increase was correlated with a higher expression of Cas9 mRNA in the tissue. The proposed strategy makes possible the generation of precise modifications in the grapevine genome without need of stable integration of the sequences encoding for reagents.
Work funded by Biofrutales Consortium and CORFO-Chile Grant 13CTI-21520-SP7

PLENARY SESSION 7- PLANT BIOTIC INTERACTIONS

THE BATTLE OF THE FUNGAL UMSRT1 AND MAIZE ZMSUT1 SUCROSE TRANSPORTERS FOR PLANT SUGAR RESOURCES

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The biotrophic fungus *Ustilago maydis* causes corn smut disease, inducing tumor formation in its host *Zea mays*. Upon infection, the fungal hyphae invaginate the plasma membrane of infected maize cells, establishing an interface where pathogen and host are separated only by their plasma membranes. At this interface the fungal and maize sucrose transporters, UmSrt1 and ZmSUT1, compete for extracellular sucrose in the corn smut/maize pathosystem. Electrophysiological analyses show that UmSrt1 has a much higher affinity for sucrose than ZmSUT1. This raised the question whether the transplantation of the fungal transporter into maize would improve the pathogen tolerance of the plant. Using the quantitative parameters of ZmSUT1 and UmSrt1, a mathematical model to simulate the competition for extracellular sucrose at the contact zone between the fungus and the host plant was developed. This approach revealed that UmSrt1 exploits the apoplastic sucrose resource, which forces the plant transporter into a sucrose export mode providing the fungus with sugar from the phloem. Importantly, the high sucrose concentration in the phloem appeared disadvantageous for the ZmSUT1, preventing sucrose recovery from the apoplastic space in the fungus/plant interface. A hypothetical plant sugar transporter with the features of UmSrt1 would not increase plant´s performance, but instead deteriorate it.
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A NEW PLASTID TARGETING MECHANISM REVEALED BY THE SYSTEMIC DEFENSE-ASSOCIATED LIPID TRANSFER PROTEIN AZI1

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Right subcelular localization of defense factors is essential for the plant immune system. The mobile signal azelaic acid (AZA) together with the lipid transfer protein (LTP)-like AZI1 are key components for systemic resistance and the priming or immunological “memory” establishment. AZI1 allows the systemic movement and uptake of AZA in Arabidopsis plants. Localization studies indicate that a pool of AZI1 exists near the site of AZA production, in the chloroplast outer envelope. However, AZI1 does not possess a classical chloroplastic transit peptide that can explain its localization. Here, we show that this LTP-like and several members of the AZI1 family use an undescribed N-terminal signature that

allows the chloroplast targeting. We will present evidence that cytoskeleton integrity, protein kinases associated to defense and specific features of the AZI1 N-terminus mediate AZI1-plastid targeting. Interestingly, ~0.3 % of the Arabidopsis coded proteins display a similar N-terminal signature. The study of some of them corroborate their plastid localization although their organelle targeting is not predicted by standard algorithms. Moreover, because we observed that AZI1 play a role and localizes to root plastids, this signal may also be functioning in underground tissues. Taken together, our results suggest the existence of a novel mode of plastid targeting/trafficking possible related to defense responses.

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TGA CLASS II TRANSCRIPTION FACTORS NEGATIVELY REGULATE THE SALICYLIC ACID PRODUCTION UNDER STRESS

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Salicylic acid (SA) is a key hormone in the plant defense response. Under stress conditions, such as UV radiation, the increase in SA levels modulate changes in gene expression. TGA class II factors, that includes the functionally redundant TGA2, TGA5 and TGA6 proteins, are important mediators for transcription of SA-controlled genes. In a previous transcriptomic analysis via RNAseq, we found that mutant plants in TGA2 class II genes (*tga256* plants) treated with UVB radiation show increased expression of genes involved in SA accumulation, compared to wild type (WT) plants. To corroborate the participation of TGA class II on the SA-biosynthetic pathway, plants were irradiated with UVC, a well-known SA-inductor stress condition. Compared to WT, the *tga256* plants show a significant increase in the expression of genes involved in SA accumulation (*PAD4*, *EDS1*, *SARD1*, *ICS1* and *EDS5*). The same effect was observed at the ICS1 protein level, the main enzyme in SA biosynthesis under stress. We complemented *tga256* plants with a construct expressing the V5-tagged TGA2 protein controlled by a constitutive promoter (*tga256*/TGA2-V5 plants). In these plants, the levels of the mentioned transcripts and the ICS1 protein show similar levels after UVC than WT plants. We also evaluate the levels of SA and we found that, according with gene expression data, *tga256* plants show increased accumulation of the hormone under UVC treatments, and that the ICS1 pathway is responsible for this effect. Together, these results suggest that TGA class II factors negatively control SA production under stress conditions.

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POSTER ABSTRACTS

PS1

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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PS2

RESPONSE OF THE EUROPEAN GRAPEVINE MOTH *Lobesia botrana* TO VOLATILES EMITTED BY THE NON-HOST PLANT *Schinus polygamus* (CAV.) CABR. (ANACARDIACEAE)

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Insects modulate its behaviour through perception of environmental compounds. Its olfactory sense allows them to respond to the emission source, being attracted or repelled.

This mechanism is used in the development of tecniques for agricultural pest management. Lobesia botrana, the grapevine moth, is controlled by sexual confusion attracting the males with sexual feromone, in Chile. This latter promotes the search for attracters for the females of this plague. Essential plant oils are an important source of molecules capable of modulate insect behaviour. The objective of this work was to determine electrophysiological response of adults of L. botrana to volatile compounds released by S. polygamus with the goal of contribute to the integrated pest management. The essential oil was obtained from branches of S. polygamus by steam distillation and characterized by gas chromatography coupled to mass spectrometry. The adult electrophysiological response was determined by electroantennographic detection. Chemical characterization of the essential oil of *S. polygamus* showed the presence of some chemical compounds reported as attracters for *L. botrana* such as α-pinene, α-terpineol y cariofilene, with relative abundances of 23,41%, 3,73% y 1% respectively. Adittionally, a high abundance of limonene was determined (19.4), previously identified as kairomona for *L. botrana*. Males and females of *L. botrana* respond significately to the essential oil *S. polygamus* with depolarizations of 1,17 mV and 0,95 mV, respectively. Results indicate an attractive effect of *S. polygamus* volatiles for *L. botrana*. Compounds identified in the essential oil must be studied individually with the purpose of incorporate them to the integrative management of *L. botrana.*

PS3

DE NOVO TRANSCRIPTOME ASSEMBLY OF *Cistanthe longiscapa* TO EXPLORE GENE EXPRESSION UNDER ARID CONDITIONS IN THE ATACAMA DESERT

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Climate change is a current phenomenon that is affecting the biodiversity of species. Under this scenario, it is expected that extreme climates will intensify in the coming years, such as the increase in periods of extreme aridity. For this reason, the study of desert plants is relevant to explore possible adaptive mechanisms to deal with aridity. *Cistanthe longiscapa* is a native and abundant plant of the Atacama Desert. One of the aridity resistance mechanism of this plants seems to be the capacity to adapt their photosynthetic pathway, suggesting that *C. longiscapa* is a CAM facultative plant. The aim of this work was to obtain de novo transcriptome of *C. longiscapa* allowing the identification of aridity resistance genes and to find transcriptomic evidences that explain the adaptive physiological changes in the photosynthetic pathway. For this, we analyzed sequences obtained by RNA-seq from leaves of plants sampled in three locations, in two moments: post-sunset (night) and dawn (day). The assembly was done using the Trinity program and validated with BUSCO program. The assembled transcriptome was annotated with non-redundant NCBI

databases using BLASTx and sequence similarity networks. We performed a differential expression analysis to identify genes related to aridity resistance. Preliminary results shown several genes differentially expressed in the day/night experimental design, mostly associated to nocturnal stomata opening and dark phase photosynthesis, suggesting that a CAM cycle is predominately operating in this desert plant.
This work was support by FONDECYT 3150588, FONDAP-CRG 15090007 and Basal PB-16.

PS4

WHOLE GENOME SEQUENCING AND RNA-SEQ OF CONTRASTING SIBLINGS FOR MATURITY DATE IN PEACH TO UNDERSTAND THE GENETIC CONTROL FOR THIS TRAIT

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Maturity date (MD) is a crucial factor for marketing of fresh fruit, especially those with limited shelf-life such as peach: selection of several varieties with differing MD would be advantageous to cover and extend the marketing season. This trait is also interesting from the genetic point of view, because of several reports about a pleiotropic effect on other fruit quality traits. We constructed a genetic linkage map using a genotyping by sequencing strategy and performed a QTL analysis with the phenotyping data of three evaluation seasons for MD from F1 population (n=183). A saturated linkage map with 498 markers (marker density of 1.4 cM/marker) was built and five consistent QTL were detected on the chromosomes 1, 2, 5 and 6 of the peach genome. Using a whole genome sequencing of contrasting siblings for this trait, we identified 28,007 genetic variations on the QTL region of which 1,303 were found on genes. We performed an RNA-seq analysis and we identified 553 genes on QTL regions with putative functional effect. Finally, 43 genes are identified as candidates (12 transcription factors) but it is necessary to validate these genes in commercial varieties. The results obtained in this work are the basis to understand the MD genetic control.
This work was supported by Genoma 4 G13i1005, FONDECYT 1160584, Consorcio Biofrutales 13CTI-21520-SP03 and 13CTI-21520-SP04.

PS5

IDENTIFICATION OF CANDIDATE GENES ASSOCIATED WITH SOLUBLE SOLIDS CONTENT USING WHOLE GENOME SEQUENCING AND RNA-SEQ ANALYSIS IN *Prunus persica*

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Prunus persica is one of the most important fruit crops in the world considering production and cultivated area. For this reason, the Chilean peach exporter industry carry out several peach breeding programs to develop new varieties to satisfy the consumer`s needs. The soluble solids content (SSC) is one of the most important fruit quality traits for the consumer, and this character determine the fruit sweetness. We constructed a genetic linkage map using a genotyping by sequencing strategy and we performed a QTL analysis with the phenotypic data of three evaluation seasons from F1 population (n=182). A saturated linkage map with 498 markers and a marker density of 1.4 cM/marker was built and one consistent QTL of 5Mbp was identified on the chromosome 5 of the peach genome. Using a whole genome sequencing of contrasting siblings for this trait, we identified 7,301 genetic variations on the QTL region. We performed an RNA-Seq analysis to determine the differential expression of the genes between contrasting siblings for SSC, and we identified 239 DEG on detected QTL for this trait. Finally, 17 genes are postulated as SSC master regulators using the combination among genetic (QTL analysis), genomic (DNA-Seq) and transcriptomic (RNA-Seq) approaches. As second step, it is necessary to validate these candidate genes in other peach populations and commercial cultivars.
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PS6

IRON ACCUMULATION IN NUCLEI

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Iron is an essential micronutrient for plants. Different approaches have been used in order to study where iron localizes in plant organs and at subcellular level. In plants, iron accumulates in different compartments depending on the tissue and cell type. Among these are apoplast in root vasculature, plastids in leaves and pollen grains, vacuoles in embryos, and nuclei in different cell types. In early maturation stages (embryo in torpedo stage) iron was localized principally in nuclei of integument, endosperm and embryo cells. This result is very surprising, indicating that vacuoles are not the most important subcellular compartment for iron storage during seed development. In later stages, iron seems to be mobilized and gradually concentrated in structures surrounding the nuclei (possibly mitochondria or endoplasmic reticulum) before being load into the vacuoles of the endodermis cells. Our results suggest that nuclei may be a reservoir of iron during seed development. The presence of iron in the nuclei of other models is also shown.

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PS7

RNA-SEQ ANALYSIS OF POSTHARVEST BEHAVIOR IN KIWIFRUIT *Actinidia deliciosa* AFTER 1-MCP AND ETHREL APPLICATIONS

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Kiwifruits belong to *Actinidae* family and *Actinidia* genus which comprises several important varieties from the commercial point of view being the majority of them included in *A. deliciosa* var. *deliciosa* and *A. chinensis* planch. var. *chinensis*. 'Hayward' (*A. deliciosa)* is a green fleshy kiwi fruit the most commercialized in the world which is characterized for its hexaploid genome (6n = 174). Nowadays there is not much information about kiwi genome and the different ploidy between the kiwi species complicates the sequencing work. Recently has been reported a draft diploid genome of 'Hong Yang' (*A. chinensis*) and the assembled genome reaches a total length of 616.1Mb and contains 39,040 genes. The aim of this study is focused in a transcriptomic approach by RNAseq analyses of 'Hayward' kiwifruits treated with Ethrel (ethylene precursor) and 1-MCP (ethylene repressor) in order to identify significative genes related to softening and respiration rate using 'Hong Yang' as reference genome. We sequenced eighteen libraries by Illumina HiSeq 2500 platform and we obtained a total of 670.195.682 reads which were trimmed with FLEXBAR software for filtering low quality reads. Filtered sequences were aligned to *Actinidia chinensis* genome using Bowtie2 software. The alignment results showed around 70.72 % of reads aligned to *Actinidia chinensis* genome and 29.28 % were not aligned. Finally, 18,036 genes were differentially expressed from a total of 79,614 genes identified. This study has allowed us to identify genes related to the fruit maturation process of the Hayward kiwi variety, which will allow us to create a gene reference framework to focus new trials on other *Actinidia* species.

Keywords
Actinidia, Postharvest, RNAseq, 1-MCP, Ethrel
This work has been supported by FONDEF project N° D09i-1136, FONDAP CRG N° 150900007, FONDECYT postdoctoral N° 3160080 and FONDECYT Start into Research N° 11150662.

PS8

MONOFLORAL HONEY FROM THE GUINDO SANTO *(Eucryphia glutinosa).* A NATURAL FOOD ENDEMIC TO THE CHILEAN FOREST

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The chemical composition of honey is directly related to the nectar of the flowers visited by the bees.The Guindo Santo is an endemic bee plant species found in the mountain areas of the Regions of Maule, Bío-Bío and La Araucanía.This melisopalynological study to determine the botanical origin and quality of the honey through the physicochemical characteristics as established by the Chilean Standard was conducted on honeys from the geographic region of Alto Bío-Bío in the province Bío-Bío, Chile.The pollen results indicate that honey from the village of Pitril is of monofloral origin and consists mainly of *Eucryphia glutinosa* (62.9%), *Gevuina avellana* (9.7%), Myrtaceae (8.6%) and 12.5% of introduced species.The physicochemical parameters (pH, % humidity, % insoluble solids, hydroxymethylfurfural, % ash and electrical conductivity) comply with the ranges established by Chilean food safety regulations.Therefore, just as the antioxidant capacity and antimicrobial activity has been established in other Chilean monofloral honeys, such as that of *Eucryphia cordifolia* (Ulmo), which is from the same botanical family as *Eucryphia glutinosa*, this honey from Guindo Santo would also present added value as an endemic, natural food unique in terms of its origin, with potential application in medicine, and optimizing what is still a subsistence economy for a population of ethnocultural value also unique in the world, that of the Pewenche people.

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PS9

TRANSCRIPTIONAL RESPONSE IN ROOT OF CHERRY ROOTSTOCK MXM60 *(Prunus avium x P. mahaleb)* UNDER DROUGHT STRESS USING RNA SEQUENCING

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Sweet cherry trees are one of the most important crops in Chile and they are established in irrigated orchards. However, due to variations in the climate and the increased aridity, drought has become a major constraint, causing crop losses wordwide. In general, sweet cherry trees are grafted on rootstocks (same or other species or interspecific hybrids of the *Prunus* genus) that determine, in part, their tolerance to drought stress. However, the transcriptomic changes and molecular mechanisms that underlie the adaptation of cherry rootstocks to water shortages are poorly understood. Therefore, 6 RNA libraries from roots of non-stressed control and drought-stressed MxM 60 plants grafted with "Bing" cultivar were constructed and sequenced. We generated 279 M raw reads which allowed "*de novo*" assembly of 49,772 genes and 107,000 transcripts with a medium average of 1308 bp. Compared with non-stressed plants, 829 genes were differentially expressed (DEGs; logFC>=2, FDR<=0.01) in the drought-stressed plants, including 419 up-regulated and 410

down-regulated transcripts. The DEGs were functionally annotated with 71 gene ontology (GO) terms. The most represented "biological process" subcategories were response to stimulus/ to abiotic stimulus/ to water and response to stress; in "cellular component" the main subcategories were cell, cell part and membranes whereas in "molecular function" most of DETs were in protein seronine/threonine kinase activity subcategory. The reliability of the RNA-seq experiment is being validated by analyzing the expression patterns of 25 DEGs using qPCR. Our result represents a valuable source of information for further studies to identify the real mechanism and genes that define drought tolerance in *Prunus*.

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PS10

AtZAT4, A C_2H_2-TYPE ZINC FINGER TRANSCRIPTION FACTOR FROM *Arabidopsis thaliana*, SEEMS TO BE INVOLVED IN POLLEN AND SEED DEVELOPMENT

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In flowering plants the male gametophyte plays a key role in the plant fertility and crop production, being essential for the generation and delivery of the sperm-cells for double fertilization, event that leads to embryo and endosperm formation during seed development. After stamen primordia specification, controlled by the B and C type MADS-box transcription factors, anther-development occurs and gametophytic and sporophytic tissues communicate and participate co-operatively in pollen-development. Several downstream-acting transcription factors are involved in regulation of anther and pollen morphogenesis, modulating the expression of specific genes of male germline. Among them, key roles are played by C_2H_2-type zinc-finger transcription factors (ZF-TFs) as determined either in *Arabidopsis thaliana* as well as in *Petunia hybrida*. In this work we analyze the role of *AtZAT4* which codes for this type of ZF-TFs in *A. thaliana*. A tissue-specific *AtZAT4* expression has been observed, being the transcriptional activity restricted to mature-flowers and seeds. Because the unviability of the homozygous-insertional mutant (*Atzat4*-/-), the phenotypic characterization of a heterozygous-insertional mutant (*Atzat4*+/-) was performed. While the development of vegetative tissues seems to be not affected, impairment in pollen-development was detected. The *in vitro* pollen germination assay shows a significant reduction in the rates of germination and pollen tube elongation in the *Atzat4*+/- mutants, however pollen viability, shows no significant difference. Therefore, as expected, the fertility in *Atzat4*+/- plants is lower than in the wild-type. In agreement with these results a significant reduction in the number of seeds per silique was determined in the *Atzat4*+/- mutant. The results suggest an essential role for AtZAT4 in both, pollen and seed development. Experiments to identify downstream target genes are in progress.

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PS11

A GENOME-SCALE METABOLIC RECONSTRUCTION MODEL OF THE PHYTOPATHOGENS *Pseudomonas syringae* pv. tomato DC3000

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Pseudomonas syringae is a phytopathogenic proteobacterium capable of infecting a wide range of plant species. It is employed as a model bacterial strain to understand plant-pathogen interaction**,** aiming at finding new targets to combat plant diseases. Its genome sequence was released in 2003, opening new avenues to understand the metabolic response of this versatile microorganism at a system level. To fully comprehend the metabolic capabilities of this microorganism requires a mathematical framework, where the reconstruction of a genome-scale metabolic model allows the integration of experimental data, genomic data, and high-throughput technologies. This work presents the first draft of the metabolic model at the genomic scale of *P. syringae* pv. tomato DC3000, which was built based on genomic, biochemical and physiological information. The *in-silico* strain (iPS1576) contains a total of 1202 genes (21.51% of the genome), 1576 metabolic reactions, of which 1282 gene–protein-reaction associations (81.35% of the total reactions of the model), and 1258 metabolites. The predictive potential of the model was challenged using experimental data from growth experiments on glucose as carbon source in batch and chemostat cultures. The genomic scale model can accurate predict the specific growth rate (~94%) of *P.* syringae pv. tomate DC3000. Therefore, the iPS1576 model will serve as a basis for understanding the complex interplay among different molecular levels with the aim to predict the resulting phenotype under different growth conditions, including inside its host plants, tomato and Arabidopsis.

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PS12

DECREASE OF AUXIN LEVELS IN FLOWERS AND POLLEN LEADS TO ABNORMAL DEVELOPMENT IN *Arabidopsis thaliana.*

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The phytohormone auxin is one of the most important molecules involved in plant development. Three-indole acetic acid (IAA) is the auxin with greater preponderance in the whole plant. The role of this hormone has been largely described during sporophytic development, but also IAA has an important role in reproductive tissues, particularly in flower development. It has been described that Arabidopsismutants defective in auxin

biosynthesis or perception, display abnormal phenotypes affecting flower morphology, stamen filament elongation, anther maturation, and the correct development of pollen grains. Interestingly, 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 literature 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 were manipulated in the whole flower using flowers grown *in vitro* and treated with PPBo, a chemical compound that inhibits the auxin biosynthesis through YUCCA genes. On the other hand, the auxin levels in pollen grains also 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 lysine, inactivating the hormone. Transgenic plants expressing this construction present phenotypes in flowers, including shorter stamen filaments, loss of short stamens and problem with pollen viability. These results suggest that auxin present in pollen grain would be important to regulate flower development, suggesting a novel role for pollen in reproductive development.
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PS13

SUBNUCLEAR LOCALIZATION OF THE MBD4L DNA GLYCOSYLASE SPLICING ISOFORMS

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DNA glycosylases are key enzymes for organisms' genome stability mediating DNA damage repair. Among them, MBD4L is a nuclear *Arabidopsis* DNA glycosylase acting during stress conditions. Interestingly, *MBD4L* gene can generate two-isoforms through the retention of a protein-coding cryptic intron (exitron). It is believed that exitron splicing events result in protein versions with alternative functional domains and/or post-translational modifications. Taking this into account, we analyzed MBD4L splicing-isoforms transcript levels, subcelular localization and contribution to damaged DNA correction. We found that the *MBD4L* alternative transcripts changed their relative levels depending on the stress applied. Surprisingly, when expressed as GFP fusions each of the MBD4 isoforms located at different subnuclear compartments in both *Arabidopsis* and *Nicotiana benthamiana* plants. Moreover, some stresses induced dynamic changes in enzyme subnuclear localization. On the other hand, although showing distinctive localization the overexpression of both MBD4L isoforms increased resistance to a DNA damaging agent. Altogether, our results indicate that MBD4L location can be driven by exitron alternative

splicing mechanisms. However, additional levels of control may determine differential subcellular requirements for MBD4L isoforms under particular circumstances. A putative model for MBD4L nuclear role/localization will be presented.

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PS14

CLONAL IDENTIFICATION OF *Vitis vinifera* CV CABERNET SAUVIGNON USING WHOLE GENOME SEQUENCING

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Grapevine is one of the most economically important fruit crops and Chile is the fifth world wine exporter. There are many grape collections and 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, clone 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. We have sequenced eleven 'Cabernet Sauvignon' clones from two Chilean wineries and obtained reads were mapped against 'Cabernet Sauvignon' genome, which was recently assembled using PacBio sequences. We expect to develop molecular markers to implement high-throughput genotyping methodologies using amplicon sequencing. The 99% of reads were mapped to the 'Cabernet Sauvignon' reference genome and an average of 3,500,000 total variants were detected between clones with a SNP frequency around 6 SNP/kbp. The comparison among all clones by PCA shows that exists some genomic differences between them. We expect to design 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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PS15

CYTOKININ IN STONE FRUITS: COMPARATIVE ANALYSIS OF CYTOKININ MODULATED GENES IN SWEET CHERRY (*Prunus avium*) AND PEACH (*Prunus persica*) FRUITS

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The non-climateric fruit, sweet cherry and the climateric fruit, peach, are Chilean high yield export crops. The international demand for these stone fruits, fresh and processed, is due to the nutritional and bioactive/medicinal properties that they contain. These desirable traits, formed during fruit maturity/ripening, are mediated by phytohormones, such as cytokinin. Recently, meta-analyses in *Arabidopsis* have revealed a conserved group of the "top 25 cytokinin-induced genes", many of which are also conserved in rice. In order to further understand the role of cytokinin in fruit maturity/ripening, the objective of this work was to 1) identify putative orthologs of these "top 25 cytokinin-induced genes" in sweet cherry and peach, 2) determine if exogenous application of cytokinin modulates the expression of these putative orthologs in fruits, 3) identify conservations and divergences in the genomic *loci* of these putative orthologs in both stone fruits. Using bidirectional blasts we have identified many putative orthologs of the "top 25 cytokinin-induced genes" in sweet cherries and peaches. Analyses of gene expression, using qPCR analyses and exploratory RNA-seq analyses, reveals a modulation in gene expression of several of these orthologs in response to exogenous application of cytokinin. Comparative analyses, of the sweet cherry and peach genomic *loci* of these orthologs, reveal conservations and divergences of several known *cis*-acting elements. By further studying these conserved and divergent *loci*, we may begin to better understand the role of cytokinin in fruit maturity/ripening and how this role has diversified between climateric and non-climateric fruits.

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PS16

GENETIC IMPROVEMENT OF DURUM WHEAT (*Triticum turgidum* L.var *durum*) GLUTEN QUALITY

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Wheat is one is the most important crop cultivated worldwide. Durum wheat (*Triticum turgidum* L. var. *durum*) is a tetraploid species used in pasta production. Grain quality is an important feature that encompasses nutritional value, yellowness, protein content and strength. For high quality pasta industrial purposes, the factors commonly accepted include rounded and vitreous kernel, high protein content (around 15%) and gluten strength. Gluten accounts for over 80% of the seed protein, and gluten is associated to gliadins and glutenins. The genetic control of the strength and extensibility in the dough is strong and depends mainly on the composition of gliadins and glutenins, with the latter being the most influential. Glutenins are divided in High Molecular Weight (HMWGs) and Low Molecular Weight subunits (LMWGs), being the former codified by *Glu-A1* and *Glu-B1*, and the latter by *Glu-A3*, *Glu- B3* and *Glu-B2*. A population comprising 288 durum wheat genotypes around the world were grown and cultivated in the 2016-2017 season in two locations, Pirque (Metropolitan Region) and Chillán (Bío-Bío Region), in order to analyze different

gluten parameters evaluating the influence of the environment on them. The gluten index is a measure of the gluten characteristics, which indicates whether the gluten is weak, normal or strong. Our results show that gluten index ranged between 1 and 97 in Pirque, whereas they varied between 1 and 99 in Chillán, being the number of genotypes with optimal gluten index values higher in Chillán. Thus, higher overall gluten quality was reported in Chillán.

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PS17

IDENTIFICATION, CLONING AND EXPRESSION PATTERNS OF *Fragaria chiloensis* NAC TRANSCRIPTION FACTOR

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Fragaria chiloensis is an endemic rosacea from Chile, being its fruit intense in flavor, attractive color and pleasant aroma. However, the fast fruit softening is one of the main problems. One NAM, ATAF1,2, and CUC gene was isolated from fruit tissues, encoding 332 amino acids. The protein contains the conserved NAC domain, subdivided into 5 sub-domains. High evolutionary proximity with others NAC transcription factors related to secondary wall formation was identified. The transcription profile at different fruit stages of maturation and vegetative tissues is reported, as well as, a structural model of FcNAC1 built by comparative modeling, and showing the highly conserved NAC domain in the amino terminal region. A 1,488 bp of the *FcNAC1* promoter and *in-silico* analysis with the presence of cis elements to hormonal responses is reported. The expression response of *FcNAC1* under hormonal treatments in fruit and using dual luciferase assay were able to determine the transcriptional activation of a promoter sequence from one gene related to cell wall remodeling. The involvement of NAC during fruit softening and senescence is still unknown, and these data allow the understanding for this biological process of particular commercial interest.

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PS18

EFFECT OF ABSCISIC ACID EXOGENOUS APPLICATION ON APPLE TREES ANTIOXIDANT METABOLISM AND PHOTOSYNTHESIS

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Fruit trees are frequently exposed to adverse environmental conditions which affect its optimal development. Abscisic acid (ABA) is a hormone involved in abiotic stress responses in plants. In apple trees, ABA has been reported as an antioxidant substances promoter. However, ABA also induces stomatal closure which may affect photosynthesis. Our objective was to determine the effect of ABA applications on "Granny Smith" apple trees (*Malus domestica* Borkh.) on antioxidant metabolites production and the effect on photosynthesis and vegetative development. ABA treatments consisted in three applications of ABA 400 ppm on five plants during three months since December to February. Five untreated plants were left for control. In leaves tissues, no significant differences ($p \leq 0.05$) were found in lipid peroxidation, antioxidant capacity and total polyphenols. ABA applications decreased 6% photosystem II (PSII) maximum quantum efficiency but did not affect chlorophylls and carotenoids contents. Stomatal conductance in treated leaves decreased from 169 to 64 µmol H_2O m^{-2} s^{-1} with a reduction of net photosynthesis (Pn). Control leaves Pn was 16.8 µmol CO_2 m^{-2} s^{-1}, while in, treated leaves, was 8.6 µmol CO_2 m^{-2} s^{-1}. Consequently, specific foliar mass and foliar area decreased in control and ABA treated leaves 11% and 16%, respectively. ABA application did not promote changes in tissues antioxidative state but it induced stomatal closure and Pn decrease, which negatively affected vegetative development.
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PS19

MOLECULAR CHARACTERIZATION OF *HYPOXIA INDUCED GENE DOMAIN* (*HIGD*) GENES IN *Prunus* ROOTSTOCKS UNDER HYPOXIA AND OTHER ABIOTIC STRESSES

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Root hypoxia produced by flooding or over-irrigation limits stone fruit tree development, particularly in orchards established on soils with restricted drainage. To overcome this problem, stone fruit trees are usually grafted on rootstocks (species or hybrid of the *Prunus* L. genus) with different degrees of tolerance to root hypoxia. In order to gain insights into the molecular basis of stone fruit rootstock responses to low-oxygen environments, we performed a large-scale transcriptome sequencing of roots from two different stone fruit rootstocks with contrasting responses to hypoxia. Among the flooding-responsive genes, we selected two outstanding candidate genes induced by hypoxia, *HIGD1* (*Hypoxia-Induced Gene Domain 1*) and *HIGD2*. *Prunus HIGD1* and *HIGD2* codified for small proteins of 78 and 97 amino acids, respectively. The expression of *HIGD1* and *HIGD2* genes was

differentially regulated by root hypoxia and *HIGD2* gene had higher expression levels in roots of tolerant rootstock. Furthermore, *HIGD1* and *HIGD2* expressions were regulated by other abiotic stresses (high and low temperatures, salt and drought) and hormonal treatments (ABA, IBA, AIA, NO, GA3, ethylene, hydrogen peroxide) suggesting a broad role in abiotic stress response in plants. Transient expression assays showed that *Prunus* HIGD1 and HIGD2 GFP-tagged proteins were localized in the plasma membrane. Over-expression of *HIGD1* in Arabidopsis confirmed their subcellular localization and their effect(s) on plant survival under hypoxia is under analysis. Our results suggest that changes in *HIGDs* expressions could be part of the adaptive mechanisms that have evolved in the *Prunus* species to survive under hypoxia or other types of environmental stress that commonly challenge stone fruit tree orchards.

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PS20

CHALCONE SYNTHASE FROM *Deschampsia antarctica*: ISOLATION AND CHARACTERIZATION OF THE GENE AND STRUCTURAL MODEL OF THE PROTEIN

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Deschampsia antarctica is a perennial grass native to Antarctica. It is a vascular flowering plant that has colonized some islands in the Antarctic peninsula and the southernmost parts of Argentina and Chile. It is naturally exposed to very harsh environmental conditions such as high levels of UV radiation and low temperatures that induce oxidative stress. Previous studies have shown that this species is well adapted to such adverse environment, which may be related to the accumulation of leaf flavonoids. Flavonoids derived from the phenylpropanoid pathway. Because of their absorptive properties they may be involved in plant protection against UV-B radiation. In this context, the gene coding for Chalcone synthase (CHS), one of the precursor enzymes of flavonoids biosynthesis, was isolated and characterized. *DaCHS* isolated from *D. Antarctica* consisted in 1197 bp, coding for a protein of 397 residues. It shares high homology with *CHS* from other monocots, and it is closely related to *CHS1* from *Hordeum vulgare*. The DaCHS protein sequence displayed the two domains of CHS. It contains all the catalytic residues which have been reported to be essential for catalytic activity, and also shares those involved in the formation of the active site pocket. The protein structure of DaCHS was obtained through homology modeling: the catalytic residues are displayed correctly into the active site. Few amino acid residues differ from the *H. vulgare´*s CHS but they are located far from the catalytic core. The data indicates that *DaCHS* could be involved in flavonols biosynthesis.

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PS21

CALLOGENESIS FROM *Prunus persica IN VITRO* LEAVES, THROUGH DIFFERENT GROWTH REGULATORS

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Prunus persica (L.) Batsch (peach) is a fruity-tree that belong to Rosaceae family. Peaches are one of the most worldwide consumed fruit, having in Chile a commercial exportation higher than kiwis and several berries. Currently, this specie is propagated by clonal lignified cuttings in nurseries, but this technique is limited to season (once a year) and also susceptible to pathogen infections in mother plants. For this reason, is necessary new plant replication sources that guarantee healthy status sanitation. One of this, is *in vitro* plant propagation obtained from somatic embryos that will permit clonal selection in sub-cultures and pathogen free tissue. The first step to obtain these embryos are a cellular callus formation (callogenesis) from a dedifferentiate plant tissue. This process is possible using external plant growth regulators control, as auxins and cytokinins. The aim of this research, was investigated the callogenesis induction from peach *in vitro* leaves in woody plant medium (WPM) supplemented with the auxin 2,4-D (1.2 mg/mL) and two cytokinins commonly used for callus formation: Kinetin (KN) or Thidiazuron (TDZ) at three different concentrations (0.5, 1.0 and 1.5 mg/mL). We observed callogenesis at day 46 from induction. Tukey test results demonstrate that the best hormone and concentration (plus 2,4-D) was Kinetin with no significant differences between concentrations. This is the first report of callogenesis from peaches *in vitro* leaves and using these two cytokinins. Our future investigation will consider somatic embryo generation from this cellular callus.
Sponsored by Biotechnology And Biochemical Laboratory.

PS22

TRANSCRIPTION FACTOR IDENTIFIED IN *Pinus radiata* D.DON OVER-EXPRESSED IN *Arabidopsis thaliana* AFFECTS THE EXPRESSION OF OTHER TRANSCRIPTION FACTORS RELATED TO STRESS

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PrMADS10 is a transcription factor isolated from *Pinus radiata* D. Don, described as differentially expressed in response to inclination (2 hours after treatment). MADS box TF have been associated to flowering and pine cone formation, but none has reported a role in stems. This radiata pine TF was expressed in one side of the trunk on inclined trees. PrMADS10 gene was overexpressed in *Arabidopsis thaliana* in order to identify its role in modulating gene associated to cell wall formation and other transcription factors. Up and down regulated genes were identified using the Affymetrix AraGene chip. A total of 1211 genes were modulated, from which 689 genes up regulated and 529 genes down

regulated. A general view of differentially expressed genes was created using MapMan. At least seventy transcription factors were modulated in their expression, from which twenty TFs were down regulated. Considering the fifty top up and down regulated genes, stress genes and transcription factors related to stress was analyze. *In silico* analysis of putative Cis elements binding to MADS-box was done with PlanPan 2.0 and Jaspar. We build a network with GeneMania in order to observe the co-expression and interaction between them. Finally, a hierarchical relationship from *PrMADS*10 to other transcription factor families like bZIP, HB and AS2 for up regulated; and, C2C2-CO-like, WRKY, JUMONJI and MYB for down regulated was build. We don´t observe phenotypic change in plant, it is possible to counteract the effects, however, by performing an overexpression in an inducible construct, the modulation of PrMADS10 over other TFs can be better clarified.

PS23

EFFECT OF ABSCISIC ACID (ABA) APPLICATIONS ON CRACKING TOLERANCE AND CUTICLE WAX COMPOSITION OF SWEET CHERRY (CV. BING)

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Rain-induced cherry fruit cracking is one of the main problems in cherry industry around the world. Different studies indicate that the primary cause of this problem is related to the increase of fruit size and the cessation of cuticular membrane components during fruit development. Abscisic acid (ABA) is an important phytohormone that promote the development and ripening of this non-climacteric fruit and the synthesis of fruit cuticular components. In order to evaluate the effect of this hormone on fruit cuticle wax composition and fruit cracking tolerance, ABA (0.1 mM) was applied during different stages of fruit development (fruit set, fruit embryo hardening and fruit color change). The results showed that the application promoted an increase the biosynthesis of C 29 alkanes and had positive effects on fruit cracking tolerance.

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PS24

UNDERSTANDING THE TOPOLOGY OF THE SYNTHESIS OF UDP-ARABINOFURANOSE AND ITS IMPACT ON THE ARABIDOPSIS SEED COAT MUCILAGE BIOSYNTHESIS

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Pectins are one of the main components of the plant cell wall non-cellulosic polysaccharides and regulates plant cellular growth and development. The monosaccharide L-arabinose is

present as a-(1®5)-L-arabinan side chains of pectic rhamnogalacturonan I and II, arabinogalactan proteins and extensins. The arabinan side chains synthesis takes place in the Golgi Apparatus by glycosyltransferases that use specifically the UDP-arabinofuranose (UDP-Ara*f*) rather than the more abundant UDP-arabinopiranose (UDP-Ara*p*) conformation. The interconversion between both conformations (UDP-Ara*p*/Ara*f*) seems to be carried out by UDP-arabinofuranose mutase (UAM) enzymes which are located at the cytosol. Indeed, it was believed that UDP-Ara*p* synthesized in the lumen of the Golgi is translocated into the cytosol to be converted into UDP-Ara*f* by UAM protein complexes, and then UDP-Ara*f* is translocated into the Golgi Apparatus for arabinan polymerization. One possible explanation is that the interconversion of UDP-Arap/Araf by UAM is strongly directed to the formation of UDP-Ara*p*, therefore the UAM compartmentalization seems to be a key process to ensure the UDP-Ara*f* synthesis. The aim of this work is to study the effect on the cell wall composition and architecture of the translocation of UAM into the Golgi lumen. In addition, we seek to clarify the formation of UAM-associated protein complexes that would assist the synthesis and utilization of UDP-Ara*f*. To perform the study, we will use the Arabidopsis seed mucilage as a tool to investigate pectin biosynthesis as a cell wall model, since the loss of function of several UAM revealed a less adherent mucilage seed coat.
Fondecyt: 3170796; Fondecyt: 1151335.

PS25

A *DE NOVO* TRANSCRIPTOME ANALYSIS IDENTIFIES SOME TRANCRIPTION FACTORS INVOLVED DURING THE RESPONSE OF RADIATA PINE SEEDLINGS TO INCLINATION

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Wood formation is a complex process particularly because when trees are exposed to some external factors such as wind or snow the normal vertical growth of the stems can be altered. Lost of stem verticality promotes the formation of compression wood, which induce morphological changes in the active cells of trunk. The understanding of the molecular mechanism involved in the response to inclination remains unclear, even the research efforts to identify the genes involved. With the aim to identify molecular players, a *de novo* transcriptome analysis was performed through Illumina technology using stem tissues from one year-old radiata pine seedlings (*Pinus radiata* D. Don) subjected to 45° inclination. Stems were longitudinally divided into upper and lower halves; samples were collected after 2.5, 10 and 24 h of inclination and RNAseq libraries were built. A total of 101,575 contigs were assembled, with a N50 of 1,831 bp. By using Augustus prediction 54,192 full-length transcripts were obtained. Biochemical pathways charts were built considering all genes from the libraries. Differential expression analysis was performed using EdgeR comparing all conditions, reducing the list to 804 differentially expressed contigs and also validated by qRT-PCR. Among them, 21 transcription factors (TF) were identified belonging to different families. TFs such as bHLH, GATA and GRAS, which have been described to be involved in cell wall modification during stress, could be coordinating the gravitropic response on pine seedlings.

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PS26

SNP AND INDEL VARIANT CALLING USING GBS AND WHOLE GENOME SEQUENCING IN PARENTS AND F1 POPULATION FROM A JAPANESE PLUM (*Prunus salicina* l.) BIPARENTAL CROSS.

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Japanese plum (*Prunus salicina* L.) is a diploid member of the Rosaceae family and an interesting target for fruit genetic improvement. NGS platforms offer determination of large amounts of sequence data, allowing to construct a more complete picture of the genomic variants in different varieties, crucial information to identify Quantitative Trait *Loci* (QTL) and genetic markers for assisted selection. In this work, our aim was to identify robust variants using previously reported GBS-dataset from a F1 progeny (<98-99xAngeleno>; Salazar et al, 2017), as well as resequencing information of the corresponding parents. Initial GBS dataset (735330418 reads) were processed in the Tassel 3.0 GBS pipeline, using *P.persica* v2.0 genome as reference, generating a final set of 43233 SNPs. After filtering for depth (> 5x) and allelic dosage of the corresponding reads, we obtained a set of 7429 segregating SNPs. To provide a comprehensive view of variants segregating in this population, we performed re-sequencing of progenitors using Illumina HiSeq4000, obtaining 313 Gb (313048618 reads) and 316 Gb (316265506 reads) for 98-99 and Angeleno, respectively. After trimming and filtering with CLC Genomics Workbench (Qiagen), we obtained 294408916 and 299709186 reads for 98-99 and Angeleno, respectively (average depth: 141x). Using the bioinformatics tools above mentioned, we merged GBS and re-sequencing datasets in order to call SNP variants present on both, obtaining an unfiltered dataset of 35320 markers. Moreover, using Pindel software, we have identified 249054 insertions and 359571 deletions considering both parents (2-900 bp). All these data are being used for fine-mapping of mutations responsible for variation in traits of commercial and nutritional importance, thus assisting to enhance Chilean fruit competitiveness from genomics.

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PS27

CHARACTERIZATION OF PHYSIOLOGICAL PARAMETERS IN *Prunus avium* IN VEGETATIVE TO DORMANCY STAGES

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Chile is the most important sweet cherry exporter in the Southern hemisphere in counter-season. This perennial fruit species presents an annual cyclical behavior. In summer, the flower buds are determined; in autumn, the tree suffers leaf abscission and enters to dormancy until the end of winter. In the dormancy stage, the buds remain closed and should accumulate chilling hours to bloom in spring. Therefore, the carbon assimilated during the vegetative period are stored in trunk and roots tissues as reserves being determinant to maintain tree metabolism during dormancy and at very first events flowering and fruit set that precede the development of new photosynthetic leaves. We characterize photosynthetic parameters in two sweet cherry varieties, '210' an early flowering and "Regina" a late flowering variety during the active vegetative and senescence to dormancy periods. The results showed that carbon assimilation (*A)* and transpiration (*E*) rates were higher in the vegetative phase compared to senescence, being the late variety the one with highest rates. These results agree with the chlorophyll fluorescence parameters measured, which reach their highest efficiency in the vegetative stage. As they reach dormancy, both varieties showed a decrease in *A* and *E*, and an increase in stomata conductance (g_s) and internal mesophyll carbon (C_i). The dormancy entry for '210' was two weeks before 'Regina', where both correlated with the decrease of photochemical quenching (qP), electron transport rate (ETR) and an increase in non-controlled photochemical quenching (qN), while controlled non-photochemical quenching remained constant during the whole period. In conclusion, a lower photosynthetic rate correlates with the variety, reflecting dormancy entrance.

CORFO 13CTI21520-SP05.

PS28

UNCOVERING C2H2 ZINC-FINGER PROTEINS ENCODED GENES IN GRAPEVINE GENOME (*Vitis vinifera* L.). THE GENE FAMILY IDENTIFICATION, PHYLOGENETIC RELATIONSHIPS AND EXPRESSION PROFILE REVEAL POSSIBLY PARTICIPATION IN REGULATION OF DEVELOPMENTAL PROCESSES

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The C2H2 **z**inc-**f**inger **p**roteins (ZFP) are a large gene family in plants involved in growth and development regulation, as well as in biotic and abiotic stress responses. To date, the genome-wide identification and characterization of this family was performed in *Arabidopsis thaliana* and other model plants, but no study has been reported in grapevine (*Vitis vinifera* L.). In this study, we executed the genome-wide identification of all grapevine *ZFP* family members (*VviZFP* family), searching in grapevine deduced proteome using HMM analysis. In addition, we report the intron-exon organization, conserved domains in protein primary structure and phylogenetic relationships to infer about the evolutionary origin of *VviZFP* gene family. Besides, an *in silico* gene expression profiling

and GO-enrichment analysis was realized in order to know more about the molecular role of *VviZFP* in plant development. A total of 94 putative grapevine-ZFP were identified and renamed on the basis of respective genomic distribution. This genomic distribution reveal seven VviZFP genes clusters possibly originated from tandem duplication events. Furthermore, the phylogenetic and structural analysis of VviZFP shows a high heterogeneity in length, number of zinc-finger (ZF) domain and presence of conserved regions like Jumanji domains (JmjC and JmjN) or EXOIII domains. Moreover, the frequency of NLS and EAR domains confirm the structure reported in other plant models. Finally, the genome-wide microarray based gene expression analysis has revealed three clusters of differential expression indicating that *VviZFP* genes could be involved in tendril, leaf, flower and fruit development stages in grapevine. Our work provides a basis for future studies of the *VviZFP* gene family evolution and to deepen in the characterization of candidates that regulate specific grapevine development processes.

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PS29

TGA FACTOR-MEDIATED REGULATION OF KEY GENES IN THE SALICYLIC ACID BIOSYNTHESIS PATHWAY.

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Salicylic acid (SA) is an essential phytohormone in the establishment of immune responses against pathogens and other abiotic stress conditions. While SA accumulation plays a key role in these responses, elevated and sustained cellular levels lead to developmental issues and general stress, and so the regulation of its synthesis and accumulation is critical for plant fitness. The biosynthesis of SA is mainly achieved through the isochorismate pathway, which relies on the enzyme isochorismate synthase (ICS1). The expression of *ICS1* has been reported to be under the control of two partially redundant transcription factors which act as positive regulators, SARD1 and CBP60g. Furthermore, other proteins have been described to play a determining role in the accumulation of SA, such as PAD4, EDS1 and EDS5. On the other hand, SA-dependent signaling cascade and gene regulation has been described as being mainly under the control of the transcription factors TGA2, TGA5 and TGA6 (clade II TGAs). These factors have been described as downstream players of the SA signaling pathway, controlling the expression of hundreds of stress and pathogen related genes. However, in this work we show that Arabidopsis plants which are mutant in these factors (*tga256*) show elevated expression of several genes involved in SA biosynthesis, including ICS1, SARD1, EDS5 and PAD4. This would point to an upstream, non-canonic participation of the clade II TGA factors. To further elucidate this relationship, we performed a bioinformatic search for putative TGA recognition sequences in the promoters of these

deregulated genes. In parallel, we also complemented *tga256* lines with TGA2-V5 to evaluate, by ChIP-qPCR analysis, the possible binding of this factor to the aforementioned promoters.

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PS30

DEVELOPMENT OF CALLOGENESIS IN *Colobanthus quitensis (Kunth) Bartl.*

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Colobanthus quitensis (Kunth) Bartl. (Caryophyllaceae) is one of the two angiosperms to have naturally colonized the Antarctic continent, overcoming both geographical and environmental obstacles. It has been considered a species that is not feasible and difficult to maintain in *in vitro* culture, requiring the development of new establishment strategies under controlled conditions. Tissue culture is indispensable in the maintenance and conservation of genotypes, particularly when conventional propagation methods prove to be difficult. The controlled environment of *in vitro* culture provides a more effective way of regenerating seedlings, achieved through direct or indirect morphogenesis. The latter is done through a callus intermediate stage, resulting in a greater number of propagules. Callus induction has not been reported in *C. quitensis*; however, it has been reported in species belonging to the same family. The objective of this work was to achieve callus induction in populations of *C. quitensis*. The Conguillio (pC) continental population and the Arctowski (pA) island population were studied. Seeds, hypocotyls, and shoots were used as explants, and callus induction was performed in MS medium in the presence of different picloram and 2.4-D concentrations. Callus were recorded after one month and with both hormones, but only 2.4-D induced callus were friable. Callus formed on all explants, with the highest induction in hypocotyls, followed by shoots, and lastly seeds, which only produced callus in pA. These results will enable the development of new strategies for the propagation and conservation of *C. quitensis* in our laboratorys Active Germplasm of Antarctic Plants.

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PS31

EFFECTS OF FE^{3+} IONS ON *IN VITRO* GERMINATION OF *Colobanthus quitensis*

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Iron is an essential nutrient for plants that is necessary for life-sustaining processes such as respiration and photosynthesis. It participates in the transfer of electrons through reversible redox reactions, cycling between Fe^{2+} and Fe^{3+}. The main effects of heavy metals on seeds are manifested by general anomalies, decreased germination and reduced elongation of roots and shoots, leading to seed toxicity and loss of productivity. *Colobanthus quitensis* (Kunth) Bartl (Caryophyllaceae) extends its range of distribution from the Antarctic continent to southern Mexico. Many ecophysiological and molecular studies have been performed on *C. quitensis* due to its adaptability to adverse conditions such as extreme temperatures, high incidence of UV rays and salinity, acidic soils and insufficient water and nutrients. High levels of Fe have recently been observed in tissues of this species, thus the objective of this study is to evaluate the effect of Fe^{3+} ions on the germination of *C. quitensis*. The seeds were maintained for 32 days in an MS medium supplemented with Iron Chloride ($FeCl_3 \cdot 6H_2O$) at concentrations of Fe^{3+} ions of 100µM and 500µM. The concentrations of Fe^{3+} ions evaluated did not produce significant differences in percentage or mean time (GT_{50}) of germination, but there were significant differences in leaf and root morphology of germinated seedlings in 500µM Fe^{3+}.
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PS32

INTEGRATIVE TRANSCRIPTOME ANALYSIS REVEALS THE GENE EXPRESSION NETWORKS UNDERLYING SULFATE RESPONSE IN *Arabidopsis thaliana*

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Sulfur is an essential nutrient for plant growth and development, forming part of proteins, the plasma membrane and cell walls among others important cellular components. In plants, sulfate is the primary sulfur source to synthesize these sulfur-containing biomolecules and, therefore, numerous efforts have been carried out to identify genes responsible for their transport and assimilation in several plant species. However, little is known about the transcriptional regulation of sulfate assimilation including the model plant *Arabidopsis thaliana*. In order to obtain new insights into the gene regulatory networks underlying sulfate response, we performed an integrative meta-analysis of transcriptomic data from sulfate-availability experiments of five different laboratories. We identified a group of 27 genes that were differentially expressed by sulfate in all experiments analyzed,

indicating that these genes have an important role for sulfate response. Analysis of the most consistent biological functions in sulfate experiments highlights biological processes not studied before in the context of sulfate response such as cell wall biosynthesis, response to stress and carbon/nitrogen metabolism. Gene co-expression network analysis uncovered relationships between sulfate-responsive genes distributed in seven functional specific co-expression modules. Gene expression patterns of these modules suggests that sulfate starvation signals activate the expression of genes related with sulfate assimilation and repress genes related with secondary sulfur metabolism. We identified new candidate genes and provided new hypothesis to advance in our understanding of the transcriptional regulation of sulfate metabolism in plants.
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PS33

THE BLOOD-FLESH PEACH AND ITS ANTIOXIDANT PROPERTIES

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The blood-flesh peach is a type of red pulp peach, whose populations in Chile are distributed between the O'Higgins and Araucanía regions. The fruit trees are not very well known because its production is limited to home gardens, for own consumption, such as fresh and jam. At the moment part of the studies of this fruit are oriented towards the nutritional characterization (i.e. antioxidants; micro/macro nutrients). Due to the pigmentation of the blood-flesh peach will be interesting to analyze its bioactive compounds. Different analysis shown that the fruit contains high levels of antioxidants as well as micro and macronutrients at the pulp and skin level. These results will help in the characterization of the peach as well as rank the different populations on the country and on the other hand will help in the rescue and the recovery of the blood-flesh peach for the country.
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PS34

EVALUATION OF THE ANTIOXIDANT ACTIVITY OF THE METHANOLIC EXTRACT OF LEAVES OF *Kageneckia oblonga* (RUIZ ET PAV)

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Antioxidant compounds, such as polyphenols are developed in plants in order to prevent cell damage caused by endogenous or exogenous radicals. *Kageneckia oblonga* Ruiz & Pav, also known as Bollen or Huayo, belongs to the family Rosaceae, is an endemic species of Chile, and lives in the regions of Coquimbo to Biobío, which has been little studied, especially its antioxidant activity. The objective of this work was to evaluate the antioxidant activity of the methanolic extract of *Kageneckia oblonga*, through the uptake of the radicals 2,2-diphenyl-1-picrylhydrazyl (DPPH) and 2,2´azinobis-(3-ethylbenzothiazoline-6-sulfonic acid) (ABTS) and thus verify how efficient was the solvent used in the process of extraction. The antioxidant capacity was evaluated by calculating the percentage inhibition of both radicals in an absorbance spectrophotometer. The extract concentration to produce a 50% inhibition of free radical (IC_{50}) absorbance was determined. The antioxidant tests with DPPH and ABTS showed a positive antioxidant activity, obtaining a maximum reduction of 89,94±0,6% y 86,82±0,8%, respectively. IC_{50} was calculated for both cases, obtaining a value of 0.34mg/mL (DPPH) and 0.18mg/mL (ABTS). With the IC_{50} values, a kinetic assay was performed for DPPH and ABTS for a period of 180 minutes, obtaining 84.81±3.4% and 79.04±10.2%, inhibition at 180 minutes. Gallic acid equivalents (GAE) and Trolox (6-hydroxy-2,5,7,8-tetramethylchroman-2-carboxylic acid) equivalents using DPPH and ABTS assay respectively, were also determined. The result obtained for GAE was 43,52±0,77 mg/gr extract and for Trolox equivalents was 199,99±9,62 mg/gr extract.
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PS35

IDENTIFICATION OF BIOACTIVES COMPOUNDS AND DIFERENTIAL EXPRESSION OF GENES IN *V. pubescens* AND *V. chilensis*, TWO PHENOTYPICALLY CONTRASTING PAPAYA SPECIES.

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Within the *Caricaceae* family, the two most economically important genera of this family are the *Carica papaya* and the group of papayas of the highlands, *Vasconcellea spp*. There are two species of *Vasconcellea* in Chile, the *Vasconcellea pubescences* that are botanically similar to *C. papaya* and *Vasconcellea chilensis* that are only conserved as wild natural resource and live in harsh environmental conditions. Biochemically, papayas fruits represent sources of various phytochemical bioactives compounds, such as phenols, carotenoids and anthocyanins as well as alkaloids and proteins with pharmaceutical, medical and industrial applications. Among the proteins there are four cysteine proteases present in the latex that regulated physiological functions such as senescence and seed germination, as well as defense against pathogens. Papain is one of the major proteases with proteolytic activity and this activity is higher in *Vasconcellea* than in *C. papaya*. A transcriptomic analysis was performed between a population of *V. pubescens* and a *V. chilenses*, showing an increase of the transcription level for papain and proteases inhibitors in *V. chilensis* compared to the commercial papaya being validated by qPCR. In addition, phenolic compounds, anthocyanins, carotenoids, micro and macro nutrients were measured.
This research was supported by CONICYT, FONDECYT/Regular N° 1150919.

PS36

STUDIES OF AtA6PR2, A PUTATIVE *A. thaliana* ALDOSE-6-PHOSPATE REDUCTASE

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Polyols or sugar alcohols are molecules associated with a series of roles in plants, such as increased tolerance to abiotic stresses like cold and saline stress, protection against reactive oxygen species by acting as a source of reductive power, and transport and uptake of micronutrients like boron. Sorbitol, a type of polyol found in species of the *Rosaceae* and *Plantaginaceae* families, is synthesised from glucose-6-phosphate by aldose-6-phosphate (A6PR) in source organs and is translocated via phloem to sink organs where sorbitol dehydrogenase oxidises it to fructose. In *Arabidopsis thaliana*, there are two open reading frames coding putative A6PRs, *At2g21250* and *At2g21260*, which we have named *AtA6PR1* and *AtA6PR2*, respectively. *AtA6PR2* possesses lower expression levels when compared to *AtA6PR1* and its function in *A. thaliana* is still unknown. To establish what role this gene may possess, several *A. thaliana* wild-type and *atsdh1-1* transgenic lines which stably express *AtA6PR2* under a strong promotor have been obtained. Additionally, insertional lines of the SALK collection for *AtA6PR2*, dubbed *ata6pr2-1* (SALK_001358) and *ata6pr2-3* (SALK_050803) have been identified and the precise T-DNA insertion sites were determined to be within the first intron of *AtA6PR2*, approximately 250 bp downstream from the start codon, and in the 3'UTR region approximately 50 bp downstream from the stop codon, respectively. *AtA6PR2* expression levels in homozygous *ata6pr2-1* mutants

were shown to be significantly lower than those of wild-type plants, and the phenotypes of these lines are currently under analysis.
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PS37

BIOCHEMICAL CHARACTERISATION OF TWO PUTATIVE ALDOSE 6-PHOSPHATE REDUCTASES, AtA6PR1 AND AtA6PR2 FROM *Arabidopsis thaliana*

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During photosynthesis, plants of the Rosaceae and Plantaginaceae families mainly translocate sorbitol. This sugar alcohol is synthesised in source organs by aldose 6-phosphate reductase (A6PR), which reduces glucose-6-P to sorbitol-6-P. The latter is converted to sorbitol, which acts as a compatible solute in conditions of abiotic stress and also facilitates boron mobilisation. However, in Arabidopsis, a sucrose-translocating Brassicaceae, two proteins with >65% amino acid identity with known plant A6PRs have been identified. Both proteins have the molecular characteristics of aldo-keto reductase-like proteins such as 3 highly-conserved sites:- site 1 (tyrosine), corresponding to the active site; site 2 (histidine), the substrate binding site; and the conserved sequence IPKS. These proteins were called AtA6PR1 and AtA6PR2. Both have been found by transient transformation of tobacco to be localised in the cytosol (GFP-fusion protein), and the expression of both genes is altered differentially when plants are subjected to abiotic stress (cold and saline). Biochemical characterisation of these two proteins was initiated by the expression of codon-optimised *AtA6PR1* and *AtA6PR2* in the heterologous system of *E. coli* BL21 (DE3) plysS. After optimising the induction conditions, the recombinant proteins are being purified in order to perform substrate specificity assays.
Fondecyt 1140527 (MH) and Conicyt Master scholarship 22160896 (KO).

PS38

POSTHARVEST MONITORING IN *Prunus salicina* FOR MARKER TRAIT ASSOCIATIONS

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Genotype by Sequencing is a powerful molecular tool for genotyping in *Prunus* species which allows us to construct very saturated genetic maps using thousand SNPs. Therefore, GBS can be used for any genomic association using different agronomic traits. In fact, there

is a great quantity of information about QTLs related to fruit quality traits in several *Prunus* species but no so much in terms of post-harvest behavior. In this work five postharvest traits were monitored in ninety-six seedlings from 98-99' × 'Angeleno' F1 population using non-destructive methods. Fruit weight, skin chlorophyll index, skin color, and respiration rate were evaluated for days 1 and 7 while firmness was evaluated for days 1, 4 and 7. Genetic map of '98-99' × 'Angeleno' F1 Japanese plum population was used to carry out a marker-trait association by General Lineal Model (GLM) and Mixed Lineal Model (MLM) as well as QTL identification by Interval mapping. Finally, important marker-trait associations and QTLs for weight loss in the LG5, chlorophyll degradation in the LG4, skin color (CIE l*a*b*) in the LG3 and slope softening in the LG5 were identified which allow to explore genomic regions linked to these traits for using molecular assisted selection.

Keywords: Postharvest, marker-trait association, QTL, *Prunus salicina*

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PS39

SWEET CHERRY CHILLING REQUIREMENTS ARE INFLUENCED BY LOCALITY AND CYANAMIDE APPLICATION

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Prunus avium L. is a fruit tree that grows in temperate climates, whose flowering depends on the fulfillment of determined chilling requirement. When chilling accumulation is lower than 50% of the requirement, bud break takes longer and flowering is erratic, reducing final fruit yield. To overcome the lack of cold and synchronize bud break hydrogen cyanamide application in the field can be used. The objective of this work was to determine the chilling requirements of the sweet cherry varieties "Royal Dawn", "Bing", "Lapins", "Regina", "Santina" and "Kordia" from production two fields located at O'Higgins region of Chileand compare the chilling requirements pre and post cyanamide application. Two commonly used chill models were used to evaluate the chilling requirements pre and post cyanamide application in the field. Sticks of each variety harboring dormant floral buds were kept in growth chambers at 4.5 °C in darkness to accumulate cold in a controlled manner and then were taken to favorable conditions in the greenhouse (25°C, long day) to analyze the percentage of bud break. It was observed that bud break increased throughsuccessive chilling hour accumulation. It was observed that "Royal Dawn" was the variety with the lowest chilling requirement while "Kordia" was the one with the highest chilling requirement. Moreover individuals "Lapins" from the different localities evaluated presented different chilling requirements. These differences may be due to the different

conditions of latitudes, altitudes and microclimates. All varieties required less chilling hour accumulation for bud break when hydrogen cyanamide was applied.
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PS40

PMEI13 AS A NEW PECTIN METHYLESTERASE INHIBITOR IMPLICATED IN MUCILAGE HOMOGALACTURONAN METHYLESTERIFICATION

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The plant cell wall is a surrounding layerlocated outside the plasma membrane which provides the cell with structural support and protection. One of the major components of the cell wall is pectin and therefore studying pectins components can help uncover relevant aspects regarding the cell wall properties. The Homogalacturonan (HG) is the most abundant pectin domain and its methylesterification has been described as a key process to confer the cell wall with its biochemical and biomechanical properties. HG domains are secreted in a highly methylesterified state into the cell wall, being the degree of methylation regulated by the activity of two classes of enzymes, the pectin methylesterases (PMEs) and its inhibitors (PMEIs). PMEs catalyze the reaction of HG demethylesterification and they are negatively regulated in the cell wall by their proteinaceous inhibitor. PMEIs prevent access to the HG substrate by covering the PMEs catalytic sites. In Arabidopsis, there are 69 putatives genes encoding for PMEIs, which suggestes a fine regulation of HG methylesterification. The Arabidopsis seed mucilage contain low amount of HG, and therefore will be used as a model to study how PMEs and PMEIs regulate HG methylesterification. In our laboratory, a screening of mutants allowed us to detect a novel gene encoding for a PMEI (*PME13*). We select 2 mutant lines for PMEI13 (*pmei13-1* and *pmei13-2*) which have the T-DNA insertion in the promotor proximal region. Preliminary results show that pmei13-1 and pmei13-2 exhibit changes in the global PME activity. Moreover, immunolabeling of adherent mucilage of *pmei13-1* and pmei13-2 show a decrease of JIM7 labeling, confirming the presence of defects in the mutant lines HG methylation.
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PS41

EFFECT OF NATURALIZED ROOTSTOCKS ON GROWTH AND PHYSIOLOGY OF SYRAH AND CABERNET SAUVIGNON UNDER WATER DEFICIT

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Grapevine production in Chile is facing increasing water problems related to aridization. We explored rootstocks as compelling mitigation strategy for increasing water use efficiency in Syrah (Sy) and Cabernet Sauvignon (Cs) vines under water deficit. Vines were grafted onto five naturalized genotypes from our collection "GermoVidNor"; G25 G32 (Copiapó); G57, G65, G70 (Huasco), collected in Chilean arid zones. Own-grafted and grafted onto commercial drought-tolerant rootstock 140-Ruggeri plants were used as controls. Vines were grown for three years in 35 L containers at random block design (4 replicates) and submitted to optimal (100% ETc) and deficit (30% ETc) irrigation. Components of shoot growth and physiology traits (leaf gas exchange, xylem water potential) were assessed throughout the season. We explored leaf area as a proxy for primary performance. Additionally, leaf tissues in maturity stage were collected for transcriptional analysis of target genes related to water stress considering hormonal, AQPs and developmental pathways. Statistical analysis included ANOVA for physiology, ANCOVA for morphology additional LSD Fisher test and relative changes in gene expression were determined using Pfaffl method normalized to *Ubiquitin*. Water deficit indeed reduced foliar rate and physiological performance. Naturalized genotype G32 displayed a superior physiological performance under deficit treatment than 140 Ru and own-grafted controls. G32 also displayed better fitness in morphologic traits mainly under Cs scion, and expression analysis of target genes displayed contrasting behavior compared to Own-grafted, suggesting that naturalized genotypes better improved drought responses than commercial rootstocks.
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PS42

MOLECULAR CHARACTERIZATION OF *CONSTANS-LIKE* GENES IN SWEET CHERRY (*Prunus avium* L.) FLOWER BUDS AND LEAVES

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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 sweet cherry trees (*Prunus avium* L.) is limited. Through a RNA-seq analysis of leaves during flowering induction period, we identified several *CONSTANS*-like (*COL*) transcripts being expressed in sweet cherry trees. Based on this information, we searched the *P. avium* genome and we found at least seven COL To establish a relationship between the putative *P. avium* COL proteins, Arabidopsis COL proteins and those from other *Rosaceae* species, such as peach,

P. mume, *P. cerasifera x P. munsoniana*, *Fragaria vesca*, apple and pear a phylogenetic tree was developed. The tree showed that the sweet cherry COL and *Rosaceae´s* COL proteins can be subdivided into three subfamilies as in Arabidopsis. As a first approach to ascertain the role of the COL gene in sweet cherry development, its temporal and spatial expression pattern was analyzed by qRT-PCR in leaves and floral buds. The *P. avium COL* genes were differentially regulated in leaves and floral buds being higher expressed in leaves than in floral buds. Furthermore, 5 *COL* genes were up-regulated in leaves together their putative target genes, *FT*-like and *SOC1*-like genes, during the flowering induction period. A spatial and temporal relationship in the expression of *PaCOLs*, *SOC1*-like and *FT*-like suggest that these genes are involved in the seasonal periodicity of flowering in sweet cherry trees.
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PS43

MOLECULAR ANALYSIS OF *Solanum lycopersicum* cv MICRO-TOM OVEREXPRESSING LIPOYL SYNTHASE *SlLIP1* or *AtLIP1*

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Agricultural crops are constantly threatened by different abiotic stresses that cause an increase in reactive oxygen species. These are dissipated by enzymatic and non-enzymatic mechanisms. Among the latter, antioxidants such as carotenoids and anthocyanins are found, and several studies have raised the content of these molecules to confer stress tolerance in different species. Lipoic acid is a powerful antioxidant whose effect on species of commercial importance has not been studied. Nevertheless, several enzymes participating in lipoic acid biosynthesis have been identified, mainly in *Arabidopsis thaliana*. Thus, it is known that lipoic acid is synthesised and attached to target proteins (lipoylation) in mitochondria by two pathways: scavenging from free lipoate by lipoyl ligase (AtLplA); and *de novo* synthesis, where lipoyl transferase (AtLIP2) and lipoyl synthase (AtLIP1) are involved. Among other targets, lipoic acid is incorporated into E2 subunits of pyruvate dehydrogenase and α-ketoglutarate dehydrogenase complexes. Additionally, two genes coding lipoyl synthase, one mitochondrial (SlLIP1) and the other plastidial (SlLIP1p) have been found in tomato (*Solanum lycopersicum*). In previous studies, tomato cv. Micro-tom was transformed stably with either *SlLIP1* or *AtLIP1* and multiple T0 generation lines obtained. In the present work, a molecular, biochemical and phenotypical characterization is being carried out using the respective homozygous plants. The molecular approach involves expression analysis of *SlLIP1*, *AtLIP1* and the lipoylated targets. The biochemical analysis includes determining the lipoylation levels of the target proteins, whilst the phenotypic analysis will determine fruit number, flowering time and plant height. Progress in these analyses will be presented.

PS44

ASSESSING UDP-RHAMNOSE/UDP-GALACTOSE TRANSPORTERS SPECIFIC ROLES IN *Arabidopsis thaliana* CELL WALL PECTINS BIOSYNTHESIS BY USING A PROMOTOR SWAP APPROACH

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The synthesis of cell wall matrix polysaccharides occurs in the Golgi apparatus through the concerted action of hundreds of glycosyltransferases. However, nucleotide-sugars are synthesized in the cytoplasm, and need to be transported into the Golgi lumen for their use as substrates for cell wall biosynthesis. Nucleotide sugars transporters (NSTs) accomplish this task and are therefore crucial for cell wall biosynthesis. UDP-Rhamnose (UDP-Rha) is a key plant cell wall nucleotide sugar precursor since it is used for the rhamnogalacturonan I (RG-I) and rhamnogalacturonan II (RG-II) cell wall pectins biosynthesis. Recent studies carried out in our laboratory led the characterization of a family of six UDP-Rhamnose/UDP-Galactose Transporter (URGT1 – 6) which transport UDP-Rhamnose and UDP-Galactose *in vitro*. However, although URGT1 and URGT2 share approximately 90% identity in their amino acid sequence, *urgt1* and *urgt2* mutant lines present specific phenotypes: *urgt1* show a decrease in galactose content in rosettes leaves while *urgt2* exhibit a decrease in seed mucilage rhamnose content, suggesting a selective role of URGTs in pectin biosynthesis. In this work, we analyze whether the URGTs are exchangeable in their role using a promoter swap approach. Thus, we examined the phenotype of transgenic plants expressing promoter-swap constructs of GFP-tagged *URGT1* and *URGT2* coding sequences. We confirmed that URGT1 and URGT2 are Golgi localized proteins irrespective of their promoter sequences and analyzed their contribution to pectin biosynthesis by biochemical and immunolabeling analysis.
Fondecyt 1151335, Fondecyt 11160787 and FONDAP CRG 15070009.

PS45

THE KEY ROLE FROM UDP-RHAMNOSE/GALACTOSE TRANSPORTERS IN THE BIOSYNTHESIS OF SEED COAT MUCILAGE

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The cell wall is a complex matrix that plays an important role in growth, structure and plant defense. This structure is mainly composed of celulosic and noncellulosic polysaccharides. The majority of noncellulosic polysaccharides such as pectins are produced in the Golgi

apparatus from nucleotide sugars that are predominantly synthesized in the cytosol. The pectin comprises four primary components, xylogalacturonan (XGA), homogalacturonan (HGA), rhamnogalacturonan I (RG-I), and rhamnogalacturonan II (RG-II). UDP-rhamnose is a key substrate because is present in the backbone of RG-I and the side chains of RG-II, at the same time the synthesis of UDP-rhamnose occurs in the cytosol, therefore is essential that this molecule gets into the lumen of the Golgi. Nucleotide sugar transporters (NSTs) have evolved to enable the transfer of nucleotide sugars into this organell. We have identified and characterized a family of six Golgi localized UDP-rhamnose/galactose transporters (URGT1→6) in *Arabidopsis thaliana*. *Arabidopsis* seeds produce mucilage, a gelatinous structure mainly composed of the unbranched pectin RG-I making it a good model to study biosynthesis and pectin modification. To study the role of URGTs, we took advantage of *Arabidopsis* seed coat mucilage. The analysis of loss of function in single, double and triple URGT mutant plants shows notorious phenotypes at the level of immunolabeling, which are supported by various biochemical evidence. Results suggest that URGT2, URGT4 and URGT6 are important in the RG-I polymere biosynthesis and they contribute in a different way.

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PS46

EFFECT OF ESSENTIAL OIL OF *Schinus polygamus* (CAV.) CABR. (ANACARDIACEAE) ON *Galleria mellonella L.* (LEPIDOPTERA: PYRALIDAE)

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Schinus polygamus (cav.) Cabr. (Anacardiaceae), is a plant native to southern America, is known as \"Huingán\", belonging to the family Anacardiaceae. It is known for its use in the practice of popular health and its antimicrobial activity, however it is unknown if this species has any insecticidal activity. Given the above, the objective of this work was to determine the insecticidal activity of the essential oil (EO) of *S. poligamus* leaves on *Galleria mellonella* (Lepidoptera: pyralidae), the large wax moth, one of the most important pest in beekeeping. For this, we evaluated the behavioral response that the moth possesses to the compounds present in the EO with a \"Y\" type olfactometer. The test consisted in subjecting adults to volatile oil stimuli to evaluate repellency or attraction at concentrations of 1000, 100, 10 and 1 ppm, 70 µl of the stimulus was deposited on a Whatman No. 1 filter paper, a vacuum pump was installed which circulated the air, dragging the volatile compounds of the EO into the decision area (simple arm), the residence time in each arm was recorded for 5 minutes. In addition, insecticidal activity was evaluated on groups of 10 larvae of *G. mellonella* at a concentration of 1000 ppm. The results obtained demonstrated an insecticidal effect of *S. Polygamus* (EO) with 57.14% mortalities on G. mellonella larvae.

The concentrations 1000, 100 and 10 ppm were repellent according to the olfactive preference index. To date there is no record regarding the insecticidal effect of S. polygamus being these results the first to demonstrate the possible insecticidal effect, also contributing information for the integrated management of this pest.

PS47

NATIVE ENDOPHYTIC FUNGI WITH POTENTIAL BIOCONTROLLER OF *Sclerotinia sclerotiorum* IN LETTUCE SEEDLING

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White rot caused by *Sclerotinia sclerotiorum* (Lib.) is a disease that affect Lettuce (*Lactuca sativa* L.), which is one of the main vegetable crop for human consumption. The objective of this work was to evaluate the endophytic colonization capacity of *Beauveria*, *Trichoderma* and *Clonostachys* strains and their biocontrol potential for White Rot in lettuce. Two treatments were done: i) lettuce plants were inoculated with $1x10^6$ conidia mL^{-1} by spray on the foliage and ii) seeds were inoculated with $1x10^8$ conidia mL^{-1} in a methylcellulose suspensión. Leaves, stems and roots were collected at 10, 20 and 30 d post-inoculation which were superficially disinfected, cut in small pieces and put on PDA, incubated at 24°C for 60 d. Then, fungi strains were re-isolated and characterized by BOX-PCR typification method to compare the fingerprintings genomes. The antagonistic activity against *S. sclerotiorum* was evaluated through dual cultures method and the inhibition growth of pathogen were measured for antibiosis and parasitims. Results show that *Beauveria* sp. would have an endophytic behaviour by foliage inoculation method, while *Trichoderma* sp., and *Clonostachys* sp. got it by seeds inoculation. Only the re-isolated *Beauveria* sp. and *Clonostachys* sp. had the same BOX-PCR fingerprinting respect to the inoculated strains. And just *Beauveria* strains show antagonistic activity inhibiting a 33% the radial growth of *S. sclerotiorum* by antibiosis, while *Trichoderma* and *Clonostachys* inhibited an 81% and 66% the radial growth of *S. sclerotiorum* by parasitims, respectively. *Beauveria*, *Trichoderma* and *Clonostachys* strains are potential biocontrol agent for *S. sclerotium* like endophytes in Lettuce.

PS48

INHIBITION OF FREE RADICALS DUE TO PHENOLS PRESENT IN AERIAL PARTS OF *Acaena pinnatifida* (RUIZ ET PAV.)

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Antioxidants are molecules of interest due to their ability to prevent or delay the oxidation of other molecules, such as lipids, proteins or nucleic acids. *Acaena pinnatifida* is a native

plant, always green which lives above the forest line present in southern Chile.The in vitro antioxidant activity of methanol extract obtained from aerial parts of *A. pinnatifida* has not been studied.Therefore, in this work the antioxidant activity of methanolic extract obtained from the aerial parts of this species was evaluated, determining the decrease of absorbance in a solution of the 1,1-diphenyl-2-picrylhydrazyl (DPPH) radical and the acid radical 2,2-azino-bis (3-ethylbenzothiazoline-6-sulphonic acid) (ABTS).In addition, the polyphenols present in the methanolic extract were quantified and a phytochemical test was performed to determine the presence of different groups of secondary metabolites.The highest antioxidant activity observed by ABTS was in a concentration of 0.50 mg/mL of extract, with an inhibition percentage of 84.33% ABTS absorbance and an IC 50 of 0.28 mg/ml.The results observed by DPPH were a maximal inhibition of 86.67% in a concentration of 2.0 mg/ml and an IC50 of 0.49 mg/ml. The antioxidant activity determined by DPPH and expressed as gallic acid equivalents was 34.69 ± 0.1 mg/g of extract and the 6-hidroxy-2,5,7,8-tetramethylchromane-2-carboxylic acid (Trolox) equivalents determined by ABTS was 147.61 ± 2.06 mg/g extract.

PS49

DYNAMICS OF HOMOGALACTURONANS IN APHID-PLANT INTERACTION

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Green peach aphid, *Myzus persicae*, is a phloem feeder insect which colonize more than 400 plants species and transmit over 100 viral diseases, thus is considered one of the most important agriculture pest worldwide. The ability of aphid to extract phloem sap relies on a slender structure called stylet placed into their mouthparts. Stylet penetrates between epidermal cells and cross the different cell layers through the cell walls and pectin rich lamella media until the sieve elements are reached and penetrated. Since homogalacturonan (HGs) is one of the most abundant polysaccharide along the stylet probing pathways, this investigation is focused on analyze this pectin during early stage (6 hours) of aphid feeding on *A. thaliana*. To accomplish this goal, our experimental strategy was based on analyze the HG methyl-esterification state by immunolabelling with LM19 monoclonal antibody and measure the global activity of the HG modifying enzymes, pectin methylesterase (PME) and polygalacturonase (PG). Our results show that PME activity increased approximately 20% in both, local and systemic tissue of infested plants, compared to non-infested condition (control) with the consequent decrease of methyl-esterification state confirmed by LM19 immunolabelling. On the other hand, PG activity was decreased in 28% and 37% in local tissue and systemic tissue respectively, compared with non-infested condition (control). These results suggest that at early stages of aphid

infestation, pectin related enzymes (PME and PG enzymes) play a significant role in the remodeling or restructuring of cell wall during aphid-plant interaction.
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PS50

CO-SUPPRESSION OF *FCSEP3* REVEALS A NEGATIVE REGULATOR ROLE ON THE ANTIOXIDANT PROPERTIES OF THE WHITE CHILEAN STRAWBERRY FRUIT

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Fragaria chiloensis is a native strawberry species characterized for an intense aroma and exotic white-pink color, but a short postharvest life. On the other hand, *F. chiloensis* fruit is also relevant for its high antioxidant properties, being considered as a functional food. The most abundant antioxidant compounds in the fruit are phenolic compounds, in special flavonoids and flavones. The biosynthesis pathway of this kind of metabolites is sharply regulated by the MBW (MYB/bHlH/WD40) transcriptional complex. In the Chilean strawberry, the negative effect of FcMYB1 as regulator of anthocyanin accumulation has been recently demonstrated. In this work, we studied the role of FcSEP3, a MADS-box transcription factor, on the antioxidant properties of *F. chiloensis* fruit. For this purpose, *F. chiloensis* fruits were transient transformed, using agroinfiltration, with FcSEP3 obtaining a clear co-suppression of the transcription of the endogenous gene. The co-suppression of *FcSEP3* in transient *in planta* transformed fruits promoted the increase in the total level of phenolics and flavonoids, and in the antioxidant capacity, without affecting the total anthocyanin content. In addition, the co-suppression of *FcSEP3* up regulated the expression level of important genes of the flavonoids biosynthesis pathway such as Leucoanthocyanidin Reductase (*LAR*) and down regulated the expression of Chalcone Synthase (*CHS*) and Chalcone Isomerase (*CHI*); no changes were observed in the remaining genes of the pathway. The results indicate that *FcSEP3* is playing a negative regulator effect on the antioxidant capacity of the fruit; however, the mechanism needs to be unraveled.
Anillo ACT 1110, FONDECYT 1171530.

PS51

STUDYING THE ROLE OF LIGHT-INDUCED GENES IN THE SYNTHESIS OF CAROTENOIDS IN THE DARK-GROWN CARROT STORAGE ROOT

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Carotenoids are pigments which provide color to flowers, fruits, and some roots. In plants, they participate in photosynthesis, are precursors of phytohormones, and provide

protection against photo-oxidative damage. Carotenoid synthesis is upregulated by light in leaves and fruits through the signal transduction mechanism induced by photoreceptors (PHYs). The orange *Daucus carota* (carrot) synthesizes and accumulates high amounts of carotenoids in the root that grows in darkness. Contrary to other organs, light inhibits the synthesis of carotenoids in the carrot root, negatively affecting the expression of carotenogenic genes such as *PSY1 and PSY2*.To understand the regulation of the synthesis of carotenoids and the effect of light in the carrot root we performed a *de-novo* RNA-seq analysis between dark-grown and light-grown roots. Surprisingly, genes involved in light signaling and photomorphogenesis as *PAR1*, *PHYA* and *FHY3*, were upregulated in the dark-grown root and down-regulated in light. The validation of the expression of these genes were performed in orange varieties and in white ones, which does not accumulate carotenoids. This allowed us to associate the candidate genes to carotenoid synthesis and not to root development. For further functional characterization, we overexpress the *AtPAR1* in carrot. Transgenic embryos present an orange phenotype and the regenerated plants show higher levels of carotenoids in roots and leaves as well as greater expression of *PSY1* and not *PSY2*, demonstrating that PAR1, a transcriptional cofactor involved in the shade avoidance syndrome, participates and is part of a machinery that regulates the synthesis of carotenoids in the carrot storage root.

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PS52

EVALUATION OF THE ANTIOXIDANT ACTIVITY OF THE METHANOLIC EXTRACT FROM LEAVES OF *Kageneckia oblonga* (RUIZ ET PAV)

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Antioxidant compounds, such as polyphenols are developed in plants in order to prevent cell damage caused by endogenous or exogenous radicals. *Kageneckia oblonga* Ruiz & Pav, also known as Bollen or Huayo, belongs to the family Rosaceae, is an endemic species of Chile, and lives in the regions of Coquimbo to Biobío, which has been little studied, especially its antioxidant activity. The objective of this work was to evaluate the antioxidant activity of the methanolic extract of *Kageneckia oblonga*, through the uptake of the radicals 2,2-diphenyl-1-picrylhydrazyl (DPPH) and 2,2´azinobis-(3-ethylbenzothiazoline-6-sulfonic acid) (ABTS) and thus verify how efficient was the solvent used in the process of extraction. The antioxidant capacity was evaluated by calculating the percentage inhibition of both radicals in an absorbance spectrophotometer. The extract concentration to produce a 50% inhibition of free radical (IC_{50}) absorbance was also determined. The antioxidant tests with DPPH and ABTS showed a positive antioxidant activity, obtaining a maximum reduction of 89,94±0,6% y 86,82±0,8%, respectively. IC_{50} was calculated for both cases, obtaining a value of 0.34mg/mL (DPPH) and 0.18mg/mL (ABTS). With the IC_{50} values, a kinetic assay was performed for DPPH and ABTS for a period of 180 minutes, obtaining 84.81±3.4% and

79.04±10.2%, inhibition at 180 minutes. Gallic acid equivalents (GAE) and Trolox (6-hydroxy-2,5,7,8-tetramethylchroman-2-carboxylic acid) equivalents using DPPH and ABTS assay respectively, were also determined. The result obtained for GAE was 43,52±0,77 mg/gr extract and for Trolox equivalents was 199,99±9,62 mg/gr extract.
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PS53

FCRGL4: FROM THE GENE TO THE ENZYME ACTIVITY

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The ripening of a fruit is a complex process, and during its course softening of the fruit occurs, in addition to other events. During softening the remodeling of plant cell wall polysaccharides takes place favored by the presence of enzymes such as glycosyl hydrolases and/or lyases. As the solubilization of pectins is intense during softening of *F. chiloensis* fruit, we decided to study enzymes involved in their metabolism, in special the metabolism of rhamnogalacturonan I (RG-I). We identified *Rhamnogalacturonan endolyase* (*FcRGL4*; PL4 family) as a gene that it is highly expressed during ripening of *F. chiloensis* fruit; in addition, *FcRGL4* transcripts are also abundant in expanding tissues such as stem and runners. On the other hand, the expression of *FcRGL4* is induced by abscisic acid treatments and repressed by auxins. The open reading frame of *FcRGL4* was cloned and then expressed heterologously in *Pichia pastoris* yeast. The recombinant protein obtained presents RG-lyase activity against rhamnogalacturonan I (RG-I) from potato, and it is also able to disassembly the mucilage of *Arabidopsis thaliana* seeds. The protein was purified 61-fold through affinity chromatography (Histidine-tag). The enzyme requires pH 5.0 for maximum activity. The disassembling of pectins such as RG-I during the ripening of *F. chiloensis* fruit could be explained by the increment in RGL activity.
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PS54

EVALUATION OF ANTIOXIDANT ACTIVITY, TOTAL PHENOLIC AND TOTAL FLAVONOID CONTENTS IN THE METHANOL EXTRACT FROM ROOTS OF *Acaena pinnatifida* (Ruiz et Pav.)

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Acaena pinnatifida (Ruiz et Pav.) is a native specie located in the Andes mountains from the Coquimbo region to the Magallanes region. One of its most remarkable features are the unfavorable external conditions for its development. Taking this condition into account, an evaluation of the antioxidant effect of the methanolic extract of *Acaena pinnatifida* was madethrough an assay with the test of the radical DPPH (2,2-diphenyl-1-picrylhidrazyl) and the cation radical ABTS (2,2-azino-bis-3-ethylbenzothiazoline-6-sulfonic acid) expressed in equivalents of gallic acid and Trolox® (6-hidroxy-2,5,7,8-tetramethyl chromane-2-carboxylic acid), respectively. The biggest discoloration effect for DPPH was observed in extract concentration of 0.5 mg/mL, reaching an inhibition of absorbance of 88,9±2,13 % and for ABTS it was observed an inhibition of 85,5±3,66% with 0.150 mg/mL of extract concentration. For the Kinetic assay with DPPH radical an IC_{50} value of 0.120 mg/mL was determined, where a stable discoloration effect was present during the time of the assay. The maximum effect was observed at 150 minutes with an inhibition of 87,3±0,71 %. In the case of the Kinetic assay with the ABTS radical, an IC_{50} of 0.0672 mg/mL was calculated, where an inhibition effect was stable during 180 minutes of this assay and its maximum inhibition effect corresponds to 95,3±1,32%. The total content of flavonoids was also determined and expressed as Catechin equivalent, which corresponds to 209.17±41.23 mg of Catechin per gram of dry extract. Phytochemicals assays for recognition of secondary metabolites were also developed, and saponins and tannins were detected.

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PS55

EFFECT OF ALUMINUM TOXICITY (AL^{3+}) ON RADICAL GROWTH, OXIDATIVE DAMAGE AND ANTIOXIDANT METABOLISM ON FLAX (***Linum usitatissimum*** L.)

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Aluminum (Al) in acid soils with a pH less than 5.0 is solubilized as a trivalent ion (Al^{3+}), which is toxic for plant. Al^{3+} cause damage in the cell wall, plasma membrane, as well as provoke inhibition of radical growth. In Southern Chile, the predominant soil type is Andisol, it is characterized by excellent physical properties, but with high Al contents. Flax (*Linum usitatissimum*) is an important species for its nutritional characteristics, high content of α-linolenic acid and bioactive compounds. In this study, we evaluated the radical growth, oxidative damage and antioxidant metabolism of thirty genotypes of flax in nutritive solution. The concentration used was 1mM as $AlCl_3$ to pH 4.8. We evaluated the relative root growth, lipid peroxidation (TBARS), polyphenols (Folin-Ciocalteau) and antioxidant

activity (DPPH). The results showed for leaves significant differences ($p<0.05$) in lipid peroxidation in the treatments 0 and 1 mM Al. In root, we observed significant differences ($p<0.05$) between radical length, lipid peroxidation, and polyphenols. In relation to flax genotypes, not statistically significant differences were observed for any of the parameters assessed. According to the antioxidant activity, this variable is not significant for treatments and genotypes. Finally, in this preliminary study the toxicity by high concentrations of Al^{3+} in flax seedlings caused inhibition of radical growth and oxidative damage that incremented the concentrations of polyphenols. However, more research to low Al concentrations is required to identify Al-contrasting genotypes.

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PS56

INTERANNUAL PLANT BIODIVERSITY ESTIMATED FROM SOIL DNA AND SEEDLING EMERGENCE IN THE ATACAMA DESERT

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Studying biodiversity in extreme environments allows us to understand how individuals and whole ecological communities are able to survive at the limits for life. We characterized plant biodiversity in an altitudinal transect along the western slope of the Andes in the Atacama Desert. Here, plants must overcome aridity, high radiation and nutritional shortage among other extreme conditions. Plant biodiversity in the hyperarid Atacama varies over time in response to fluctuating environmental conditions from inter-annual to decadal timescales. Multiple life habit strategies are utilized in this environment such as annuals, which commonly avoid drought years by forming soil seed banks that germinate when conditions are suitable. To establish the composition of these plant communities we performed plant diversity surveys over seven consecutive years along an altitudinal transect. We observed a total of 71 different plant species with significant inter annual variation (31 to 63 species) and species persistence (years of appearance, from one to seven years). Environmental DNA in surface soil samples complemented the surveys and revealed hidden plant diversity. DNA barcode analysis revealed seven new taxa in the area, but tended to show broad distributions of different plant DNA. To complement field and molecular surveys, we further performed an analysis of soil seed banks using the seedling emergence method. The soil seed bank proxy shows that viable seeds have wider ranges than observed for plant species during surveys (in agreement with the DNA barcode method). Our results show higher than anticipated plant richness and composition along the transect. These

wider ranges provide adaptive flexibility at the community level to changes in climate in Atacama Desert.

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PS57

NACL UPTAKE AND PLANT NUTRITIONAL IMBALANCE: IONOMICS ON *Prunus* SPP. ROOTSTOCKS AND SALT STRESS

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Fruit production is one of the agricultural items with greater dynamism and growth in Chile, being one of the engines of the export industry. Stone fruit tree orchards are one of the most important fruit producers in Chile representing a 25% of the total area planted with fruit trees. Nowadays, extreme temperatures, lower water availabity and soil salinization, represent a hard challenge for agriculture given by the global climate change. The most important agricultural crops and stone fruit trees are not among the most salinity tolerant plant species and their yields fall as consequence of growing in saline soils. The inability of stone fruit trees to tolerate salinity could result in substantial yield losses and decreased fruit quality. Furthermore, salinity also limits plant vegetative development and induces leaf senescence. These detrimental effects are broadly given by the nutritional imbalance in the whole plant concomitant to the massive NaCl uptake. Through Ionomics, the mineral nutrient composition of roots and leaves of two *Prunus* rootstock genotypes contrasting in their adaptive response to salinity was assessed by ICP-MS. After 14 days of saline irrigation (1/2 Hoagland + NaCl 120 mM), the salt-sensitive rootstock 'Mazzard F12/1' evidenced a higher root capacity of sodium uptake (11,72 fold higher in stressed vs control plants), in contrast to roots of the salt-tolerant rootstock (5.6 fold). In addition, Mazzard F12/1 showed the highest variation al leaf level (18.15 vs 7.20 fold detected in Mariana 2624). Thus, the salt-sensitive *Prunus* roootstock accumulated higher Na contents which implied a disturbance of the essential element composition of this genotype compromising the plant survival which are summarized in this work.

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PS58

GENOME-WIDE ASSOCIATION MAPPING FOR FLOWERING AND MATURITY IN TROPICAL SOYBEAN: IMPLICATIONS FOR BREEDING STRATEGIES

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Knowledge of the genetic architecture of flowering and maturity is needed to develop effective breeding strategies in tropical soybean. The aim of this study was to identify haplotypes across multiple environments that contribute to flowering time and maturity, with the purpose of selecting desired alleles, but maintaining a minimal impact on yield-related traits. For this purpose, a genomewide association study (GWAS) was undertaken to identify genomic regions that control days to flowering (DTF) and maturity (DTM) using a soybean association mapping panel genotyped for single nucleotide polymorphism markers. Complementarily, yieldrelated traits were also assessed to discuss the implications for breeding strategies. To detect either stable or specific associations, the soybean cultivars (N = 141) were field-evaluated across eight tropical environments of Brazil. Seventy-two and forty associations were significant at the genome-wide level relating respectively to DTM and DTF, in two or more environments. Haplotype-based GWAS identified three haplotypes (Gm12_Hap12; Gm19_Hap42 and Gm20_Hap32) significantly co-associated with DTF, DTM and yield-related traits in single and multiple environments. These results indicate that these genomic regions may contain genes that have pleiotropic effects on time to flowering, maturity and yield-related traits, which are tightly linked with multiple other genes with high rates of linkage disequilibrium. In addition, the results reported from this study are being used to select and accelerate the soybean breeding program of Dow Agrosciences in Brazil.
Coordination of Higher Personal Education of Brazil.

PS59

GENOME IDENTIFICATION AND TRANSFERABILITY OF MICROSATELLITE MARKERS BETWEEN ATRIPLEX SPECIES

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Species of the genus Atriplex (Chenopodiaceae) are halophytes and able to photosynthesize under low soil water availability and high temperatures. Several Atriplex species are known for their high biomass generation, which made them candidates for solid biofuels production. Besides, Atriplex sp. also can be used as animal forages, especially in drought periods. Most of the 21 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. The aim of this work is to develop microsatellite (SSR) markers from genome sequencing of *A. desertícola and A. atacamensis,* and study their transferability with other atriples species. We have generated and characterized genome sequences using Illumina technology, Hiseq2500 paired-end, specifically. A quality control and a pre-processing of the sequences including trimming and filtering were realized. Assembly of the nucleotide sequence reads was performed using the SOAPdenovo software. Finally, the software MISA was used to found microsatellite markers of *A. deserticola and A. atacamensis*. In this work, we provided microsatellite markers from high throughput next generation sequencing of the *A. deserticola* and *A. atacamensis* genomic DNA. These SSR markers were compared and 100 SSR markers conserved between both, *A. atacamensis* and *A. deserticola* were evaluated in 11 different Atriplex sp. These markers could be used in germplasm analysis, accessing genetic diversity and linkage mapping of *A. deserticola, A. atacamensis* and other *Atriplex* species.

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PS60

WATER STRESS EFFECTS ON PEPPER (*Capsicum annuum* L.) FRUITS AND PLANTS

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Plants react to environmental constraints by triggering secondary metabolism leading to defence end products at the whole plant level. Sweet pepper is known to contain metabolites valued for human health, leading to the idea that production under controlled water deficit might lead to healthier fruits, however, compromising yield. We have evaluated the effect of reduced water availability on the plant physiology and on fruits properties of *Capsicum annuum* L. on 6 genotypes; red (R), yellow (Y) and brown (B) fruit peppers (two of each colour). Watering treatments consisted on the replacement of 100% evapotranspiration (ETP), 80%ETP and 60%ETP, from darkening to full coloration of the fruits, assessing xylem water potential (Ψ_x), photosynthesis (A) and stomatal conductance (g). Also, assessing plant growth, fruit dry mass and soluble solids (SS) in fruits (°Brix). Except for one Y variety (1807), genotypes rapidly reduced gs upon water shortages, maintaining the water status of plants with. However, no immediate reductions in A were observed, but until later in the season. Even though all the varieties reduced their fresh biomass, dry biomass of shoots and roots were slightly affected, being the 1807 Y variety, the more sensitive. The pericarp thikness of the fruits were strongly and rapidly affected by the water restriction, in contrast to their SS content. Interestingly, high variability was found on the effect of deficit irrigation on plants and fruit responses in the 6 varieties of sweet pepper. The results will be discussed in relation to the fruit composition and agronomical perspectives of controlled water deficit in sweet peppers.

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PS61

PARAHELIOTROPISM IN BEAN VARIETIES: IMPACT ON CROP LIGHT INTERCEPTION AND YIELD

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Beans (*Phaseolus vulgaris* L.) are among the most world wide consumed legumes and its importance lies in the high protein content in seeds. Upon environmental constraints, and similar to other leguminous species, bean plants are capable of moving their leaflets, avoiding the direct light interception. Such response, known as paraheliotropism is believed to be an efficient mechanism for reducing photoinhibition at the leaf level upon stressing environments, even thou they occur up to a lesser extent in optimal agronomical conditions. Therefore, paraheliotropism might reduce the intercepted light, potentially affecting yield. We aimed to assess the correlation between the extent of paraheliotropism on crop light interception and crop yield in eight bean varieties, commercially and non-commercially bred, in the field. Differences in the extent of the paraheliotropic movement in apical leaflets were observed between varieties, but with no differences in the crop light interception, nor in the final yield. Besides, from flowering onwards, higher paraheliotropic movement of apical leaves correlated with higher crop light interception suggesting that lower light interception in the upper canopy is compensated by a better light spatial distribution as the crop reaches higher leaf area index (LAI) values, coincident with the reproductive growth.

PS62

DIFFERENTIAL PREHARVEST METHYL JASMONATE APPLICATIONS IN STRAWBERRY INDUCES A DISTINCT PHYSIOLOGICAL AND FUNGAL DEFENSE-RELATED RESPONSES DURING FRUIT POSTHARVEST STORAGE

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Preharvest applications of methyl jasmonate (MeJA) are effective for pathogen control and improving quality during fruit postharvest. However, the information about the number and time of applications to achieve the best response is unknown in strawberry. Thus, we

performed three MeJA treatments (M1, M2 and M3), which consisted in differential applications of 250 µmol L^{-1} MeJA at flowering (M3), large green-turning fruit (M2 and M3), and ripe fruit stages (M1, M2 and M3) of *Fragaria* x *ananassa* (cv. Camarosa). Then, we analyzed their effects in fruit quality and physiological parameters (such as anthocyanin and proanthocyanidins contents) along with incidence of *Botrytis cinerea* (Bc) and other fungal pathogens at 0, 24, 48 and 72 h of postharvest storage. Fruit weight loss was greater in control than MeJA-treated fruits, and color parameters a* and Chroma exhibited significant greater values for M2 and M3 treatments at 0 h. M3 fruit showed the greatest anthocyanin content at 24 and 48 h. Bc incidence was lower in M2 and M3 fruit at 24 and 48 h in Bc-inoculated fruit, whereas control fruit exhibited the highest incidence values at 48 and 72 h in water-inoculated fruit. Interestingly, *Penicillium*-related infection was observed only in control fruit at 72 h. We concluded that preharvest MeJA applied at ripe stage decrease the rate of fruit weight loss but earlier applications during fruit development improve others parameters such as color, anthocyanin content and the incidence reduction of fungal postharvest pathogens.

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PS63

CONTRASTING PHOTOSYNTHETIC RESPONSE OF *Cistanthe longiscapa* UNDER ARID CONDITIONS IN THE ATACAMA DESERT

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The Blooming Atacama Desert is a rare phenomenon that occur when rainfalls exceed the threshold (>12mm/yr) that trigger the blooming of hundreds of endemic species. Within it, *Cistanthe longiscapa,* an annual plant that survive 3-4 months under arid conditions after blooming, is the dominant. A mechanism to survive under arid conditions is to improve the Water Use Efficiency (WUE), this can be done either by reducing the stomatal opening in a C3 plant, thus restricting water loss and carbon gains; or by developing a CAM photosynthesis that limit the carbon gain to the night, decreasing the water loss by transpiration. In particular, *C. longiscapa* have demonstrated to be able of developing both photosynthetic pathways, depending on local climatic conditions. The aim of this work is to determine if different photosynthetic pathway can be favored under local conditions. For this, we studied ecophysiological parameters related to photosynthesis and drought resistance in two locations: the first, close to Vallenar (28°03' Lat. S), and the second, close to Copiapo (27°38' Lat. S), we measure traits like succulence degree, relative water content, leaf mass: area ratio (LMA), $\partial^{13}C$ Isotopic composition, % Nitrogen, % Carbon, chlorophyll content and day/night Δ leaf acidity. Our results show that exist marked differences between the plants from the two locations: plants from the northern locality presents traits related with drought resistance and CAM photosynthesis, while plants in the southern

locality showed parameters related to C3 photosynthesis. These results suggest an adaptive response in *C. longiscapa* under arid conditions and help to explain their plentiful growth under limited water availability in the Atacama Desert.
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PS64

GENETIC DIVERSITY OF SOME ATRIPLEX SPECIES AL ESTACIÓN EXPERIMENTAL LAS CARDAS, UNIVERSIDAD DE CHILE (IV REGION)

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Species of the genus Atriplex (Chenopodiaceae subfamily) are plant halophytes, able to photosynthesize under low soil water availability and high temperatures. Atriplex species arouse a great interest, due to its biomass and palatabilty with potential as biofuel and animal forage, respectively. Its distribution is almost global from subtropical to temperate and subarctic regions, including Australia, North America, South America and Eurasia. Most of the 21 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. The aim of this work is to stablish the genetic diversity of some Atriplex species at Estación Experimental Las Cardas (IV Region, Chile) using SSR markers. In our lab, we have generated microsatellite markers of *A. deserticola and A. atacamensis* from high throughput next generation sequencing, 100 of these SSR markers conserved between both, *A. atacamensis* and A. *deserticola* were evaluated in different Atriplex sp. Of them, 10 were selected as highly polymorphic and used in this study about biodiversity of Atriplex species. These markers could be used in other germplasm analysis, accessing genetic diversity and linkage mapping of *Atriplex* species.
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PS65

POLYPHENOL OXIDASE (PPO) IN LETTUCE (*Lactuca sativa* L.) AS POSSIBLE TARGET FOR USING CRISPR/CAS9 SYSTEM

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The use of minimally processed products is increasing by the conveniences offered by its use. In lettuce (*Lactuca sativa* L.) one of the principal problems in using this industrial process is its susceptibility to enzymatic browning, with polyphenol oxidase (PPO) activity being one of the main responsible. Polyphenol oxidase is an enzyme encoded in the nucleus that is subsequently transported to the plastids, where it is associated with the internal membrane of the thylakoid. For its part, the phenolic substrate is located in the vacuole. Subsequent to the damage generated by the cut enzymatic, browning occurs because these subcellular compartments are lost, generating the oxidation of phenolic compounds to quinones. The production of colored compounds is responsible for the loss of nutritional and organoleptic properties of the product. The lettuce genome (id28333 Genome Center Michelmore Lab unmasked vv8) was analysed bioinformatically for the presence of PPOs orthologues. We found a sequence with 52% identity at the amino acid level. The cloning of PPOs from lettucewas performed successfullyand the deduced peptide of these fragment showed molecular characteristics corresponding to PPOs from other plant species. Also, we set the optimal conditions of light and temperature of growth in greenhouse for lettuce. Finally, we are working in *in vitro* transformation of seedlings of lettuce using the LsPPO::CRISPR/Cas9 system.Future studies will focus on determining the subcellular localization transiently-transformed leaves from *N. tabacum* using the fusion constructs LsPPO::sGPF and LsPPO::mRFP.

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PS66

HYPERSENSITIVE RESPONSE MECHANISM CONTRIBUTE TO PARTIAL RESISTANCE TO SOUTHERN CORN RUST IN TROPICAL MAIZE

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Southern corn rust, caused by *Puccinia polysora* Underw., is a biotrophic fungus that has destructive potential on the susceptible host and is a significant problem for corn producers in America. In Brazil, the yield losses have been estimated at up to 44% on susceptible maize hybrids. In this study, the genetic architecture and identification of genomic regions, including putative candidate genes, associated with southern corn rust (SCR) resistance was investigated performing a genome-wide association (GWAS) study. A genotyping by sequencing was performed to carry out a GWAS study using high-quality single nucleotide polymorphism (SNP) markers (268k) and phenotypic data from two environments on a panel of 164 maize inbred lines that includes popcorn and field corn. Fifteen SNPs were identified as significant for SCR resistance. The associated SNPs were co-localized with previously reported QTL regions, and some of which were novel and adjacent or inside of candidate

resistance genes with functions that would seem likely to be involved in hypersensitive response (HR). HR should act as a mechanism of resistance to SCR that is primarily effective against biotrophic diseases. In addition, the co-localized of candidate genes associated to other maize diseases indicates that resistance to SCR may be controlled by pleiotropic genes. Once the associated SNPs are validated, they will be useful for marker-assisted selection and for a better understanding of maize resistance to southern corn rust.

PS67

IDENTIFICATION OF DEVELOPMENT-REGULATED MICRORNA/TARGET MODULES IN *Arabidopsis thaliana* ROOTS

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The plant root system senses, explores and uptakes nutrients from the soils. At a given time, root system architecture is the result of the integration of external cues experienced by the plant into intrinsic developmental programs. Thus, plasticity of RSA is a dynamic process that changes during plant life cycle according to specific plant requirements to optimize growth in heterogenous and changing environments. Despite the importance of roots for plant growth and productivity, little is known on root plasticity regulators and their impact during different stages of plant development. This is of paramount importance for developing biotechnological applications that target the improvement of root systems for growth in stress conditions such as limiting nutritional conditions. Post-transcriptional gene silencing by small RNAs (sRNAs) is a key determinant of plant developmental processes. To date, the patterns of expression of some sRNAs have been studied in detail during Arabidopsis development in shoot tissue and have been shown to be crucial for timing of phase change. Although root-expressed sRNAs controlling primary and lateral root growth have been identified, their role during specific stages of plant development, the gene regulatory networks (GRNs) that they control, or their role in adaptation to environmental conditions have not yet been identified. In this work, we predicted Arabidopsis microRNA targets using bioinformatics programs and experimental data from available degradome-seq analyses and we analyzed their developmental expression patterns using root transcriptomics datasets. We were able to identify and experimentally confirm diverse development-regulated microRNA/*TARGET* modules in roots. Using available interactomics data, together with our results, we generated miRNA-controlled GRNs expressed at different developmental time points in the root.

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PS68

FUNCTION OF REGULATORY NETWORKS CONTROLLED BY MIR156 / SPL AND MIR172 / AP2 IN THE GROWTH AND RESPONSE TO NITROGEN DEFICIENCY IN ROOTS OF *Arabidopsis thaliana*.

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As sessile organisms, plants have developed sophisticated mechanisms to adapt to environmental conditions which include continuous sensing of their surrounding environment and transduction of these signals into modulation of growth, development and physiology. One of the most important environmental conditions that control organismal responses is nutrient availability. Although there have been significant advances into dissecting how nutrient signals are sensed and transduced by plants, these studies analyze the effect of nutritional changes in a specific time point of the plant life. Plants produce different types of organs at different times throughout their life cycle, thus these different stages of development should have different nutritional demands. Plant development can be divided into discrete phases that include heterotrophic, autotrophic, juvenile, adult and reproductive development. Since each of these developmental stages is expected to express specific genes and gene regulatory networks (GRNs), it is expected that plant responses to nutrients vary accordingly over their life cycle. microRNAs are important regulatory factors in plant development. Among microRNAs, miR156/SPL and miR172/AP2 modules are key microRNAs whose temporal expression in shoots controls the timing of adult and reproductive plant phase change. Furthermore, these microRNAs are differentially expressed in Nitrogen(N)-limiting conditions. Using transcriptomics data and bioinformatics tools, we found that expression of these modules is also regulated in a consistent manner in plant roots. GRN analysis together with phenotypical analysis of plants expressing altered levels of these microRNAs and/or their targets suggest a role for these microRNAs in early post-germinative root development in N-limiting conditions.
FONDECYT-#1170926, Proyecto-#OI101040-Universidad Mayor.

PS69

ANTIOXIDANT ACTIVITY OF AQUEOUS EXTRACT OBTAINED FROM THE ROOTS OF *Acaena pinnatifida* RUIZ & PAV. (ROSACEAE)

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Acaena pinnatifida Ruiz & Pav (ROSACEAE) is a shrub native to Chile, has a wide range of distribution from the 30 ° S (IV region of Coquimbo to XII region of Magallanes) and is characterized by inhabiting open places with little vegetation in conditions of low temperature and rainfall. In the present study, the antioxidant activity of the root extract was determined, using free radicals DPPH (2,2-diphenyl-1-picryl-hydrazyl) and ABTS (2-

azino-bis (3-ethylbenzthiazoline-6-sulfonic acid)) expressed as Gallic Acid equivalentsand Trolox (6-hydroxy-2,5,7,8-tetramethylchroman-2-carboxylic acid) equivalents respectively, indicating that the mean inhibitory concentration (IMC_{50}) for the DPPH test (IMC_{50}= 262 ppm) was 292 mg (6621,51) Gallic acid / g extract and for the ABTS test (IMC_{50} = 122 ppm), 470 mg (8844,6) Trolox / g dry extract. An immediate antioxidant reaction was observed in the kinetics assays, reaching the stationary stage at 10 minutes with 80% inhibition for DPPH and at 13 minutes with 97% inhibition for ABTS. The spectrophotometric analysis using Folin-Ciocalteu Reagent of the *A. pinnatifida* extract, revealed that polyphenols content in gallic acid equivalents was 113, 8 ± 0,012 mg. Qualitative phytochemicals assays revealed the presence of anthraquinones, saponins and terpenoids in *A. pinnatifida*.

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PS70

NITROGEN SOURCE AND CONCENTRATION DETERMINATE THE DIAMETER AND YIELD OF ROOT IN CHICORY (*Ciclorium intybus*) FOR INULIN ACCUMULATION

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Cichorium intybus L is an erect perennial herb with a fleshy taproot. Actually, the chicory is an important crop for industrial extraction of inulin, a polysaccharide with a negligible impact on blood sugar and thus is suitable for diabetics. Nitrogen (N)-based fertilizer increse agricultural productivity but have detrimental effects on the environment. The nitrogen use efficiency (NUE) is crucial for sustainable agriculture. It is involving the uptake, assimilation and utilization. Understand better this process in chicory can involve increse the yield of inulin production and reduce the impact of agricultural effects in the environment. The present research had as aim determinate the adequate nitrogen source, levels and timing for improve the root development and consequent inulin accumulation in chicory. We evaluated the seedling development using different nitrogen sources (NH_4NO_3, KNO_3 and $CO(NH_2)_2$) and concentrations (0,2g/l, 0,4g/l and 4g/l) . We selected the better N source and it was evaluated in greenhouse in 2l pots for different concentration of amonium nitrate (T1=1kg/m^3; T2=0,05g/m^3 and T3=0g/m^3). They were evaluated at 45, 60 and 90 days from seedtime. Both assays were evaluated root and leaf parameters of yield. Plate assay showed that develop of seedling was highly inhibited by higher and lower concentration of nitrogen. The pot assay showed that the higher concentration had the higher leaves number, leaf longitud, fresh leaf weight, fresh root weight and root diameter, however, these results were in general significantly at the day 90. In resume, the optimal concentration of N for aerial organs and root development depend of the stage and source of N, while the effect in root morphology is discussed.

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PS71

REGULATION OF NAC TRANSCRIPTION FACTORS SLNAC43 AND SLNAC49 DURING ABIOTIC STRESS AND AUXIN IN TOMATO

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Water deficit is the main factor affecting the growth and productivity of crops. The tomato is one of the most cultivated vegetables in the world. It is an important source of vitamins, minerals and antioxidants. The cultivated tomato is sensitive to drought stress in the first development stages. On the other hands, the wild parents such as *S. peruvianum* and *S. chilense* show highly desirable characters related with tolerance to biotic and abiotic stresses. The study of these species could be important insight for improve the tolerance to water deficit in plants. The transcription factors (TFs) regulate the expression of different sets of genes. Between them several families of TF are involved in the response to drought stress. More specifically, the family of NAC TFs has been described to be involved in processes such as plant development, senescence, defense and response to stress. Studies have demonstrated the role of these transcription factors in the tolerance to stress. The aims of this study have been directed to analyze the expression of NAC TFs genes SlNAC43 and SlNAC49. They have been related in tomato with response to oxidative damage and auxin respectively. Here, we evaluated the effect of osmotic stress, salt and auxin in the expression of both genes in *S. peruvianum* and *S. lycopersicum* during early period of treatments. These gene are induced mainly in *S. peruvianum* by water stress. These data are correlated with the accumulation of hydrogen peroxide and level of lipoperoxidation.
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PS72

ARABIDOPSIS RNA BINDING PROTEIN RBP31A ASSOCIATE WITH LARGE TRANSCRIPT POOLS INFLUENCING THE CORRECT FORMATION OF THE POLLEN GRAIN AND POLLEN TUBE CELL WALL.

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To achieve a successful fertilization the pollen grain should mobilize and guide their sperm cells into the embryo sac through the growing pollen tube. This process requires careful control of their metabolic processes as well as the expression of the specific set of genes required for this unique process of rapid and dynamic deposition of cell wall precursors at the growing pollen tube. RBP31a is an RNA binding protein which modulates chloroplast transcripts stability and immunity response to pathogens by affecting RNA metabolism. To go further in RBP1a function, RNA-seq analyses were conducted in *rbp31a* and WT pollen grains. This analysis showed that the lack of RBP31a ribonucleoprotein produced an abnormal accumulation of transcripts of genes involved in the cell wall catabolism, defense and plastid biogenesis. Additionally, pollen grains from *RBP31a* mutants exhibit severe changes in the rheological properties of the pollen tube, showing defects in pectin deposition and abnormal branching growth compared to the tip growth of a WT pollen tube. Furthermore, *in vitro* pollen germination of *rbp31a* mutants revealed the secretion of cell wall, emerging from the growing tube. The integration of these results suggests that the dynamic cell wall-associated response and the formation of the pollen grain and pollen tube share common metabolic pathways of cell wall formation.
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PS73

IN SILICO MOLECULAR ANALYSIS OF THE JASMONOYL-ISOLEUCINE PUTATIVE RECEPTORS IN *Fragaria vesca*

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The phytohormone jasmonoyl-isoleucine (JA-Ile) regulates fundamental processes in plants. The woodland strawberry (*Fragaria vesca*) is a model plant for the Rosaceae family, in which the JA-Ile signaling pathway is poorly understood at the molecular level. JA-Ile mediates binding of the JAZ repressor protein to COI1 to form a functional JA-Ile receptor in Arabidopsis. The aim of this work was to understand the molecular basis of the interaction between the *F. vesca* COI1 (FvCOI1) and JAZ1 (FvJAZ1) or JAZ8 (FvJAZ8) mediated by JA-Ile. The FvCOI1 and FvJAZ1/8 3D structures were built by homology modeling methods, which were further refined and validated by molecular dynamics simulation (MDS). A molecular docking approach along with MDS analysis were used to evaluate the interaction capacity between a putative degron-like present in FvJAZ1 and FvJAZ8 with the FvCOI1-JA-Ile and FvCOI1-JA complexes. Unexpectedly, we found that FvJAZ1 has a variant degron sequence respect to the canonical degron sequence observed in AtJAZ1. The MDS results showed that the FvCOI1-JA-Ile-FvJAZ1 complex was the most stable among all the analyzed ones, and the FvJAZ1 degron interacted directly with FvCOI1 and JA-Ile. The

present research provides novel insight into the molecular interactions between key JA-Ile perception components in the model plant *F. vesca*.
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PS74

THE HISTONE ACETYLATION IS INVOLVED IN THE BORON TOXICITY RESPONSE IN *Arabidopsis thaliana*

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Boron is an essential micronutrient for plant growth and development. Despite the great importance of boron, only a narrow range of concentrations between deficiency and toxicity is considered optimal. Toxic effects of boron might include inhibition of cell division, defects in cell wall development, metabolic disruption, decrease of photosynthetic pigments and an increase in accumulation of total soluble and insoluble sugars. Adaptation to environmental stress requires genome-wide changes in gene expression. Histone modifications are involved in gene regulation, but the role of histone modifications under boron stress is unknown. In this work, evidence that the histone acetylation is involved in boron toxicity response in *Arabidopsis thaliana* is shown. The histone acetyltransferase GCN5 loss-of-function plants are hypersensitive to boron toxicity, reducing significantly the root growth and chlorophyll content. In addition, the yellowed leaves phenotype of plants grown in higher boron concentration was reverted when plants were additionally treated with Trichostatin A (TSA), a broad-spectrum histone deacetylase inhibitor, suggesting that TSA can antagonize the toxic effect of boron in leaves. A phenotypic screening using histone deacetylase mutant plants will reveal which genes are involved in this response. Environmental stresses, such as boron toxicity, cause significant yield losses annually. Further studies on how chromatin modifications are involved in plant stress response will contribute significantly to our understanding of the molecular mechanisms underlying plant response to environmental stresses, which may ultimately be applicable to improve agricultural productivity.
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PS75

IN SILICO AND FUNCTIONAL CHARACTERIZATION OF DIFFERENTIALLY EXPRESSED TONOPLAST INTRINSIC PROTEIN (TIP) IN *Prunus* ROOTSTOCKS WITH CONTRASTING RESPONSE TO WATERLOGGING

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Crop plants are exposed to a variety of environmental factors that unfavorably affect their growth and productivity. Abiotic stresses, such as heat, waterlogging, freezing, drought and salinity, result in the production of reactive oxygen species (ROS) and the generation of oxidative stress, which can cause several cellular damages. Aquaporins (AQPs) are ubiquitous and multifunctional membrane proteins present in plants. AQPs transport a wide range of substrates such as ammonia, arsenite, boron, carbon dioxide, glycerol, urea, and others. Recently, it has been reported that members of some Tonoplast Intrinsic Protein (TIP) are also able to transport hydrogen peroxide. In order to obtain a better understanding of the role of TIP in response to abiotic stresses, two *Prunus TIP* genes with contrasting transcriptional profile between hypoxia-tolerant and hypoxia-sensitive genotype were analyzed. *In silico* analysis were used to construct structural models based on comparative modeling of the putative pore regions of TIPs from genotypes with contrasting responses to hypoxia stress. We determinate potential substrates of these selected TIPs using molecular simulations, homology modeling and structural comparison. Furthermore, structural differences between genotypes were studied. Finally, a functional analysis was performed through a hydrogen peroxide permeability assay in *Saccharomyces cereviceae* using an endogenous knockout mutant AQP strain (aqy-null strain) and complemented with TIP genes of interest inserted into the yeast expression vector pYES2.1-/V5-His-TOPO. Results of this study show significant differences between the analyzed genes, both in the computational as in the functional analysis.
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PS76

SPECIES OF KIWIFRUIT (*Actinidia spp.*) SHOW DIFFERENT RESISTANCE LEVELS TO THE PATHOGEN *PSEUDOMONAS SYRINGAE* pv *ACTINIDIAE* (Psa)

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Pseudomonas syringae pv. *actinidiae* (Psa) is the causal agent of the canker kiwifruit disease which generates severe consequences for the production of kiwifruit in Chile, Europe, Asia and New Zealand. The kiwifruit industry has produced several varieties in order to improve the yield and organoleptic features of this fruit. However, all of these varieties have been shown to be susceptible to Psa since the 2011 global outbreak of Psa, which also affected

Chile. The main cultivar grown here is the *A. deliciosa* var. *Hayward*, but recently the use of *A. chinensis* varieties has been increasing. Interestingly, it has been suggested that distinct varieties of this crop show different levels of damage under Psa infections. Thus, we are interested in defining the levels of resistance in the varieties grown in Chile and whether this resistance levels are associated to differences in the defense response mediated by salicylic acid (SA), a key regulator of plant defense responses. To asses this, we inoculated 3-4-month-old plants with a Psa isolated in Chile and quantified bacterial proliferation and area of damage in the inoculated leaves. Among the varieties and species evaluated, we observed that *A. arguta* was the most resistant to Psa attack, and the most susceptible was *A. chinensis* var KC8. In this species, we are currently evaluating the expression level of defense genes associated to the SA-defense pathway during early times of Psa inoculation along with the SA levels on basal and Psa-infection conditions.
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PS77

SUGAR AND RIPENING, A TRANSCRIPTOMIC ANALYSIS TO UNDERSTAND THE REGULATORY PROCESS OF GRAPE BERRY DEVELOPMENT

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Grape berry (*Vitis vinifera* L.) is a non-climacteric fruit, in which the main regulatory process that induce ripening are still unclear. Due to the change in the sugar content is one of the most important event occurring during ripening, in this work the possible ripening inductive role of sugar was studied, and for this, berries of cv. Red Globe treated with different sugar solutions, were analyzed. The results showed that sugar treated berries were bigger and entered veraison earlier than the control ones, and concomitantly showed an increase in the anthocyanins and sugar content. We performed a transcriptomic analysis using RNAseq platform, which revealed that 387 genes change their expression pattern by sugar treatment. The Enrichment analysis of Gene Ontology terms, on the other hand, showed that several genes associated to different metabolic processes, such as cell wall modification, carboxylic acid metabolism, among others, were enriched. Finally, in order to identify the putative regulators that participate in the ripening regulation, a co-expression analysis was carried out. The network analysis revealed that 192 genes were co-expressed, of which, 8 transcription factors could be involved in this process. Our results showed that sugar treatments accelerate grape berry ripening and induce transcriptomic changes that probably participates in this process. Suggesting that during grape berry development, sugar could be an important metabolite signal that induce ripening. Also, we identified 8

putative transcription factors that could be part of the transcriptomic regulation of this process.

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PS78

THE ROLE OF ATPLCS IN THE NITRATE SIGNALING PATHWAY OF *Arabidopsis thaliana* ROOTS

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Nitrogen (N) is an essential macronutrient for plant growth and development. Different N nutrient/metabolites can also act as signal molecules that regulate gene expression and a myriad of biological processes in plants. Understanding molecular components involved in N sensing and signaling and how plants sense and respond to changes in N availability are essential to improve nitrogen-use efficiency and crop yield. We show that Ca^{2+} is a second messenger in the NRT1.1-dependent nitrate signaling pathway in Arabidopsis. Moreover, our data indicates the nitrate transceptor NRT1.1/AtNPF6.3 activates a phospholipase C (AtPLC) that is required for increased levels of inositol 1, 4, 5- trisphosphate (IP_3) and an increase in cytoplasmic Ca^{2+} concentration ($[Ca^{2+}]_{cyt}$). We also showed this NRT1.1-PLC-Ca^{2+} pathway impacts gene expression of nitrate-responsive genes in roots of *Arabidopsis thaliana*. Here we used transcriptome analysis to identify genes that require PLCs in a nitrate-dependent manner at a genome-wide level. Moreover, ongoing characterization of AtPLC proteins highlights the role of root-specific isoforms for nitrate responses. Our findings suggest a model where nitrate is sense by NRT1.1 and a phospholipase C activity mediates the increase of Ca^{2+} required for changes in expression of canonical nitrate-responsive genes. Identifying and characterizing the function of the different players involved in nitrate signaling pathways and their functional relationships is essential to understand N responses in plants.

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PS79

MOLECULAR CHARACTERIZATION OF TRADITIONAL YELLOW MAIZE VARIETIES FROM COIHUECO, ÑUBLE PROVINCE, CHILE

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Morphological studies have revealed that there is variability within and among the different populations of yellow maize grown by small farmers in Coihueco commune, Ñuble province, distinguishing at least three distinct morphotypes, one of which may be associated with a maize described for Chile. Knowing diversity and relationships between populations is important for conservation and promoting their direct or indirect use. In this study 12 SSR were used to characterize the diversity of 28 traditional maize accessions: 11 from Coihueco,17 accessions conserved at the La Platina Germplasm Bank, INIA, Chile, used as references to associate the yellow maize to a specific Chilean racial type. Diverse indices show the existence of diversity between and within populations. Amova revealed that 81% of variability was due to differences among individuals. The PCoA and the dengrogram showed that the yellow maize of Coihueco conform at least 4 subgroups that are associated with samples belonging to the Curagua, Amarillo de Ñuble and Ocho Corridas maize races, evidencing admixture between distinct types of maize. Structure identified two genetic groups. It is necessary to expand the reference samples to obtain a better classification.
FIA Project PYT-PYT-2015-0387; Fontagro Project FTG/Rf-15460-GF, INIA/Min. Economía Red de Bancos de Germoplasma Project 501679-71; INIA/MINAGRI Conservación de Recursos Genéticos Project 501453-71.

PS80

IMPROVED OF WATER USE EFFICIENCY IN Arabidopsis thaliana PLANTS BY OVEREXPRESSION OF THE CITRUS TRANSCRIPTION FACTOR MYB61

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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 *CsMYB61* homologous gene of *AtMYB61* in *A. thaliana*, under the transcriptional control of a specific stomatal promoter *CsMYB15*, increases the WUE in arabidopsis plants under water stress. To do this

we identified, isolated and sequenced the *CsMYB61* coding region and also the promoter *CsMYB15*. The protein encoded by *CsMYB61* has characteristic domains and motifs of other *AtMYB61* 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, *pCsMYB15* directs the expression of the reporter gene *GUS* in stomata by red light induction. *A. thaliana* lines over-expressing *CsMYB61,* have a normal phenotype under *in vitro* and greenhouse conditions. WUE assessment under water stress shows increase in several *A. thaliana* lines. This approach opening the possibility to use this strategy in others agricultural species.

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PS81

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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PS82

Hoffmannseggia doelli: CHARACTERIZATION OF AN EXTREMOPHILE PLANT FROM ATACAMA DESERT

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Under the current global climate change scenario, the discovery and characterization of plant species adapted to extreme environmental conditions has become increasingly important. *Hoffmannseggia doelli* ("mutukuru") is an endemic perennial herb of the Chilean Atacama Desert that grows between 2900 and 3800 meters above sea level (m a.s.l.) in the western Andes Mountains. Its growing habitat is characterized by high radiation (³620 watt/m^2), low water availability (~ 76 mm annually) and nutrient-poor soils. Under these conditions, *H. doelli* is able to develop a tuberous root, which has served as a food source for Atacama natives over centuries. This work constitutes the first attempt to establish *H. doelli* cultures under laboratory conditions. We optimized growth conditions as a foundation for future physiological and genetic studies that will help to unravel the strategies that allow its growth under extreme abiotic conditions. We showed that under our experimental conditions *H. doelli* germinate and growth. We can also obtain tuberous roots in 45 days. We are currently sequencing the *H. doelli* genome, in an effort to advance our knowledge about this species and the identification of genes involved in tolerance to extreme abiotic conditions.

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PS83

NITRATE ADDITION TRIGGERS SPECIFIC CHANGES IN THE TRANSCRIPTOME OF ACTIVE *Medicago truncatula* NODULES

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Nitrate not only reduces nodulation in legumes but also down-regulates the activity of existing nodules. The goal of the present study was to identify early events after nitrate application that would precede and possibly initiate the physiological inhibition of nodule activity. The hypothesis is that early events are locally induced and nodule-specific and would reveal possible hubs for the later observed changes in the transcriptome that coincide with declining nodule activity. Nodulated *Medicago truncatula* plants were grown

in a quasi-flow-through nutrient solution culture and the nodule activity was monitored. After addition of 5 mM nitrate to the nutrient solution, nodule activity remained stable for at least two hours. One hour after nitrate application RNAseq analysis of leaves, roots and nodules was carried out. Nitrate had no effect on the leave transcriptome, while in roots, the nitrate uptake system and enzymes for nitrate reduction and N incorporation were induced. The nodule transcriptome showed large shifts in gene expression already after 1 h nitrate addition. A large proportion of the affected TUs were expressed nodule-specific. The reduction of a great number of TUs for NCR-peptides, together with a beginning decline in leghemoglobin expression were two notable effects. Overall, the nitrate induced changes in the nodules proved to be complex and multifold. It is concluded that therefore an uncoupling of nitrate application and reduction of nitrogenase activity will be a difficult task.

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PS84

INTERACTION BETWEEN *Arabidopsis thaliana* AND *Sinorhizobium meliloti* FOR IMPROVED PLANT GROWTH AND NITROGEN NUTRITION

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Nitrogen (N) is an essential macronutrient whose availability in the soil has a critical role in plant growth and development in natural as well as in agricultural environments. Plants acquire N directly from the soil and in some cases N can be provided by interacting with N-fixing bacteria. This type of interactions is well described in legumes, but are also observed in some non-legume plant species, that are unable to form nodules. Understanding these plant-bacteria interaction mechanisms could have important agronomic implications, reducing the use of N-fertilizers in non-legume crops. Our goal was to evaluate a functional association between a non-legume model plant, Arabidopsis thaliana, and a N-fixing model bacteria, Sinorhizobium meliloti, to study and identify molecular mechanisms underlying this association. We found A. thaliana growth under N-limiting conditions is enhanced by S. 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 plants indirectly acquired atmospheric N, where 14N isotope predominates. We also determined bacterial root colonization through different types of microscopy, locating the bacteria in the outer layer of the root. This was also corroborated by an endophytic assay where it was shown that S. meliloti is not an intracellular bacterium when interacts with Arabidopsis. Finally, we demonstrated that Arabidopsis homologs of key regulatory genes involved in legume:rhizobium interactions are required for Arabidopsis growth promotion mediated by S. meliloti. Our results suggest a non-canonical interaction between A. thaliana and S. meliloti RMP110, without nodule formation, or intracellular colonization of the bacteria, but with conserved molecular

mechanisms of legume:rhizobium interactions for improved growth under N-limiting conditions.

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Regulation 15090007.

PS85

CONTENTS OF CARBOHYDRATES IN STEM AND STARCH IN KERNELS OF FOUR CEREALS GROWN IN GREENHOUSE

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Cereals such as wheat and barley have carbohydrate reserves that are stored mainly in the stem as water soluble carbohydrates (WSC) and are composed predominantly of fructans called graminanes. The accumulation of soluble carbohydrates in the stem is influenced by environmental and genetic factors. In this work, we study the dynamic of water soluble carbohydrates (WSC) in the stem and the accumulation of starch in kernels of four cereal species: bread wheat (*Triticum aestivum L.*), durum wheat (*Triticum turgidum var. durum L.*), barley (*Hordeum vulgare L.*) and triticale (*Triticosecale Wittmack*) exposed to two well-watered (control, no stress condition) and 60% lower than the control (moderate water stress condition), starting from the flag leaf stage (terminal water stress). The quantification of WSC in two segments of the stem (upper two and lower internodes) was performed by the anthrone method and starch in kernels using the kit Starch de Boehringer Mannheim, R-BIOFARM. The concentration and content of WSC in the different internodes were reduced in the water stress condition. Triticale showed the highest levels of WSC in the stem and weight of spike. Bread and durum wheat showed a similar content of WSC in the two water conditions. Barley presented the lowest WSC in the stem and weight per spike, but it produced higher number of spikes. The pattern of starch accumulation in kernels showed no differences between the water availability, but was higher in barley.

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PS86

A CHILEAN CORE COLLECTION FOR SWEET CHERRY (*Prunus avium* L.) BREEDING BY THE MEANS OF DIVERSITY AND FRUIT QUALITY MOLECULAR MARKERS

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Sweet cherry (*P. avium* L.) production in Chile involves an increasing area the last decade. However, if we cannot access to new varieties with improved fruit quality in the future, our competitiveness could be limited. Supported by the state, the Chilean industry has implemented its own breeding programs for sweet cherries such as the INIA-SCBP (INIA-Sweet Cherry Breeding Program). Obtaining a germplasm collection has been one the most important goal, which mainly comes from Europe and North America breeding programs. Until now more than 60 genotypes have been collected, and it is increasing in size. These sweet cherry varieties, and clone individuals, constitute a genetic pool carrying desirable allele genes to build up our future new sweet cherry varieties. Large size of parental collection often complicates the characterization, evaluation, utilization and maintenance of the conserved germplasm for most species; this situation is much more important in sweet cherry with big trees that require extensive field surface and significant maintenance labor. Therefore, a core collection with a minimal set of progenitors representing the genetic diversity but carrying the best alleles to improve the fruit of sweet cherry is desirable. Using a set of 18 SSR, including 5 markers associated to color, fruit size, maturity time and cross compatibility, with criteria of maximum genetic diversity, best allele combinations for desirable quality of cherry fruits and cross compatibility, a minimal group of genotypes as core collection for the INIA-SCBP is proposed
FONDECYT REGULAR 1161377; INNOVA CORFO 09PMG 7243.

PS87

THE FIRST DRAFT OF THE SWEET CUCUMBER (S*olanum muricatum*, AITON) GENOME SEQUENCE

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Sweet cucumber (*Solanum muricatum* Aiton) also known as pepino dulce, is an herbaceous perennial plant that is grown for its sweet edible fruit. Native to the Andean region, it was likely introduced by the Incas in Chile. At the present time, it is mainly cultivated in north-central regions of Coquimbo and Valparaíso. Never important as tomatoes or potatoes, several countries had introduced this species as crop, including establishment of breeding programs to obtain new varieties. INIA collected the most representative material

cultivated by farmers in the north-central regions of Chile, which is maintained as genetic backup at Pan de Azúcar Experimental Station (INIA-Intihuasi, La Serena). Also, this material represents the germplasm collection to initiate breeding activities, to obtain improved varieties with better agronomical qualities and high content of compounds that protect the human health. In order to understand molecular and genetic mechanisms associate to important traits, and to facilitate the selection of parent and progenies a genomic platform of pepino is desirable. In this study, first time the genome sequence of *Solanum muricatum* has been deciphered. The genome was sequenced employing Illumina paired-end libraries, de novo assembly was constructed using the software program SOAPdenovo2. The genome was assembled into 320871 scaffolds (N50 contig length 7 kb) and covers a total of 918 Mb, and GC content of 38.99%. We compare assembly with genomes of tomato and potato. Ab initio gene prediction combined with prediction based on homology and transcriptome of *Solanum muricatum* available, was made. This genome assembly is a valuable tool for identifying the genetic control of key traits in pepino and will enable wide applications such as marker-assisted and genomic selection that will enhance the speed and efficiency cultivar development.

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PS88

CELL WALL AND METABOLITE COMPOSITION OF BERRIES OF *Vitis vinifera* (L.) CV THOMPSON SEEDLESS WITH DIFFERENT FIRMNESS

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Firmer berries are highly appreciated by table grape consumers. The factors that influence changes in berry firmness during postharvest remain poorly understood. In the present study, we evaluated the firmness of berries of *Vitis vinifera* (L.) cv. Thompson Seedless from different orchards of central valley of Chile. We selected two orchards with contrasting berry firmness and evaluated polar metabolites and cell wall polysaccharide composition. Our results suggest that berries obtained from the orchard that produced softer berries accumulated more soluble arabinose and rhamnose at veraison than firmer berries, based on metabolomic analyses. This correlates with information obtained of cell wall monosaccharide determinations. On the other hand, orchards that produced harder berries had less rhamnose, arabinose and glucose monosaccharides on its cell wall components; altogether metabolome profile indicated that more soluble catechin at veraison developmental stage. Analogously, at harvest the cell wall monosaccharides had the same pattern already explained between soft and firm berries, except for glucose that had an

opposite behavior. Additionally, the polar metabolites measured at harvest showed a different distribution than veraison. Thus, this study offers new insights about a connection between polar metabolites, cell wall polysaccharide changes and berry firmness, suggesting that is possible to use metabolomic tools to identify potential biomarkers associated to table grape berry quality.

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PS89

METABOLOMIC PROFILES ASSOCIATED TO SOLUBLE SOLID CONTENT AND MEALINESS SUSCEPTIBILITY IN PEACH (*Prunus persica* L. BATCH) DURING POSTHARVEST

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The soluble solid content (SSC) and susceptibility to develop mealiness are among the most important parameters in the quality of peach fruit. Especially because of long periods of cold storage lead to the development of a physiological disorder known as chilling injury. In the present study we evaluated fruit quality parameters such as SSC and mealiness development of a peach segregating population (O´Henry x NR-053). We selected two groups of peaches, that contrast in the SCC at harvest and another group that contrasts in the mealiness susceptibility after cold storage. In these phenotypes, untargeted metabolomic profile of polar compounds was evaluated by GC-TOF-MS. Principal component analysis (PCA) showed peaches with high SSC were different in their metabolomic profile in relation to peaches with low SSC. Partial least square with discriminant analysis (PLS-DA) showed that fucose and isoleucine was the metabolites related to high SSC peach. On the other hand, sorbitol and digalacturonic acid was the metabolites related to low SSC. In the evaluation of metabolomic composition in peaches that developed mealiness. After cold storage, PCA showed that mealy peaches were different in they metabolomic profile from the peaches that not presented mealiness symptoms. PLS-DA indicated that succinic acid and valine were metabolites highly correlated with fruit that developed mealiness after cold storage. All the metabolites mentioned are potential candidates for biomarkers of peaches for SSC and mealiness susceptibility phenotype respectively. (Fondef Genoma G13I0005).

PS90

FIRST DRAFT GENOME SEQUENCES OF *Prunus* SP ROOTSTOCKS OBTAINED BY THE MEANS OF *DE NOVO* ASSEMBLING

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Stone fruit (*Prunus* L.) production in Chile covers around 43,000 ha that includes a wide variety of soils and climates requiring a large diversity of rootstocks. Nowadays, most rootstocks cultivars are clonally propagated, but some are still being propagated by seeds. Belonging to subgenera *Amygdalus* L. (peach group), *Prunus* Focke (plum group), and *Cerasus* Adans. (cherry group), several modern rootstocks are generated by inter-specific crosses, including some inter-subgenera crosses. A better understanding about the molecular response to different stimulus such as abiotic and biotic stresses will contribute to the breeding efforts. At molecular level, different phenotypic responses should be associated with allelic diversity at gene regulatory and/or ORF regions. Available *Prunus* reference genomes, such *P. persica* (L.) and *P. mume* (Siebold & Zucc), are useful platforms to support molecular studies, especially within the same species. However, they have serious limitations when sequences from gene regulatory regions, which are much more diverse among species and subgenera, are compared. To get the regulatory sequence of genes involved in hypoxia stress response and other stimulus, genome sequences of 'Mariana 2624' (*P. cerasifera* x *P. munsoniana* W. Wight & Hedrick), 'Mazzard F12/1' (*Prunus avium* L.), 'Adara' (*P. cerasifera* Ehrh.), and 'Rainier' (*P. avium*) were obtained by the means of *de novo* assembling using Illumina paired-end libraries. *De novo* assembly was constructed using the software program Platanus. Genome coverages were 200, 209, 231 and 290 Mb for 'Rainier', 'Adara', 'Mazzard F12/1' and 'Mariana 2624', respectively. These drafts complement the available public *Prunus* platform.

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PS91

WRKY7, -11 AND -17 TRANSCRIPTION FACTORS, ARE REPRESSORS OF UNFOLDED PROTEIN RESPONSE GENES THROUGH bZIP28 TRANSCRIPTION FACTOR, DURING PAMP-TRIGGERED IMMUNITY IN *ARABIDOPSIS THALIANA*

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Plants have evolved sophisticated mechanisms to protect themselves from pathogens. The recognition of pathogens triggers a signaling cascade, which leads to the biosynthesis of salicylic acid, ROS, callose and the upregulation 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 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.To get insights about the molecular mechanisms involved in WRKYs mutant resistance phenotype and UPR, we analyzed the expression of the main components of the signaling pathways suggesting that bZIP28 transcription factor plays a key role in the regulation of ER chaperones upon plant exposure to Flg22. We show that triple *wrky*-mutant plants are more effective at establishing a defense response against *Pst* DC3000 infections. Additionally, triple *wrky* mutant plants exhibited a larger number of callose deposits and accumulates more transcript of ER chaperones in response to Flg22. Also, *wrky* mutant accumulates more transcript of *bZIP28* suggesting that WRKY7, 11 and 17 acts as transcriptional repressors of this gene. Using Arabidopsis protoplast assays we tested if WRKY7, 11 and 17 can bind bZIP28 promoter trough W box *cis*-elements. Based on these results, we postulate a fine-tuning model of basal defense response regulation in Arabidopsis, including the negative control of gene expression associated with UPR genes controlling the physiological response of plant-pathogen interaction.
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PS92

COMPARATIVE GENOMICS FOR THREE SWEET CHERRY VARIETIES

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Sweet cherry (*Prunus avium*, 2n=2x=16) belongs to the *Rosaceae* family and is one of the most produced and exported fresh fruit from Chile, the main producer of the Southern Hemisphere.Developing of sweet cherry varieties well adapted to local conditions, with high crop yields represents a major challenge and genomic-based breeding programs could help to address it. Despite its commercial importance, there's a lack of genomic information in order to facilitate the identification of features associated to agronomical important traits. Our proposal was to perform an *in silico* comparative genomics strategy to search for meaningful structural differences between three sweet cherry varieties 'Karina', 'Kordia' and 'Royal Dawn', comparing them to the recently published genome of 'Satonishiki' Japanese sweet cherry variety. A whole genome sequencing strategy using

Next-Generation Sequencing technologies was performed, obtaining paired libraries with a total of 434.6 million of reads for 'Karina' variety, 214.2 million for Kordia' variety and 273.6 millions for the 'Royal Dawn' variety. These reads were mapped to the genomic sequences of 'Satonishiki' with a mapping efficiency of 90.5%, 87.9% and 86.6% respectively. Furthermore, we have successfully mapped 7078 SNP publically available to the reference genomic sequences in order to guide the variant discovery. Finally, using the mapped reads, we have constructed a partial draft for each of the three varieties (N50 ~0.22 Mbp and longest scaffold ~1.4 Mb) for using in further genomic studies.
FONDEF G09I1008 and CORFO 13CTI250-SP05.

PS93

ROLE OF *GSTU7* IN THE ANTIOXIDANT RESPONSE MEDIATED BY TGA CLASS II TRANSCRIPTION FACTORS

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Oxidative stress in the cell is produced by the accumulation of reactive oxygen species (ROS) above basal conditions, and is the principal consequence after the exposition to some abiotic stress factors like the herbicide methyl viologen (MV) and UV-B radiation. TGA class II (TGA2, 5 and 6) transcription factors (TFs) have an important role in the defense response against these stresses. *Arabidopsis thaliana tga256* mutant displays an increased sensibility to oxidative damage compared to *wild type* plants. We inquired about how TGA class II TFs are mediating this defense response. RNA-seq analyzes developed in our laboratory showed that under UV-B treatments TGA class II TFs controls the expression of a set of genes with antioxidant functions. Among these, the tau class glutathione S-transferase *GSTU7*, which has one of the most elevated basal expression levels within the GSTs, has a conserved TGA box (the sequence to which TGA class II TF's bind) in its promoter, and a reported *in vitro* glutathione peroxidase activity. All the current evidence leads us to hypothesize that the expression of *GSTU7* is directly regulated by TGA class II and that it is important for the antioxidant response mediated by these TF's. Here we evaluated the direct interaction between TGA2 and *GSTU7* promoter, and demonstrated that *GSTU7* has an important role in the response to oxidative stress caused by MV. Finally, we show the advances in the generation of the molecular tools needed to evaluate the ability of *GSTU7* to complement the *tga256* phenotype under oxidative stress conditions.
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PS94

GENETIC ANALYSES FOR ANTHOCYANIN CONTENT IN A JAPANESE PLUM F1 PROGENY

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Anthocyanin compounds are key elements as colour determinants and functional compound in plant-derived foods. The discovery of genetic markers for assisted selection of new varieties with increased functional compound content, as well as identification of candidate genes controlling fruit secondary metabolite content, are central objectives in our research. In order to pursue these aims in a commercially important species for Chilean fruit production, we performed an initial genetic analysis for individual anthocyanin content in a Japanese plum (Prunus salicina L.) F1 progeny obtained from the cross between the selection 98-99 and the cultivar Angeleno. HPLC-DAD was employed for anthocyanin profiling in skin (SK) and flesh (FL) methanolic extracts from fruits harvested at commercial maturity in 90 F1 individuals, for which genotypic data for 4058 SNPs were available after Genotyping-By-Sequencing. Two HPLC signals (peaks), previously identified as cyanidin-3-glucoside (C3G) and cyanidin-3-rutinoside (C3R) were detected in concentrations hundreds to thousand times higher than the other detected peaks. C3G and C3R, as well as minor-content anthocyanins (here called "M" and "K"; identification under progress) showed significant genetic contributions to phenotypic variance ($p < 0,001$). Parametric and non-parametric QTL-analyses (Interval Mapping and Kruskal-Wallis, respectively) were performed using linkage mapping for both parents, separately. Significant marker-trait associations ($p < 0,05$) were detected mainly for compounds present in skin samples. QTLs located in linkage-groups (LG) 1, 3, 4, 5 and 7 of Prunus genome explained between 38% and 45% of the total phenotypic variance. The results here presented, constitute a first step for genetic architecture of secondary metabolite content characterization in Japanese plum fruits.

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PS95

VALIDATION OF MIRNAS INVOLVED IN REGULATION OF GENE EXPRESSION ASSOCIATED WITH DORMANCY AND COLD REQUIREMENT IN SWEET CHERRY (*Prunus avium*).

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Sweet cherry (*Prunus avium L.*) is a flowering plant belonging to Rosaceae family that is grown on temperate climates. In the early fall the temperature and daylight hours decrease promote the entry to the dormancy state, an evolutionary phenomenon relevant for survival during the adverse conditions on winter. Dormancy is divided into three stages, para-dormancy, endo-dormancy and eco-dormancy in which certain requirements must be completed in order to resume grown. The first requirement corresponds to cold accumulation during winter (endo-dormancy) and then warm accumulation at the beginning of spring (eco-dormancy) to finally lead to flowering. There are several genome regions that are transcribed but do not encode for proteins, many of these transcripts produce sRNAs (small RNAs) which regulate biological processes by modifying gene expression. Micro RNAs (miRNAs) are a type of sRNA that generates direct mRNA cleavage, translational silencing or transcriptional silencing by DNA methylation after the recognition of their target sequences. In our laboratory, the analysis of sRNAs during dormancy was made in flower buds of *Prunus avium* cv. 'Bing' by high throughput sequencing. miRNAs with differential expression patterns were identified during bud dormancy in sweet cherry. Among them it was observed that miRNA miR156 increases its expression towards eco-dormancy, and by using an *in silico* analysis it was observed that the *PavSPL13* gene that is related to flowering in *Arabidopsis* was recognized by miR156.
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PS96

REAL-TIME MONITORING OF GLUTATHIONE REDOX STATE CHANGES UPON OXIDATIVE STRESS TO EVALUATE THE ANTIOXIDANT ROLE OF GSTU IN *Arabidopsis*

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Methyl Viologen (MeV) is a non-selective herbicide that induces oxidative stress in plant cells mainly by affecting the chloroplast. MeV transfers electrons from the Photosystem I to molecular oxygen (O_2), generating superoxide (O_2^-). In non-plant organisms, MeV accepts electrons from the complex I of the mitochondrial electron transport chain and transfers them to O_2, producing O_2^-. Cellular superoxide dismutases efficiently convert O_2^- to hydrogen peroxide (H_2O_2), which triggers the oxidative response in the cell. This response oxidizes lipids, alters the redox state of the main antioxidant buffers in the cell, ascorbate and glutathione, and induces the expression of a set of antioxidant genes, among them, glutathione S-transferases of the tau subfamily (*GSTU*s). Here, we assess *in vivo* real-time

changes in the glutathione redox state upon treatments with MeV by using the genetically encoded sensor Grx1-roGFP2 and evaluate this tool for the functional characterization of GSTUs. For this purpose, we developed a plate reader-based high-throughput approach to monitor glutathione redox state dynamics at high temporal resolution in seedlings and leaf discsof *Arabidopsis* plants, by ratiometric analysis of the roGFP2 fluorescence. Upon treatments with specific electron transport inhibitors, we also established the contribution of chloroplasts and mitochondria to the overall superoxide production. Furthermore, we tested the relevance of candidate antioxidant *GSTU*s genes in the containment of the oxidative stress by expressing the sensor in *GSTUs* mutants and over-expressing lines of *Arabidopsis*. By comparing the sensor response in these lines, we observed strikingly different sensitivities towards MeV-induced response, indicating the involvement of GSTs in the response to photo-oxidative stress.

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PS97

PHENOTYPIC AND GENE EXPRESSION CHANGES ON PEDICEL IN RESPONSE TO EXOGENOUS GIBBERELLIC ACID TREATMENT ON TABLE GRAPE

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Gibberellic acid (GA_3) treatments have been previously linked to negative effects such as berry drop which can be a serious postharvest problem in terms of exportation of grapes for fresh consumption. The characterization of susceptibility to berry drop suggests that there is genotype-dependent response to GA_3 treatments. For example, genotype 'L#23' had shown to be up to 10-fold more susceptible to berry drop than 'Thompson Seedless' (three seasons of evaluation). Further analysis suggest that this phenomenon could be affected by morphological changes on the pedicel as consequence of GA_3, with major stiffness on treated group. RNA-sequencing on pedicel tissue was performed to characterize and identify differentially expressed genes, considering a total of 32 libraries, including: two genotypes ('L#23' and 'Thompson Seedless') and two levels of treatment (Control and GA), with four biological replicates for each group and paired-end sequencing. Differential expression analysis identified a set of 1098 and 1525 up-regulated genes by GA_3 on 'L#23' and cv. 'Thompson Seedless', respectively (p-value≤0.01, FDR≤0.05, logFC≥2). Gene set enrichment analyses from such sets suggested the involvement of xylem development, flavonoids, phenylpropanoids and cell wall organization processes, among others. Validation through qPCR from a subset of selected genes on several

developmental stages proved the usefulness of the transcriptomic approach in order to develop molecular tools to characterize a complex trait such as berry drop. This is the first work providing transcriptional information on pedicel tissue for *V. vinifera* L. table grape considering regular management conditions.
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PS98

ONE POLYCISTRONIC AMIRNA TO TARGET THREE DIFFERENT GENES

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Artificial miRNAs have been widely used as a tool to target exogenous and endogenous genes in plants. In previous works, we have described the use, synthesis, and mobility of small RNA molecules derived from artificial versions of the *Vitis vinifera* 319e miRNA (avvi-miR319e). In the present work, we developed the proof of concept for the avvi-miR319e capability for multiple gene silencing by generation of in tandem versions of the avvi-miR319e. A 500 bp polycistronic molecule was designed, in which 3 amiRNAs were content. The secondary structure of the polycistronic design was verified using Mfold. The polycistronic amiRNA functionality was evaluated by use of an amiRNA targeting GFP (*gfp*-amiRNA) located at each possible (i.e. first, middle, third) position in message, in 3 different polycistronic constructs. Other amiRNAs in the message included relevant grapevine virus sequences. Stable lines of double transgenic *N. benthamiana gfp*$^{+}$/*polymirna*$^{+}$ showed that regardless the position in which the *gfp*-amiRNA was positioned, the *gfp* expression was significantly reduced. Further stem-loop PCR analysis proved that all 3 amiRNAs conforming the polycistronic message on each construct (i.e. for gfp and viruses), were correctly generated in every transgenic line. Results demonstrated that a polycistronic amiRNA based on avvi-miR319e is functional and produced 3 molecules that should silence, in a specific and efficient manner, 3 different target genes.
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PS99

MASS PROPAGATION SYSTEM FOR FRUIT TREES: SWEET CHERRY AND AVOCADO

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Difficulties associated with mass propagation of fruit species, provide an opportunity for the use of temporary immersion systems (TIS). Here we describe the successful establishment of two different culture procedures: a) for no recalcitrant, easy budding genotypes such as the sweet cherry (SC) rootstocks and varieties, and b) for extremely

recalcitrant genotypes such as avocado (Av) rootstocks. Two starting populations were established using internodal segments from SC and Av, and the propagation medium (PM; DKW-derivative) and MS (Murashige-Skoog) medium for SC and Av, respectively. For SC propagation, segments were cultured under TIS and the pipeline was defined by a 14 d TIS, leading to whole plant generation after 45 d of additional culturing in solid-rooting medium. For Av, the procedure required 21 d of TIS culture and rooting was achieved using solid medium for additional 75 d. Both SC and Av showed genotype-dependent responses, although they yielded successfully acclimatized plants in greenhouse. TIS productive parameters were defined for the SC and Av these propagation pipelines, as judged by number of shoots, biomass, elongation and sucrose consumption by the explants. Results showed that culture of SC rootstocks was significantly improved by TIS. The number of immersions influenced all productive parameters. The best values were obtained with the SC rootstocks Maxma-14 and Colt. For Av, whereas the use of solid media did not allow any successful productive propagation, a mixture between TIS and solid procedure allowed for the elongation and multiplication of explants, with the rootstock Dusa showing the best responses. Results demonstrate that TIS improves or enables mass propagation approaches of these fruit tres and represent promising alternatives for scale-up procedures. Funded by Biofrutales, CORFO 13CTI-21520-SP8, FONDEF G09i1008.

PS100

INTERACTION BETWEEN *Arabidopsis thaliana* AND *Sinorhizobium meliloti* FOR IMPROVED PLANT GROWTH AND NITROGEN NUTRITION

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Nitrogen (N) is an essential macronutrient whose availability in the soil has a critical role in plant growth and development in natural as well as in agricultural environments. Plants acquire N directly from the soil and in some cases N can be provided by interacting with N-fixing bacteria. This type of interactions is well described in legumes, but are also observed in some non-legume plant species, that are unable to form nodules. Understanding these plant-bacteria interaction mechanisms could have important agronomic implications, reducing the use of N-fertilizers in non-legume crops. Our goal was to evaluate a functional association between a non-legume model plant, *Arabidopsis thaliana*, and a N-fixing model bacteria, *Sinorhizobium meliloti*, to study and identify molecular mechanisms underlying this association. We found *A. thaliana* growth under N-limiting conditions is enhanced by *S. meliloti* RMP110. This enhancement is in part mediated by bacterial N-fixation. Dilution of 15N labeling when Arabidopsis plants were grown with *S. meliloti* indicated plants indirectly acquired atmospheric N, where 14N isotope predominates. We also determined bacterial root colonization through different

types of microscopy, locating the bacteria in the outer layer of the root. This was also corroborated by an endophytic assay where it was shown that *S. meliloti* is not an intracellular bacterium when interacts with Arabidopsis. Finally, we demonstrated that Arabidopsis homologs of key regulatory genes involved in legume-rhizobium interactions are required for Arabidopsis growth promotion mediated by *S. meliloti*. Our results suggest a non-canonical interaction between *A. thaliana* and *S. meliloti* RMP110, without nodule formation, or intracellular colonization of the bacteria, but with conserved molecular mechanisms of legume-rhizobium interactions for improved growth under N-limiting conditions.

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PS101

ECOLOGICAL GENOMICS IDENTIFIES PROCESSES REQUIRED FOR ADAPTATION IN ATACAMA DESERT

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Understanding biological processes that underlie plant resilience to extreme abiotic conditions is a major challenge for plant biologists. This knowledge is essential to develop biotechnologies that could be used to improve crops in an era of climate change or to expand the limits of agriculture to marginal lands. We have characterized three pristine and extreme ecosystems from central Atacama Desert. The western slopes of the Andes provide a natural altitudinal gradient of environmental parameters, such as rainfall and temperature, which defines three vegetational belts: The pre-puna (2400 – 3300 m a.s.l), the puna (3300 – 4000 m.a.s.l.), and the high Andean steppe (4000 – 4500 m.a.s.l.). Diverse plant communities succeed each other at these different environments, yet, very little is known about the underlying genetic mechanisms that allow them to inhabit these extreme and dissimilar environments. We sequenced the transcriptome of 32 most abundant and ecologically important plant species in order to explore gene functions. We also performed

a metagenomics analysis of the soil bacteria that congregate at their rhizosphere. Our studies provide new insights into mechanisms for evolution of plant abiotic stress tolerance, and improve our understanding of the highly unique ecosystem of the Atacama Desert.
FONDAP Center for Genome Regulation.

PS102

IDENTIFICATION OF GENES ASSOCIATED WITH SOFTENING RATE IN *Prunus persica* USING QTL AND EXPRESSION QTL

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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, 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. Using this information, we found 133 eQTL co-localizing on LG4 with a LOD score between 3.00 and 19.89. 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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PS103

TIPS AND TRICKS OF ANTIBODY PRODUCTION AND WESTERN BLOT, HOW TO OBTAIN GOOD RESULTS?

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Antibodies are a popular tool used in plant cell biology research. They can be either custom made or purchased from a commercial supplier. In either case their production is a complex process, consisting of three very important components which has to be carefully considered. These are: Antigen-Animal-Testing. Which source of antigen is most optimal for your project: peptide, recombinant protein or a native protein isolated from tissue? Which animal species to choose? Are certain species making better antibodies compare to others? Do I have any controls to validate produced antibody? What controls should be used? What to do if my antibody is not giving any signal in a western blot?

PS104

PLANT BIODIVERSITY IN THE ATACAMA DESERT

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Studying biodiversity in extreme environments allow us to understand how individuals and whole ecological communities are able survive at the limits for life. We characterized plant biodiversity in the hyperarid core of Atacama Desert as a first step to understand the unique features of Atacama plant communities that allowed them to survive under harsh abiotic conditions. In Atacama, plants must overcome aridity, high radiation and nutritional shortage among other extreme abiotic conditions. Plant biodiversity in the hyperarid Atacama varies over time in response to fluctuating environmental conditions from inter-annual to decadal timescales. Multiple life habit strategies are utilized in this environment. However, one common life form are annual plants, which can avoid drought years by forming soil seed banks that germinate when conditions are more suitable. In order to determine the composition of plant communities in the western slope of the Andes in the Atacama Desert, we performed plant diversity surveys over seven consecutive years in an altitudinal transect. We observed a total of 71 different plant species with significant inter annual variation (31 to 63 species) and species persistence (years of appearance, from one to seven years). Environmental DNA in surface soil samples complemented the surveys and revealed hidden plant diversity. DNA barcode analysis revealed 7 new taxa in the area, and a wide distribution of plant DNA. To complement field and molecular surveys, we performed an analysis of soil seed banks using the seedling emergence method. The soil seed bank proxy shows that viable seeds have wider ranges than observed plants. Our

results show an increasing plant richness and composition in the study area, and an adaptive flexibility of the communities to the changes in the climate gradient of the Andes in Atacama Desert.

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