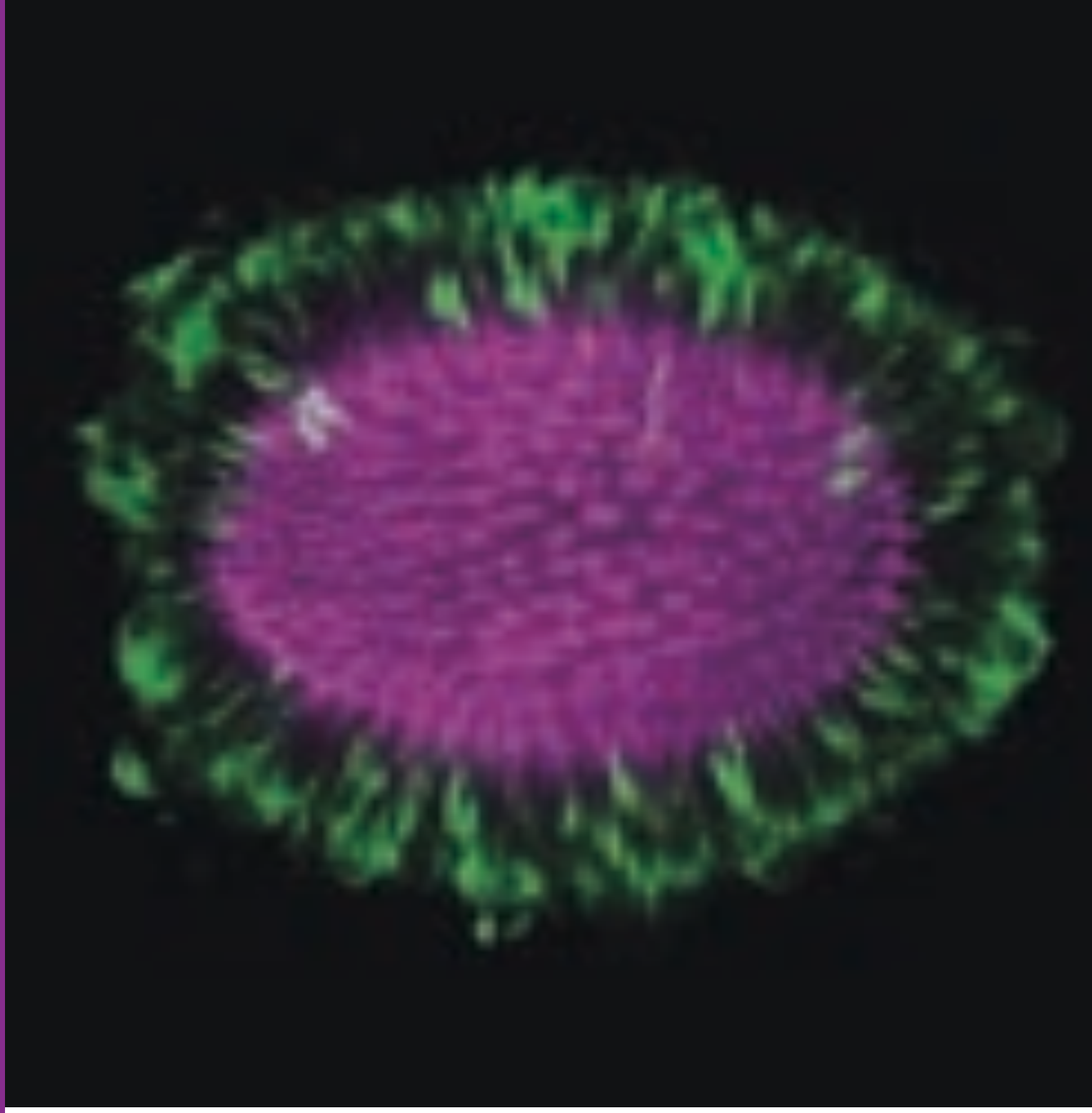

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IX REUNIÓN DE BIOLOGÍA VEGETAL REBIVE-2014

biología vegetal

1 al 4 de diciembre, Región de Coquimbo · Chile

IX Reunión de Biología Vegetal ReBiVe-2014

1 al 4 de diciembre
Región de Coquimbo · Chile

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Scientific Program

Monday -December 1, 2014

Hotel Check-in starts at 16:00 PM – Hotel Enjoy La Bahía Reception.

11:00 - 16:00 Registration – Hotel Enjoy La Bahía Pre Foyer.

11:00 - 17:00 Poster Set Up (ODD numbered posters) – Foyer Hall

15:00 - 15:30 Opening Welcome – Bahía 1 Room.

Dr. Julio Kalasich B., Director Nacional Instituto de Investigaciones Agropecuarias INIA.

Dr. Nibaldo Avilés, Rector Universidad de La Serena

15:30 - 16:30 Plenary Lecture I – Bahía 1 Room

Dr. Ralph Scorza. UTILIZATION OF EARLY FLOWERING GENES TO ACCELERATE THE GENETIC IMPROVEMENT OF LONG-GENERATION CYCLE PLANT SPECIES. USDA Appalachian Fruit Research Station, Kearneysville, WV**.**
Chair. Dr. Andrés Zurita-Silva

16:30 - 17:00 Coffee Break – La Bahía Foyer

17:00 - 18:20 Oral Session I – Bahía 1 Room
Chairs: Andrés Zurita & Paula Pimentel

17:00 MOLECULAR CHARACTERIZATION OF CYTOKININ RESPONSIVE GENES DURING STONE-FRUIT DEVELOPMENT IN *Prunus persica*.
Karen Mujica, Claudia Huerta, Elena Barindelli, Camilo Avendaño, Fernanda Rodriguez and **Lee Meisel.**

17:20 CONSTRUCTION OF HIGH DENSITY SWEET CHERRY (*Prunus avium* L.) LINKAGE MAPS USING MICROSATELLITE MARKERS AND SNPs DETECTED BY GENOTYPING-BY-SEQUENCING (GBS) TECHNOLOGY.
Verónica Guajardo, Simón Solís, Boris Sagredo, Felipe Gainza, Ksenija Gasic, Carlos Muñoz and Patricio Hinrichsen.

17:40 DETERMINATION OF THE DNA METHYLATION AND EXPRESSION KINETIC OF DORMANCY ASSOCIATED MADS-BOX (DAM) GENES IN SWEET CHERRY (*Prunus avium*) DURING BUD DORMANCY RELEASE.
Karin Rothkegel, Soraya Bravo, Humberto Prieto and Andréa Miyasaka Almeida

18:00 RESPIRATORY CHANGES IN BUDS OF *Vitis vinifera* DURING THE TRANSITION FROM PARADORMANCY TO ENDODORMANCY: A SHIFT FROM AEROBIC RESPIRATION TO FERMENTATION.
Francisca Parada and Francisco Pérez.

18:20-19:20h Plenary Lecture II – Bahía 1 Room

Dr. Omar Sabag. SCIENCE BEHIND THE SCENES: MYTHS AND FACTS OF THE PEER REVIEW PROCESS.
Universidad de La Serena.
Chair. Dr. Cristián Ibáñez

20:00 - 21:30 Dinner - Hotel Enjoy La Bahía, Bingo Restaurant.

21:30 - 23:00 Poster Session I (ODD numbered posters) – Stands Rotonda Foyer

Tuesday - December 2, 2014

7:00 - 11:30 Poster Set Up (EVEN numbered posters) – Foyer Hall

9:00 - 10:00 Plenary Lecture III – Bahía 1 Room

Dr. Sandrine Ruffel. NITROGEN-SYSTEMIC SIGNALLING CONTROLLING ROOT RESPONSE TO HETEROGENEOUS NITRATE AVAILABILITY IN *Arabidopsis*.
Biochimie et Physiologie Moléculaire des Plantes, Institut Claude Grignon, France.
Chair. Dr. Rodrigo Gutiérrez

10:00 - 11:20 Oral Session II – Bahía 1 Room
Chairs: Alejandra Moya & Michael Handford

10:00 PHOSPHOINOSITIDE - LOCALIZED BIOSYNTHESIS LINKS ENDOCYTIC TRAFFICKING AND HEAT SHOCK RESPONSE IN *Arabidopsis thaliana*.
Ricardo Tejos, Cecilia Rodriguez-Furlán and Lorena Norambuena.

10:20 JASMONATE-DEPENDENT GENE EXPRESSION LANDSCAPE DURING SALT STRESS IN *Arabidopsis thaliana* ROOTS.
Pablo Vergara, Orlando Acevedo, Camilo Valenzuela and Pablo Figueroa

10:40 CHARACTERIZATION OF 4 POLLEN SPECIFIC KINASE CODING GENES FROM *Arabidopsis thaliana*.
Noel Lucca, Miguel Ángel Ibeas, Camila Peralta, Catalina Pavez and Gabriel León

11:00 FUNCTIONAL ANALYSIS OF *P. avium FT* AND *TFL1* IN *Arabidopsis thaliana*.
Antonia Yarur, Michelle Gatica, Gabriel León and Andrea Miyasaka Almeida.

11:30 - 12:00 Coffee Break – La Bahía Foyer

12:00 - 13:00 Oral Session III – Bahía 1 Room
Chairs: Andrea Miyasaka de Almeida & Carlos Figueroa Lamas

12:00 VOLTAGE-SENSOR TRANSITIONS OF THE INWARD-RECTIFYING K+ CHANNEL KAT1 FROM *A. thaliana* INDICATE A LATCHING MECHANISM BIASED BY HYDRATION WITHIN THE VOLTAGE SENSOR.
Wendy González, Cécile Lefoulon, Rucha Karnik, Annegret Honsbein, Paul Vijay Gutla, Christopher Grefen, Janin Riedelsberger, Tomás Poblete, Ingo Dreyer and Michael R. Blatt.

12:20 MOLECULAR MODELLING AND DOCKING SIMULATIONS OF FRUIT-RELATED α-EXPANSINS FROM *Vasconcellea* AND *Fragaria* GENUS.
Carlos Gaete-Eastman, Felipe Valenzuela, Luis Morales-Quintana, Raúl Herrera and María Alejandra Moya-León.

12:40 MOLECULAR AND STRUCTURAL CHARACTERIZATION OF THE TRANSPORTER PrMATE1 INVOLVED IN THE ASSIMETRICAL GROWTH OF RADIATA PINE IN REPONSE TO INCLINATION.
Patricio Ramos, Luis Morales-Quintana, Maria Alejandra Moya-León and Raúl Herrera.

13:00 *Daucus Carota* LYCOPENE B-CYCLASE (*LCYB1*) PROMOTES INCREMENT IN PLANT FITNESS THROUGH POSITIVE REGULATION OF CAROTENOID, GIBBERELLIN AND CHLOROPHYLL GENES.
Ariel Cerda, Kevin Simpson, Juan Camilo Moreno, Claudia Stange

13:15 – 14:45 Lunch – Hotel Enjoy La Bahía, Bingo Restaurant.

15:00 – 16:00 Plenary Lecture IV – Bahía 1 Room

Dr. Kranthi Varala. BIGPLANT: A PHYLOGENOMICS APPROACH TO UNCOVER GENETIC UNDERPINNING OF TRAITS
Center for Genomics and Systems Biology, Department of Biology, New York University, USA.

Chair. Dr. Rodrigo Gutiérrez

16:00 - 16:30 Coffee Break – La Bahía Foyer

16:30 – 17:30 Oral Session IV – Bahía 1 Room
Chairs: Mónika Valdenegro & Claudio Meneses

16:30 MOLECULAR CHANGES DURING DEVELOPMENT AND RIPENING OF RASPBERRY FRUIT (*Rubus idaeus* CV HERITAGE).
Lida Fuentes, Liliam Monsalve, Luis Morales-Quintana, Dante Travisany, Juan Pablo Martínez, Mónika Valdenegro, Alejandro Maass, Bruno Defilippi and Mauricio González-Agüero**.**

16:50 AUXINS AND ABA ARE REGULATING THE SOFTENING OF *Fragaria chiloensis* FRUIT. Lizana R, Stappung Y, Herrera R and Moya-León M.A.

17:10 POSTHARVEST TREATMENT OF HYDROGEN SULFIDE DELAYS THE SOFTENING OF CHILEAN STRAWBERRY FRUIT BY DOWN-REGULATING THE EXPRESSION OF GENES INVOLVED IN PECTIN CATABOLISM.
Sebastian Molinett, Raúl Herrera and María Alejandra Moya-León.

17:30 FUNCTIONAL EVALUATION OF THE REGULATORY REGION OF AGAMOUS LIKE 11 (VvAGL11) IN *Vitis vinífera* L.
Braulio Soto F, Nallatt Ocarez and Nilo Mejía.

18:00 - 19:00 Plenary Lecture V – Bahía 1 Room

Dr. Jeroni Galmés. SUPERCHARGING PHOTOSYNTHESIS: ON THE WAY FROM NATURE TO BIOENGINEERING APPROACHES.
Research Group on Plant Biology under Mediterranean Conditions. Universitat de les Illes Balears, Spain.
Chair. Dr. León Bravo

20:00 - 21:30 Dinner - Hotel Enjoy La Bahía, Bingo Restaurant.

21:30 – 23:00 Poster Session II (EVEN numbered posters) – Stands Rotonda Foyer.

Wednesday - December 3, 2014

9:00 - 10:00 Plenary Lecture VI – Bahía 1 Room

Dr. Nathaniel Street. EXPLAINING THE GENOMIC KNOWN UNKNOWNS AND DISCOVERING UNKNOWN UNKNOWNS IN NORWAY SPRUCE AND EUROPEAN ASPEN.
Umeå Plant Science Centre, Umeå University, Sweden.
Chair. Dr. Cristian Ibáñez

10:00 - 11:20 Oral Session V– Bahía 1 Room
Chairs: Mauricio González & Lida Fuentes

10:00 ANATOMICAL, PHYISIOLOGICAL AND BIOCHEMICAL CHANGES IN WILD TOMATOES DICTATED DIFFERENTIAL MECHANISMS TO TOLERATE DROUGHT STRESS.
Gerardo Tapia, Boris Muñoz, Nicolas Bravo, Oscar Arrey, Maximo González, Jorge Burgos and Victoria Moya.

10:20 TRANSCRIPTOMIC APPROACH TO UNRAVEL SALT TOLERANCE OF ALGARROBO (*Prosopis chilensis*) TREES.
Cristian Ibáñez, Alexander Vergara, Nathaniel Street and Claus Westphal.

10:40 PHYSIOLOGICAL AND TRANSCRIPTOMIC CHARACTERIZATION OF *Cistanthe longiscapa* DURING SEED GERMINATION.
Daniela Elizondo, Paula Vizoso, Scarleth Bravo, Francisca Blanco, Claudio Meneses and Ariel Orellana.

11:00 NITROGEN AND CARBON METABOLISMS IN QUINOA UNDER DROUGHT STRESS CONDITIONS.
Bascuñán-Godoy L, Reguera Maria, Abdel-Tawab Yasser and Blumwald Eduardo.

11:30 - 12:00 Coffee Break – La Bahía Foyer

12:00 - 13:00 Oral Session VI – Bahía 1 Room
Chairs: Erika Salazar & Boris Sagredo

12:00 ADVANCES IN THE GENETIC IMPROVEMENT OF MANDARIN AND LEMON-TREE IN CHILE.
María-José Montañola, Andrea Galaz, Marina Gambardella and Johanna Mártiz.

12:20 THE ASSOCIATION BETWEEN REPRODUCTIVE TISSUES AT PRE- AND POST-ANTHESIS IS PROPOSED AS A CONTROL OF KERNEL WEIGHT POTENTIAL IN WHEAT (*Triticum aestivum* L.).
Jaime Herrera and **Daniel Calderini.**

12:40 GENETIC DIVERSITY AND POPULATION STRUCTURE OF TWO DOMINANT PLANT SPECIES OF THE HIGH ANDEAN WETLANDS OF CHILE'S NORTE CHICO. Alejandra J. Troncoso, Nicolas Gouin and Angéline Bertin.

13:15 – 14:45 Lunch – Hotel Enjoy La Bahía, Bingo Restaurant

15:00 – 16:00 Plenary Lecture VII – Bahía 1 Room

Dr. Gabriel Krouk. A SYSTEMS VIEW OF NITROGEN SIGNALING INTERACTIONS.
Biochimie et Physiologie Moléculaire des Plantes, Institut Claude Grignon, France.
Chair. Dr. Rodrigo Gutiérrez

16:00 - 16:30 Coffee Break – La Bahía Foyer

16:30 – 17:30 Oral Session VII – Bahía 1 Room
Chairs: Francisca Blanco & Felipe Gainza

16:30 FUNCTIONAL CHARACTERIZATION OF SALICYLIC ACID-INDUCIBLE GENES CODING FOR GLUTATHIONE S-TRANSFERASES AND GLUTAREDOXINS IN THE DEFENSE RESPONSE TO STRESS IN *Arabidopsis thaliana*.
José Manuel Ugalde, Alejandro Fonseca, Paula Salinas and Loreto Holuigue.

16:50 RESISTANCE LOCI *RUN1* AND *REN1* IN *Vitis vinifera* ARE ASSOCIATED TO THE ACTIVATION OF AN ETI-LIKE MEDIATED IMMUNE RESPONSE AGAINST *Erysiphe necator*.
Rudolf Schlechter, Mario Agurto, Camila Almendra, Grace Armijo and, Patricio Arce-Johnson.

17:10 VVNAC1, A TRANSCRIPTIONAL REGULATOR INDUCED UNDER A VIRAL COMPATIBLE INTERACTION IN *Vitis vinifera*.
Anibal Arce, Mindy Muñoz, Consuelo Medina and Patricio Arce-Johnson.

18:00 – 19:00 Technical Conference – Organizing Plant Biology Society.
Closing Ceremony, Best Oral and Poster Presentation Awards
Chair: Andrés Zurita

20:00 - 21:·30 Dinner – Hotel Enjoy La Bahía, Bingo Restaurant

22:30 After Dinner

Thursday – December 4, 2013

8:00 - 11:00 Breakfast – Hotel Enjoy La Bahía

Hotel Check- out before 12:00 PM- Hotel Enjoy La Bahía Reception

Plenary Lectures

Fotografía: Gentileza de Dr. Andrés Zurita

PL1

UTILIZATION OF EARLY FLOWERING GENES TO ACCELERATE THE GENETIC IMPROVEMENT OF LONG-GENERATION CYCLE PLANT SPECIES.

Ralph Scorza[1], Chris Dardick[1], Ann M. Callahan[1], Chinnathambi Srinivasan[1], Doug Raines[1], Mark Demuth[1], Ted M. DeJong[2], Jay Harper[3], Sarah Castro[2]

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The tree fruit industry is facing challenges of climate change, reductions in available labor, the need for reduced chemical inputs, the spread of exotic pests and pathogens, and consumer demands for improved fruit quality. To meet these challenges breeding new adapted fruit cultivars is critical. Current limitations of fruit breeding include long juvenility periods, significant field costs, and yearly limitations on flowering and fruiting related to dormancy. Much research has focused on marker assisted selection (MAS), germplasm characterization, and genetic engineering (GE) as means to advance tree fruit breeding. However, these strategies are all still limited by long generation cycles. We have developed a system to shorten the breeding cycle of fruit trees and other long-breeding-cycle crops. We have overcome the juvenility and environmental limitations of flowering and fruiting by incorporating a gene that induces trees to flower early and continually. This “FasTrack” breeding system has reduced the generation cycle of plum from 3-7 years to less than one year. The system allows for the rapid incorporation of important traits into plums and other long-generation-cycle crops and then in the final generation, when substantial improvements are clearly evident, only seedlings that do not contain the early flowering gene are selected, and these are not considered in the USA to be genetically engineered. The selected trees may then be used directly as new varieties, or as improved lines for further breeding. The ‘FasTrack’ breeding technology provides tree fruit and other long generation-cycle crop breeders with the ability to produce improved cultivars relatively rapidly to meet new market demands, climate change, and invasions of new diseases and pests in a way never before possible with conventional breeding.

Acknowledgements: USDA-NIFA-SCRI, USDA-ARS, California Dried Plum Board.

PL2

SCIENCE BEHIND THE SCENES: MYTHS AND FACTS OF THE PEER REVIEW PROCESS

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An important part of the generation and dissemination of scientific knowledge is determined by the socio-discursive practice of evaluating and judging the work of our colleagues. This practice, anchored in the very essence of scientific endeavor, is the Peer Review Process. Any researcher that intends to publish his or her ideas must deal with this process, so we all have a personal story to tellregarding the experience of passing through peer review lenses. Although empirical research on peer review is quite abundant, results are inconclusive regarding some key elements of the process: Is the process fair and reliable? What do referees evaluate? Do they agree on their recommendations? In the light of such questions, Iwill critically revise some of the research on the peer review process, from what is fairly well established to future lines of inquiry, as well asshow someof its implications forthe scientific literacy of future generations.

Keywords: Scientific industry, peer review, sociology of science, research articles.

Funding: FONDECYT N° 1130290.

PL3

NITROGEN-SYSTEMIC SIGNALLING CONTROLLING ROOT RESPONSE TO HETEROGENEOUS NITRATE AVAILABILITY IN *Arabidopsis*.

Sandrine RUFFEL[1*], Ying Li[2], Daniela Ristova[2], Arthur Poitout[1], BenoitLacombe[1], Dennis Shasha[2], Kenneth Birnbaum[2], Gabriel Krouk[1], Gloria Coruzzi[2]

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[2]Center for Genomics and Systems Biology, Department of Biology, NewYork University. New York, NY 10003, USA.

For all living organisms, the capacity to sense and adapt to environmental change is one of the foremost challenges for survival and propagation. The short-term adaptation of the physiology and development to external fluctuations is even more critical for sessile organisms like plants, giving a particular interest to network signaling controlling these mechanisms. Root plasticity is primordial to optimize water and nutrient acquisition and depends on the integration of local and systemic signaling. Indeed, it is well established that roots have the ability to sense and proliferate in nutrient-rich zones (local signal) and invest more of these resources in roots when the internal nutrient availability is limited (systemic signal). One major challenge remains to understand how plants coordinate this nutrient signaling network in the infinite scenario that they may encounter. We focused on signaling mechanism controlling root development and nitrogen metabolism in response to contrasted nitrateenvironments, in *Arabidopsis*. Using the split-root system (in which physically isolated root systems of the same plant were challenged with different environments), we characterized developmental and transcriptomic responses to nitrogen-related signaling in roots. The split-root conditions highlighted plants ability to integrate information from isolated appendages and tune their molecular and developmental strategies to heterogeneous environments. First, we demonstrated that cytokinin biosynthesis forms one critical component of root-shoot-root communication in this system. Second, we provided arobust temporal transcriptomic response to local *versus* systemic nitrogen-signaling, constituting an interesting resource to derive additionalbiological hypotheses of this system functioning, in particular throughthe integration to massive and publicly available genomic data. The conclusion will give a broad picture of our knowledge of N-related long-distance communication by replacing our results in light of the recent new findings on mobile signals in plants.

Acknowledgments: National Science Foundation (Arabidopsis 2010 Genome grant), the National Institutes of Health, and the Plant Biology and Breeding Department of the French National Institute for Agricultural Research for their funding support.

PL4

BIGPLANT: A PHYLOGENOMICS APPROACH TO UNCOVER GENETIC UNDERPINNING OF TRAITS

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Phylogenomics as an approach to discover gene-to-trait associations has only recently become feasible. With an increasing number of plant genomes and/or "gene spaces" becoming available we can now begin to analyze the gain and loss of traits from an evolutionary perspective. The BigPlant pipeline is an ambitious effort to reconstruct the complete evolutionary history of all plant genes starting from the early land plants (e.g., Mosses) to the commercially grown crop plants. By reconstructing the phylogeny of all completed plant genomes from every protein-coding gene we are able to determine which genes are repeatedly associated with the appearance of a trait. This ability to identify the genetic signature of convergent evolution provides a novel way, beyond the traditional genetics (forward and reverse) and association (QTL, GWAS etc.) approaches, to identify genes underlying traits of interest. We have harnessed the power of BigPlant to identify approximately 100 new members of the molecular toolkit needed to establish symbiosis with ArbuscularMychorhizae (Delaux et al. PLoS Genetics 2014). An intermediate stage of the BigPlant pipeline establishes the membership and relations of all members of a gene family across all plants. We used this stage to identify and classify all members of the Nitrate transporter family (Leran et al. TiPS 2014). With the increasing number of plant genomes and their phylogenetic distribution in the coming years and the increasing ease of determining the "gene-space" for any species of interest we will be able to apply this approach to any trait that has appeared multiple times across a range of plant species.

Acknowledgements: The BigPlant project was developed through a unique collaboration between New York University, American Museum of Natural History, New York Botanical Garden and Cold Spring Harbor Lab.

PL5

SUPERCHARGING PHOTOSYNTHESIS: ON THE WAY FROM NATURE TO BIOENGINEERING APPROACHES

Jeroni Galmés[1], John A. Andralojc[2], Marc Carriquí[1], Miquel Àngel Conesa[1], Mario A. Fares[3], Jaume Flexas[1], Marcel Font-Carrascosa[1], Jorge Gago[1], Eustaquio Gil-Pelegrín[4], Carmen Hermida-Carrera[1], Ralf Kaldenhoff[5], Maxim V. Kapralov[6], Alfred J. Keys[2], Marcus Koch[7], Arantxa Molins[1], Ülo Niinemets[8], Martin A.J. Parry[2], José Javier Peguero-Pina[4], Juan Alejandro Perdomo[1], Miquel Ribas-Carbó[1], Spencer M. Whitney[6], Hipólito Medrano[1]

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[4]Unidad de Recursos Forestales, Centro de Investigación y Tecnología Agroalimentaria, Zaragoza, Spain.

[5]Darmstadt University of Technology, Applied Plant Science, Germany.

[6]Plant Science Division, Research School of Biology, The Australian National University, Australia.

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[8]Institute of Agricultural and Environmental Sciences, Estonian University of Life Sciences, Estonia.

Future improvements in yield potential are to come by novel bioengineering strategies specifically focused on processes limiting crop productivity that have not been addressed so far. Among them, the fundamental primary processes of photosynthesis have been barely improved since breeding began and remain as the major route forfurther substantial improvements. Within the photosynthetic C_3 mechanism, increasing the concentration of CO_2 at the site of carboxylation and improving the Rubisco catalytic properties have been targeted as step changes to increase the CO_2 assimilation capacity. The present talk will update the most recent findings and next future prospects to enhance crops photosynthesis via bioengineering approaches focused on the leaf capacity to transfer and assimilate CO_2. First, the biochemical and physiological basis of leaf mesophyll conductance (g_m) and Rubisco catalytic traits will be provided, and related to the mathematical models of leaf photosynthesis. Existing natural variability will be then examined in the search for naturally improved versions of g_m and Rubisco. Finally, how these naturally improved versions represent an exceptional opportunity to supercharge photosynthesis through genetic modification of crops will be reviewed and linked to specific methodological approaches.

Acknowledgements: project AGL2013-42364 (Plan Nacional, Spain) awarded to J Galmés. CONICYT-MEC 80130020.

PL6

EXPLAINING THE GENOMIC KNOWN UNKNOWNS AND DISCOVERING UNKNOWN UNKNOWNS IN NORWAY SPRUCE AND EUROPEAN ASPEN.

Nathaniel Street

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Umeå Plant Science Centre, Department of Plant Physiology, Umeå University, Sweden.

We have sequenced the genomes of two Swedish forest trees, each of which presents distinct challenges: The 20 Gbp genome of Norway spruce (*Piceaabies*) is both gigantic and repetitive while the much smaller 500 Mbp genome of European aspen (*Populus tremula*) is highly heterozygous. Both cases push current assembly approaches using short read second generation sequencing data to their limits. Despite these challenges useful assemblies of both genomes have been produced and are allowing us to explore and explain 'known unknowns' in each genome. For example, in Norway spruce we have shown that the large genome resulted from the slow and steady accumulation of a diverse set of LTR TEs that were not subsequently removed by unequal recombination and that created extremely long introns. The availability of the genomes has also allowed us to discover previously 'unknown unknowns'. In Norway spruce, profiling of 24ntsRNAs, which are known to silence TEs via methylation, revealed a highly tissue-specific expression and much lower abundance in general than in other plants. In both aspen and Norway spruce, RNA-Seq based transcript profiling has revealed an extensive set of long non-coding RNAs (lncRNA) that are under active biological regulation and that have been widely conserved. Armed with these genomes we are now using a systems genetics approach to explore the 'known unknown' of how natural variation of complex phenotypic traits is controlled and to assign phenotypic links for known genes of unknown function. Progress on this approach using the example of leaf shape variation in aspen will be presented.

PL7

A SYSTEMS VIEW OF NITROGEN SIGNALING INTERACTIONS

Medici A.[1], Bargmann B.O.[2], Para A.[2], Li Y.[2], Varala K.[2], Marshall-Colon A.[2], Ruffel S.[1], Crawford N.M.[3], Birnbaum K.D.[2], Coruzzi G.M.[2], and **Krouk G.[1]**

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[2]Center for Genomics and Systems Biology, Department of Biology, NewYork University. New York, NY 10003, USA.

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A drastic change in plant Nitrogen (N) nutrition results in systematic adaptations ranging from metabolic to growth changes. Interestingly, experimental evidences support the idea that it exists dedicated signaling pathways involved in the tuning of growth in response to nutritional status of the plant. On the other hand, growth can influence nutrition partly through hormones action. This constitutes a feed-forward loop that entangles nutrition and growth (Krouk et al., 2011). This constitutes our biological model. We aim to get deeper insights into such signaling interactions. To this purpose, two approaches will be presented. First, genome wide investigations have been made to understand the effect of combinatorial interactions between nitrogen and hormone treatments in the control of i) gene expression and ii) root development. Multi-dimensional networks have been built and functional validations of the predicted roles for the genes belonging to these networks are currently made. Second, by studying the genome wide effect of nitrate regulated transcription factors [technique named TARGET; (Bargmann et al., 2013)], we yielded several insights into i) gene regulatory network complexity in Arabidopsis (unpublished), ii) transcription factor dynamics (Para et al., 2014),iii) potential connections between nitrate and phosphate signaling in the control of root growth control (Medici et al., in revision). All these aspects will be presented and discussed.

Bargmann, B.O., Marshall-Colon, A., Efroni, I., Ruffel, S., Birnbaum, K.D., Coruzzi, G.M., and Krouk, G. (2013). TARGET: a transient transformation system for genome-wide transcription factor target discovery. Mol Plant **6,** 978-980.

Krouk, G., Ruffel, S., Gutierrez, R.A., Gojon, A., Crawford, N.M., Coruzzi, G.M., and Lacombe, B. (2011). A framework integrating plant growth with hormones and nutrients. Trends Plant Sci **16,** 178-182.

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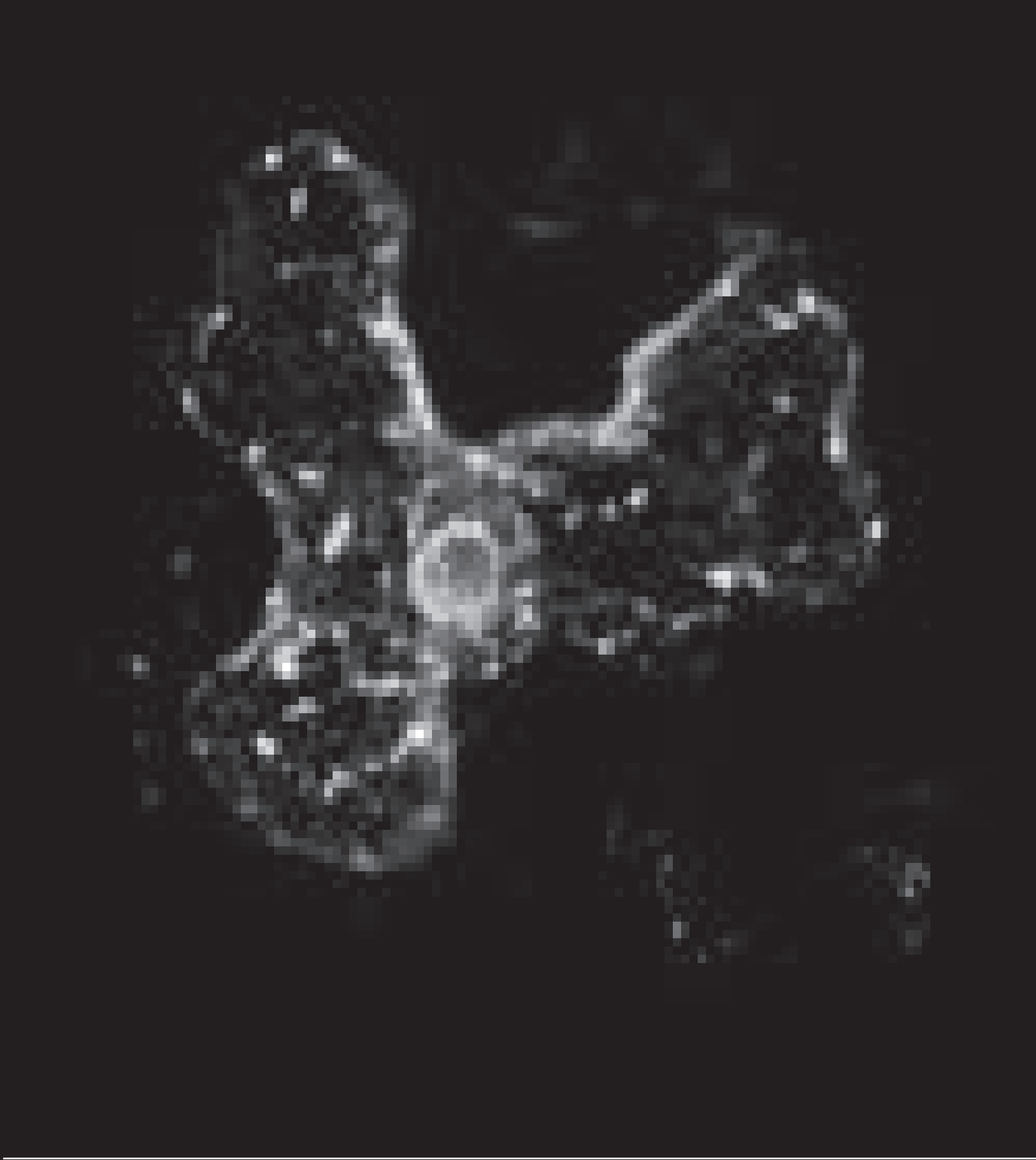

Oral Sessions

Fotografía: Gentileza de Henry Temple M.Sc.

OSI1

MOLECULAR CHARACTERIZATION OF CYTOKININ RESPONSIVE GENES DURING STONE-FRUIT DEVELOPMENT IN *Prunus persica*

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The phytohormone cytokinin plays a major role in plant development. Recently we have reported the identification and comparative analyses of genes associated with cytokinin signaling and homeostasis pathways in two hardwood tree species: *Populus trichocarpa* and *Prunus persica* (Immanen et al., 2013). Cytokinin levels have been reported to accumulate differentially during stone fruit development, with increases in cytokinin during pre-lignification and post-lignification stages of fruit development, whereas levels are lower during the lignification stage. This variation in cytokinin levels during fruit development suggests that genes associated with cytokinin signaling and homeostasis pathways may be differentially expressed during stone fruit development. To better understand the role that cytokinin responsive genes play in stone fruit development, we have performed RNA-seq and qPCR analyses of peach fruits treated with exogenously applied t-zeatin at different stone-fruit developmental stages. These analyses reveal a developmental stage specific expression of specific gene family members of the cytokinin signaling and homeostasis pathway in peach fruits. Additionally, cytokinin responsive genes were identified during pre-lignification, lignification and post-lignification stages of stone-fruit development in *Prunus persica.* Transient overexpression of a putative type-B response regulator (*PpeRR1*) in peach fruits increased the expression of putative downstream genes, *PpeShy2* and *PpeRR6*. This result demonstrates that transient overexpression of transcription factors in fruits, may be used to test the conservation of downstream target genes between model species such as Arabidopsis and crop species such as peach. Our results demonstrate that the cytokinin response pathway that has been described in Arabidopsis is conserved in Peach, and that this response pathway is differentially expressed during peach stone-fruit development.

Acknowledgements: CONICYT Fondecyt /Regular N°1121021

OSI2

CONSTRUCTION OF HIGH DENSITY SWEET CHERRY (*Prunus avium* L.) LINKAGE MAPS USING MICROSATELLITE MARKERS AND SNPs DETECTED BY GENOTYPING-BY-SEQUENCING (GBS) TECHNOLOGY

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Linkage maps are valuable tools in genetic and genomic studies. For sweet cherry, linkage maps have been constructed using mainly microsatellite markers and, recently, using single nucleotide polymorphisms (SNPs) from a sweet cherry SNP chip. Genotyping-by-Sequencing (GBS), a new methodology based on high-throughput sequencing, holds great promise for identification of high number of SNPs and construction of high-resolution linkage maps. In this study, GBS was used to identify SNPs from a sweet cherry crossing population. The physical position for each SNP was determinate by using the peach genome as a reference, given the high synteny level across *Prunus* species. These SNPs and 34 microsatellite markers were used for the construction of linkage maps. Parental and consensus high-density maps were constructed by genotyping 166 siblings from a 'Rainier' x 'Rivedel' crossing. Using this population, 462, 489 and 985 markers were mapped for 'Rainier', 'Rivedel' and the consensus map, respectively. Maps spanned 549.5 cM for 'Rainier', 582.6 cM for 'Rivedel' and 731.3 cM for the consensus map. Eight linkage groups showing a high synteny with the peach genome v1.0 were obtained. The order of mapped microsatellite was comparable to previous available maps. It was not possible to compare the position of mapped SNPs with previous maps due to the small number of shared SNPs. These new genetic maps provide valuable information on the sweet cherry genome, as the basis to identify QTLs and genes relevant for breeding the species.

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OSI3

DETERMINATION OF THE DNA METHYLATION AND EXPRESSION KINETIC OF *DORMANCY ASSOCIATED MADS-BOX* (*DAM*) GENES IN SWEET CHERRY (*Prunus avium*) DURING BUD DORMANCY RELEASE

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Bud dormancy release in *Rosaceae* depends on accumulation of chilling hours (CH). *DORMANCY ASSOCIATED MADS-BOX* (*DAM*) genes in peach are negative flowering regulators and strong candidates for the regulation of bud growth cessation and dormancy maintenance. Toget an insight in the molecular mechanism of dormancy release in sweet cherry (*Prunus avium*); we identified the presence of six putative *DAM* genesby high-throughput genomic DNA sequencing. Phylogenetic analysis of the putative *Prunus avium DAM* genes identified showed a strong similarity to the six *Prunus persica DAM* genes previously described. To study a possible epigenetic regulation of *PaDAM* genes during dormancy release, we performed a bisulfite analysis in regulatory regions of *PaDAM3* and *PaDAM5*. We show that DNA methylation in the first intron of *PaDAM3* could be involved, with the maintenance ofits repression during bud break. In parallel, the kinetic of gene expression of *PaDAM3* and *PaDAM5* (floral repressors) showed a progressive decrease with CH accumulation and no expression is observed during bud break and flowering time. Moreover, relative expression of *Flowering locus T* (*PaFT*)*,* a floral activator and candidate target gene of *DAM,* increased at 439 CH reaching its maximum at 1142 CH, at bud break. These results suggest that CH accumulation repress *DAM* genes, releasing *PaFT* expression and maybe other floral activators during dormancy and flowering regulation.

Acknowledgements: FONDEF G09I1008; FONDAP CRG 15070009; Basal PFB-16.

OSI4

RESPIRATORY CHANGES IN BUDS OF *Vitis vinifera* DURING THE TRANSITION FROM PARADORMANCY TO ENDODORMANCY: A SHIFT FROM AEROBIC RESPIRATION TO FERMENTATION

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During the transition of grapevine buds from paradormancy (PD) to endodormancy (ED), metabolic change occurs that make possible the survival of the buds throughout the winter. In this study we showed that latent buds reduced drastically their O_2 consumption during ED and recovered its normal rate of respiration before budburst. Moreover, the lower effect of temperature on the rate of respiration in dormant than in non-dormant buds, besides the stimulatory effect of dormancy-breaking compounds H_2CN_2 and NaN_3 on O_2 consumption of dormant buds, suggests that ED is associated with a low rate of bud respiration. To understand at the molecular level the restrictions that limit O_2 consumption in dormant buds, analysis of expression of genes related to tricarboxylic acid cycle (TCA), carbohydrate metabolism, mitochondrial electron transport chain (m-ETC), fermentative and pentose phosphate pathway (PPP) was performed by RT-qPCR before, during and after the entry of buds into ED. The results indicate that genes encoding enzymes of TCA cycle and m-ETC have low expression during dormancy and increase before budburst. In contrast, genes encoding enzymes of the fermentative pathway and of the PPP have high expression levels during the ED period, decreasing drastically before budburst. The concentration of sucrose, glucose and fructose decreased during ED and increased before budburst. From all this evidence, we concluded that in the entry of grapevine buds into ED a shift from aerobic respiration to fermentative pathway occurs.

Acknowledgements: This work was supported by FONDECYT Nº 1140318

OSII5

PHOSPHOINOSITIDE-LOCALIZED BIOSYNTHESIS LINKS ENDOCYTIC TRAFFICKING AND HEAT SHOCK RESPONSE IN *Arabidopsis thaliana*

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Environmental stresses, such as temperature changes, drought or salinity, induce an array of cellular adjustments that facilitate plant acclimation and survival. Among the phosphorylated membrane lipids, the phosphatidylinositols (PtdIns) can be phosphorylated to generate potentially seven phosphorylated PtdIns forms, the so-called phosphoinositides (PI). The dual PI function as scaffolding molecules and precursors of other secondary messengers, as well as their intracellular differential distribution, makes PIs important mediators of a wide variety of cellular processes like membrane trafficking, membrane homeostasis, nuclear signaling, and more prominently for stress responses. Here we show that a sudden increase in temperature (Heat Shock, HS) in *Arabidopsis thaliana* generates rapid changes in intracellular distribution of organelle and plasma membrane protein markers, and perturbs the uptake of the endocytic tracer FM4-64. We observe that the phosphoinositide markers YFP-PHPLCγ1 [which labels PtdIns(4,5)P2] and YFP-PHFAPP1 (a marker for PI4-P), together with the PI-metabolizing enzyme PIP5K1 are also modulated in content and subcellular distribution in response to HS. We discuss the data in the context of the role that PI relocalization and de novo metabolism may have on the subcellular response, the endocytosis modulation, and the overall plant heat shock response

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OSII6

JASMONATE-DEPENDENT GENE EXPRESSION LANDSCAPE DURING SALT STRESS IN *Arabidopsis thaliana* ROOTS

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Jasmonate (JA) is an essential phytohormone controlling plant responses to environmental stresses. The build-up of sodium salts on the soil surface is a critical agricultural problem affecting world´s irrigated croplands. Understanding plant tolerance to salinity is therefore important. Our previous RT-qPCR analysis showed that JA early responsive genes are up-regulated by sodium salt stress in a JA-dependent manner in *Arabidopsis thaliana* roots. However, the role of JA in salt stress responses is currently unknown. The root transcriptome analysis could reveal key components of the JA-mediated response triggered by salt stress. To elucidate which salt-induced genes are dependent on JA signaling pathway we performed RNA-Seq analysis for gene expression profiling using Illumina's HiSeq sequencing system™ to sequence mRNAs from WT *Arabidopsis* roots and *coi1-2* (a mutant partially impaired in JA perception) after 3h of 150 mM NaCl treatment. We identified 115 genes induced by salt treatment at higher level in WT plants than *coi1-2*. Based on gene ontology, we found that transcription factors and enzymes were highly represented in WT roots. On the other hand, we detected 69 genes showing a higher induction by salt treatment in *coi1-2* plants, where enzymes and several salt-responsive genes were highly represented. Root growth inhibition assay showed that JA biosynthesis or signaling mutants are more tolerant to salt stress than WT plants. MYC2/3/4 are key transcription factors activating early JA responsive genes and therefore are good candidates to activate salt responsive genes dependent on JA. Therefore, we evaluated whether MYC2/3/4 play a role in controlling expression of those RNA-Seq detected genes by measuring steady-state mRNA levels in roots by RT-qPCR analysis in *myc2 myc3 myc4* null-mutant and WT plants under salt stress. Together, these results link JA signaling pathway activation with changes in gene expression and root growth triggered by salt stress in *Arabidopsis*.

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OSII7

CHARACTERIZATION OF 4 POLLEN SPECIFIC KINASE CODING GENES FROM *Arabidopsis thaliana*

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Pollen grains are the male gametophyte of plants and thus are essential for plant reproduction and productivity. However, despite their biological and agronomical importance, little is known about the molecular mechanisms that regulate its development and function. In Arabidopsis, the mature pollen grain contains three haploid cells: a large vegetative cell and two small sperm cells. Upon contact with the stigma, the pollen grain must germinate and a pollen tube growth directionally towards the ovules, carrying both sperm cells for the double fertilization process. Currently, little is known about the molecular mechanisms involved in pollen development, tube growth and tube guidance inside female tissues. Using microarray data we have previously identified 4 genes encoding kinases proteins (*PSK1-4*, for *POLLEN SPECIFIC KINASE*) that are expressed during the last stages of pollen development, germination and tube elongation and became candidate genes for functional analysis. To analyze the physiological relevance of these genes, we have generated transgenic plants expressing specific amiRNAs for these genes under the control of a pollen-specific promoter (LAT52) and we have analyzed pollen development and tube elongation in insertional mutant and transgenic plants expressing amiRNAs. Our results suggest a role for *PSK2* in pollen-ovule interaction, specifically in the short distance guidance of the pollen tube towards the micropyle. On the other hand, pollen tubes from *PSK4* insertional mutant and transgenic plants lackthe callose plug normally found in wild type pollen tubes. Also, we have determined the sub-cellular localization of each kinase protein using *35S:PSK-GFP* constructs byagroinfiltration experiments in tobacco leaves and in pollen tube using endogenous and *LAT52* specific promoter. Taken these together, our results suggest that *PSK2* and *PSK4* have an important role for pollen function in *Arabidopsis thaliana*.

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OSII8

FUNCTIONAL ANALYSIS OF *P. avium FT* AND *TFL1* IN *Arabidopsis thaliana*

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Different environmental cues and molecular pathways regulate flowering development, where the most important are the photoperiod and vernalization. These converge in a master gene named *FLOWERING LOCUS T* (*FT*). *FLOWERING LOCUS T (FT)* and *TERMINAL FLOWER 1 (TFL1)* genes have been shown to be important in the control of the switch between vegetative and reproductive growth in several plant species. These are paralogous genes with high similarity in their sequence, however TFL1 acts as an antagonist to FT by repressing flowering. In this work we cloned *FT* and *TFL1* from sweet cherry (*Prunus avium* var. Van and Brooks) and generated different Arabidopsis transgenic plants to analyze their function in flowering. The phylogenetic analysis of the amino acid sequences showed high identity of the cloned sequences to *FT* and *TFL1* orthologous genes from other Rosaceae species and Arabidopsis. Edi-0 Arabidopsis ecotype, which requires vernalization to flower, was transformed with a construct for overexpression of *PaFT.* These transgenic plants showed an early flowering phenotype without cold treatment. On the other hand, transgenic Arabidopsis in the Col-0 ecotype that overexpress *PaTFL1* have a late flowering phenotype. *tfl1* mutant transformed with *PaTFL1* under the control of endogenous Arabidopsis *TFL1* promoter recovered the wild type phenotype, showing that this gene is functional. Our results showed that *FT/TFL1* gene family is highly conserved in sequence and function among plant species, with *FT* involved in flowering and *TFL1* in vegetative growth in perennial plants (sweet cherry) as well as in annual plants (Arabidopsis).

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OSIII9

VOLTAGE-SENSOR TRANSITIONS OF THE INWARD-RECTIFYING K^+ CHANNEL KAT1 FROM *A. thaliana* INDICATE A LATCHING MECHANISM BIASED BY HYDRATION WITHIN THE VOLTAGE SENSOR

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The Kv-like K^+ channels at the plasma membrane, including the inward-rectifying KAT1 K^+ channel of *Arabidopsis*, are important targets for manipulating K^+ homeostasis in plants. Gating modification, especially, has been identified as a promising means by which to engineer plants with improved characteristics in mineral and water use. Understanding plant K^+ channel gating poses several challenges, despite many similarities to that of mammalian K_v and *Shaker* channel models. We have used site-mutagenesis to explore residues that are thought to form two electrostatic counter-charge centers either side of a conserved Phe residue within the S2 and S3 α-helices of the voltage sensor domain (VSD) of K_v channels. Consistent with molecular dynamic simulations of KAT1, we showed that the voltage dependence of the channel gate is highly sensitive to manipulations affecting these residues. Mutations of the central Phe residue favored the closed KAT1 channel, whereas mutations affecting the counter-charge centers favored the open channel. We interpret these findings in context of the effects on hydration of amino-acid residues within the VSD and with an inherent bias of the VSD, when hydrated around a central Phe residue, to the closed state of the channel.

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OSIII10

MOLECULAR MODELLING AND DOCKING SIMULATIONS OF FRUIT-RELATED α-EXPANSINS FROM *Vasconcellea* AND *Fragaria* GENUS.

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Fruit softening is associated to cell wall modifications produced by a set of hydrolytic enzymes and proteins. Expansins are proteins with no catalytic activity, which have been associated with several processes during plant growth and development, including fruit softening. Many fruit-specific α-expansins (EXPA) have been identified at the transcriptional level in a variety of species, although more effort is needed to understand the mechanism of action. Unfortunately, isolation and purification of EXPA family protein has proven difficult, thus limiting structural and functional studies. A 3D model for VpEXPA2, was built for the first time by comparative modelling strategy. VpEXPA2 modelshows a cellulose binding domain with a β-sandwich structure, and a catalytic domain with a similar structure to the catalytic core of endoglucanase V (EGV) from *Humicola insolens*. VpEXPA2 protein contains essential structural moieties related to the catalytic mechanism of EGV, such as the conserved HFD motif. The lack of catalytic activity of this expansin and its preference for cellulosic substrate (cellodextrin) are discussed in light of the structural information obtained from the VpEXPA2 protein model. In addition, to investigate about the protein structureof two ripening-related family members from *Fragaria chiloensis*, the 3D models of FcEXPA1 and FcEXPA2werebuiltby comparative modeling methodology. The models obtained for FcEXPA1 and FcEXPA2display similarstructural-features to VpEXPA2. Additionally, the interaction of FcEXPA1 and FcEXPA2with a set of putative substrates such as xyloglucans (XGs) and cellodextrin was explored using molecular docking simulations. The results obtained suggest that stable conformational complexes are formed, with favorable affinity energies for the binding of XGs and cellodextrin. The data is congruent with a probable role of FcEXPA1 and FcEXPA2 proteins in the disassembling of the cellulose-XG matrix during ripening of Chilean strawberry fruit.

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OSIII11

MOLECULAR AND STRUCTURAL CHARACTERIZATION OF THE TRANSPORTER PrMATE1 INVOLVED IN THE ASSIMETRICAL GROWTH OF RADIATA PINE IN REPONSE TO INCLINATION

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Plants are continuously exposed to gravity force that eventually could affect their vertical growth. In trees, the inclination response is a widely studied biological phenomenon; however, the molecular mechanism is still unknown. Based on a Suppressive Subtractive Hybridization (SSH) transcriptomic approach, the bioinformatic analysis revealed that several categories of genes showed differential expression. One of the most interesting groups of genes was the related to the flavonoid compounds and to transport of those metabolites within the cell. A gene encoding a Multidrug And Toxic compound Extrusion (MATE) family protein was identified and the full-length sequence was obtained. Their deduced amino acid sequence and phylogenetic tree analysis with other MATE-like proteins indicated that PrMATE1 encode a putative PA transporters. Their relative expression was analyzed by qPCR showing a significant induction after inclination, in a temporal and spatial manner along the stem. Additionally, expression analysis in different tissues showed a specific behavior in response to inclination. Treatment with auxin showed a strong down-regulation in stem of seedlings exposed to inclination. Through molecular modeling, structural model of PrMATE1 was generated, displaying a structure consisting in 12 α-helices, which are according to the presence of the 12 transmembrane domains described to these type transporters. The results obtained leading to a greater understanding of the molecular mechanism that governs this biological process.

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OSIII12

Daucus Carota LYCOPENE B-CYCLASE (LCYB1) PROMOTES INCREMENT IN PLANT FITNESS THROUGH POSITIVE REGULATION OF CAROTENOID, GIBBERELLIN AND CHLOROPHYLL GENES.

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In plants, carotenoids are isoprenoid pigments synthesized in plastids and are involved in light harvesting, photoprotection and phytohormone synthesis. In addition, β-carotene, the main carotenoid of carrots, is precursor for vitamin A and possesses high antioxidant properties. Carotenoids derived from the precursor geranyl-geranyl-diphosphate (GGPPS) as well as chlorophylls and gibberellins. One of the most important enzymes involved in carotenoid biosynthesis is lycopene β-cyclase (LCYB) that catalyzes the conversion of lycopene into β-carotene. In *Daucus carota*, two *lcyb* genes have been described (*lcyb1* and *lcyb2*). During development, *Dclcyb1* is expressed preferably in leaves but is essential for carotenoid synthesis in the whole plant. When expressed in *Nicotiana tabacum*, *Dclcyb1* produces 2-fold increase in total carotenoids and in β-carotene. Interestingly, these lines showed a significant increase in plant height, leaf size and whole plant biomass (1.4 to 1.7 fold increase), besides a trend in early flowering regard to the wild type plant. Plus, the photosynthetic efficiency (F_v/F_m ratio) is increased in all lines. Given that these transgenic tobacco lines presented an increase in carotenoids, as well as in photosynthesis and fitness parameters, we analyzed the expression level of key genes involved in carotenoid, chlorophylls and gibberellic acid biosynthesis by qRT-PCR. We found a significant increase in the expression of genes involved in the biosynthesis of common precursors for these pathways (*ggpps* and *dxs2* genes). Additionally, key carotenogenic genes, *Ntpsy1, Ntpsy2* and *Ntlcyb2* were induced, as well as those involved in gibberellins (*cps* and *ks)* and chlorophyll (*chs)* synthesis. These results let us to propose that *Dclcyb1* produces a positive feedback affecting the expression of isoprenoid gene precursors and genes involved in carotenoid, gibberellin and chlorophyll pathways. Thus, transgenic plants present an enhanced fitness measured as plant height, leaf size, biomass, flowering, seed production, photosynthetic efficiency and carotenoid/chlorophyll composition.

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OSIV13

MOLECULAR CHANGES DURING DEVELOPMENT AND RIPENING OF RASPBERRY FRUIT (*Rubus idaeus* CV HERITAGE).

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Raspberry (*Rubus idaeus*) is an economic important fruit, with a rapid ripening and softening rate. However, the molecular mechanism involvedin ripening evolution of this fruit has been seldom studied. To understand the ripening evolution: firmness, ethylene production, indole-3-acetic acid (IAA) content, changes in cell-wall andlevels of transcriptsrelated to softening, ethylene and auxin signaling weredetermined. Raspberry exhibited an increased softening, ethylene production; respiratory rate and cell-wall disassemble according to the ripening progress, being higher in ripe fruit. While, auxin content was higher in half-ripe fruit. In addition, a RNA-Seq approach showed a total of 2,409 transcripts identified as differentially expressed. The qPCR analysis showed that ethylene biosynthesis genes, 1-aminocyclopropane-1-carboxylic acid synthase (*RiACS1*) and 1-aminocyclopropane-1-carboxylic acid oxidase (*RiACO1*) was higher expressed in receptacle and increased in the ripe stagessimilar to genes related to pectin modification, polygalacturonase (*RiPG*) and pectatelyase (*RiPL*).On other hand, the transcripts that codifies to acid Indole-3-Acetic acid-amidosynthetase, which isrelated to regulation of auxin homeostasis by IAA conjugation to amino, werefound with different and particular expression pattern. Finally, treatment of half-ripe fruit with 1000 ppm of ethylene and 1600 ppm of 1-methylcyclopropene (1-MCP) showed that inhibition ofethylene perception delayed the loss of firmness during storage at 10 °C by 5 days. The results suggest that ethylene is involved in softening during ripening evolution of raspberry. Even though, we reported changes in the IAA content and levels of transcripts related to this hormone, further studies are ongoing to elucidate the auxin role on development and ripening of this fruit.

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OSIV14

AUXINS AND ABA ARE REGULATING THE SOFTENING OF *Fragaria chiloensis* FRUIT

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The native Chilean strawberry fruit (*Fragaria chiloensis* (L.) Mill) has potential as an exotic fruit in the international market, however its fast softening limits its commercialization. *F. chiloensis* is a non-climacteric fruit and the control of ripening remains unclear, although auxins (Aux) and abscisic acid (ABA) may have a role on it. In *F.* × *ananassa*, the commercial strawberry, Aux levels in the receptacle increased from fruit set until unripe big size fruit, and declined after that until the end of development, while ABA displayed a constant increase. To understand the control of ripening in *F. chiloensis* fruit, the expression level of genes involved in ABA biosynthesis (*FcNCED1,* 9-cis-epoxy carotenoid dioxygenase) and perception (*FcPYR7*) was analyzed during development and ripening by qPCR. In addition, the effect of Aux and ABA treatments on the transcription level of *FcNCED1* and *FcPYR7*, and some softening related genes, was analyzed. Results showed that ABA biosynthesis and perception genes increase their expression level notoriously at turning stage and remained high until the end of ripening. Aux treatment induces the expression of *FcNCED1* and *FcPYR7*. ABA treatment induces *FcPYR7* transcription but reduces that of *FcNCED1*. ABA also induces the transcription of softening related genes such as *FcXTH1* and *FcExp2*, although does not change others (Fc*XTH2, FcEG* and *FcPL).* These data suggest that Aux and ABA are coordinating the ripening development in the Chilean strawberry fruit.

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OSIV15

POSTHARVEST TREATMENT OF HYDROGEN SULFIDE DELAYS THE SOFTENING OF CHILEAN STRAWBERRY FRUIT BY DOWN-REGULATING THE EXPRESSION OF GENES INVOLVED IN PECTIN CATABOLISM

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Hydrogen sulfide (H_2S) plays several physiological roles in plants, such as seed germination, root organogenesis, biotic/abiotic stress tolerance, senescence of cut flowers, etc. Despite these evidences, the physiological role that H_2S plays in *Fragaria chiloensis* remains unknown. In this work, the effect of H_2S treatment at harvest was tested during the post-harvest shelf life of Chilean strawberry fruit and its implications on softening. The treatment with H_2S gas released from the H_2S donor NaHS prolonged the postharvest shelf life of strawberry fruits in a dose-dependent manner. Chilean strawberry fruits treated with the most effective concentration of H_2S sustained significantly higher fruit firmness and kept lower respiration rate than non-treated fruit. No differences in titratable acidity or soluble sugars were recorded between treated fruit and non-treated. Further investigation evidenced during the first post-harvest days that H_2S treatment significantly down-regulated the expression of genes encoding for enzymes involved in pectin catabolism, such as polygalacturonase, pectate lyase and pectin methylesterase. Interestingly, a gene that encode for an isoform of expansin (FcEXP2) showed a similar expression pattern. These evidences suggest that H_2S as gasotransmitter prolongs the post-harvest shelf life of the Chilean strawberry fruit and prevents its fast softening rate by the suppression of pectin catabolism soon after the H_2S treatment.

Acknowledgments: ANILLO ACT 1110 project.

OSIV16

FUNCTIONAL EVALUATION OF THE REGULATORY REGION OF *AGAMOUS LIKE 11* (*VvAGL11*) IN *Vitis vinifera L.*

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Seedlessness in table grapes is one the most desired traits in this industry. Integrating multiple genomic tools we identified *VvAGL11* as the gene responsible for the absence of seeds in table grapes. *VvAGL11* reveals homology with proteins identified in model species such as *STK/AGL11* from *Arabidopsis*, *TAGL11* from tomato and *FBP7/FBP11* from *Petunia hybrida*. All MADS-box transcription factors are involved in floral organ development, and after anthesis involved in seed and fruit development. In Thompson Seedless (Sultanina) we identified two alleles for *VvAGL11*, a seedless dominant and a seeded one. Gene expression analysis performed at key stages of berry and seed development revealed a lower expression of *VvAGL11* in homozygous genotypes for the seedless allele and in heterozygous seedless genotypes compared to homozygous seeded genotypes. The characterization of seedless allele revealed several polymorphisms (SNPs and INDELs) in key regulatory elements that could drive the differential expression pattern. In this work we propose that seedlessness in table grapes is caused by variations in the regulatory region of *VvAGL11* that might be responsible for the different expression patterns of the seeded and seedless alleles. Both promoter alleles were fused to the reporter gene beta-glucuronidase (GUS) to validate the hypothesis. Allele specific expression was analyzed by quantitative PCR and by GUS enzymatic assays that were performed in stable transgenic tomato lines (cv. Micro-Tom). Both analyses showed that the basic unit defined as promoter, composed of 1.500 bp upstream the TATA-box, are sufficient to drive specific expression and that the seedless allele contains variations that abolish its functionality.

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OSV17

ANATOMICAL, PHYISIOLOGICAL AND BIOCHEMICAL CHANGES IN WILD TOMATOES DICTATED DIFFERENTIAL MECHANISMS TO TOLERATE DROUGHT STRESS

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Wild tomatoes *Solanum chilense* and *Solanum peruvianum* share the same cluster in the section Lycopersicon far away of *S. lycopersicum.* Geographically, both species are distributed in different areas in the north of Chile. *S. peruvianum* predominate at sea level, near of agricultural soils, while *S. chilense* grow between rocksfrom sea levels to 3.000 m.Both species are clearly different from *S. lycopersicum* in their morphology and green color of their leaves and stems.The present research had as objective to identify anatomical, biochemical and transcriptomic responses of these wild tomatoes to tolerate water stress and compare them with cultivated tomato *S. lycopersicum*. Experiments in greenhouse and growth chamber conditions were carrying out considering two treatments: optimal watering (NW) and restricted watering (RW). Samples were collected for determination of foliar area, stomata density, rate of stem growth (RG), osmotic potential, total sugars, proline, chlorophyll content, and lipid peroxidation. We also analyzed leaf transcriptomic profiles by RNA-seq in two species. The results of variables evaluated for *S. chilense* and *S. peruvianum* were relativized in comparison to *S. lycopersicum*. The three species showed significant differences respect to RG in NW and RWas well. The principal component analysis showed that in general *S. chilense* was associated to higherAdaxial/Abaxial rate of stomata density compared with *S. peruvianum*. The higher RG of *S. peruvianum* during RW coincided with higher oxidative damage and soluble sugars accumulation. Contrarily, the higher osmotic potential observed in *S. chilense* during RW was related tohigher proline accumulation. Additionally this species showed a lower oxidative damage. Analysis of gene expression are associated and discussed in relation to these physiological changes.

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OSV18

TRANSCRIPTOMIC APPROACH TO UNRAVEL SALT TOLERANCE OF ALGARROBO (*Prosopis chilensis*) TREES

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In arid environments, plants have to deal daily withseveral abiotic stresses such as drought, salinity, high UV radiationand cold orheavy metal toxicity. *Prosopis* genus is a group of trees adapted to arid environmentssince Miocene (12 million years ago) and in Chile, native Algarrobo (*Prosopis chilensis*) is the widest distributed among *Prosopis* species. Previously, we found that *P. chilensis*trees belonging to Choapa Valley (31° S, Coquimbo region) showed the best performance to tolerate salt stress at both germination and physiological responses. Using RNA-Seq approach, we aimed to sequence the transcriptome of our most saline-tolerant trees to dissect its metabolic pathways involved in the salt tolerance. We extracted RNA from leaves, stems and roots exposed hydroponically to 450 mMNaCl (ψ-2.29 MPa) and cDNAs libraries from saline and non-saline tissues (shoots, stems and roots) were prepared and sequenced by Illumina™ technology. Contigswere assembled by Trinity software and a matrix counts using RSEM package was prepared. Differential expression analysis using edgeR package and functional categories assigned by BLASTx-allowed us to identify near to 22.000 transcripts significantly up or down-regulated by salt stress, half coming from shoot tissues (leaves and stems) and the rest from roots. Using GO terms and a pairwise enrichment analysis, functional tags related to vacuole membranes, cell plate assembly, ß-glucosidase activity, metal ion transport, RNA splicing, Terpenes and glutathione metabolismswere found. Our results represent the first RNA-Seq-based expression study performed in *P. chilensis*and it contributes to understand the metabolic pathways and other molecular strategies displayed by this tree to respond to salt stress.

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OSV19

PHYSIOLOGICAL AND TRANSCRIPTOMIC CHARACTERIZATION OF *Cistanthe longiscapa* DURING SEED GERMINATION

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The “Blooming of the desert” is a world-renowned phenomenon that develops at the Atacama Desert in northern Chile (26-30°S). This phenomenon occurs between the months of September and November in years when rainfall is unusually high (>10 mm), when seeds of ephemeral species have accumulated a minimum of water volume between May and August. The ephemeral species that bloom in the Atacama Desert are able to detect the favorable environmental conditions to germinate and complete their life cycles. It is essential to identify genes that are involved in the germination of these seeds in these extreme conditions. This could be an important breakthroughin the development of newcrop cultivars. *Cistanthe longiscapa* is one of the dominant species in the “Blooming of the desert”, and we use it as a model to get insight into the genes that are required for germination under drought stress. DNA and RNA extraction to obtain high quality nucleic acids were optimized from different tissues of *C.longiscapa*. RNA from seeds exposed to water for 1, 5 and 12 hours were used to identify differentially expressed genes between conditions using RNA-seq. Here we described that *C. longiscapa* has a several survival strategies such as: delayed germination, density dependence of seed, nictinastic movement in their flowers and anfistomatic leaves. Moreover the transcriptomic analysis revealed that genes expressed in seed germination are concordant with the biological process that involved the seed germination in model species such as *Arabidopsis thaliana*.

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OSV20

NITROGEN AND CARBON METABOLISMS IN QUINOA UNDER DROUGHT STRESS CONDITIONS

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Drought is one of the major environmental factors limiting crop productivity worldwide. Water stress also restricts primary nitrogen assimilation by impairing the activity and function of Nitrogen-related enzymes such as the nitrate reductase (NR) or the chloroplast isoform of the Glutamine Synthase (GS2). It has also been shown that a coordinated regulation of carbon and nitrogen metabolisms is necessary to improve tolerance to stresses including drought. *Chenopodium quinoa* Willd. (Amaranthaceae) is well adapted to extreme conditions including water scarcity and recently has gained attention due to the remarkable high protein content of their seeds becoming in a great model for the study of nitrogen in a drought tolerant plant. We have analyzed the effects of water stress during grain filling on carbon and nitrogen partitioning in two quinoa genotypes naturally adapted to different climatic conditions: Faro (O'Higgins Region) and BO78 (Araucanía Region). Metabolomic, carbon and nitrogen enzymatic assays suggested a common strategy to overcome water stress, by means of fast recovery inducing the synthesis of important ROS scavengers and osmolites, especially those related with the Ornithine cycle. Changes in nitrogen metabolism driven by water stress relief lead to improvements of seed quality mostly in BO78 genotype, which presented a more steeped metabolic change on nitrogen related enzymatic activities when compare to Faro genotype. These results provide new insights regarding the role of water stress regulating carbon and nitrogen partitioning in plants targeting pathways responsible for the outstanding capacity of quinoa to tolerate water stress.

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OSVI21

ADVANCES IN THE GENETIC IMPROVEMENT OF MANDARIN AND LEMON-TREE IN CHILE

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In the 90's the main planted cultivar was mandarin 'Clemenules', but from the year 2000, with the aim of expanding the harvest season, growers started planting 'W.Murcott'. This resulted in the occurrence of cross-pollination between the two species hence fruits started showing the presence of seeds. This has caused great economical loses to the industry. The PUC with the support of five nurseries and an export company started a breeding program of mandarin and lemon in 2007. The objective was to obtain new seedless cultivars by inducing mutations with gamma radiation, *in vitro* rescue of triploids, and obtaining parental tetraploides by the use of colchicine and somatic hybridization. An experimental field was established with 5700 and 2500 irradiated mandarin and lemon trees in Pomaire. After three years some preliminary selections have been made: 14 and 164 mandarins and lemons have shown to be low seeded, four thornless lemon trees, and four ornamental plants. One hundred and eighteen triploid hybrids have been obtained by cross-pollination of diploid parentals, these plants are currently under juvenility handlings. Also, nineautotetraploid plants have been obtained by the use of colchicine and are ready to be used as parental in interploid crosses. We finally have succeeded to develop our somatic hybridization protocols to create new allotetraploid hybrids.

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OSVI22

THE ASSOCIATION BETWEEN REPRODUCTIVE TISSUES AT PRE- AND POST-ANTHESIS IS PROPOSED AS A CONTROL OF KERNEL WEIGHT POTENTIAL WHEAT (*Triticum aestivum* L.)

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The future human and environmental conditionshighlight theneed of increasing crop production for humankind food security. Among crops, wheat (*Triticum aestivum*) is one of the key crops for the achievement of this aim. However, to increase yield potential of wheat, the negative relationship between kernel weight and grain number should be counteracted. Therefore, it is necessary a better understanding ofthe physiological bases driving kernel weight potential. The objective of this study was to evaluate the association between traits developed at both pre-anthesis (ovaries) and post-anthesis (pericarp) considering that ovaries become the pericarp of kernels, andthought that imposes a physical restriction to kernel growth. Two wheat cultivarscontrasting in kernel weight potential and similar phenology (Bacanora and Kambara) were sown at field conditions under two planting rates: 44 and 370 plm^{-2}in a split plot design with three replicates. The experiment was conducted in the "Estación Experimental Agropecuaria Austral" (Universidad Austral de Chile). Floral ovaries were sampled ten days before anthesis in two-flower position of the spike (F1 and F2) from five spikes per replicate. From flowering onwards the pericarp of 8 kernels (positions G1 and G2) harvested from 4 spikes per replicatewere dissected. Ovaries and kernels were, sized and weighted. At harvest, kernels of positions G1 and G2 also were sized and weighed. The carpels were between 0.99 and 1.17 mm long, 1.12 and 1.20 mm wide and 0.91 and 0.99 mm high in Bacanora and Kambara, respectively. At 12 days post flowering the pericarp reached the maximum weight. Final kernel weight ranged from 50.5 to 74.8 mg, which was affected ($p<0.05$) by genotype, plant rate and position within the spike. The time-course of carpel and kernel dimensions (length, width and height) recorded in the experiment showed that kernel potential is determined before pollination.

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OSVI23

GENETIC DIVERSITY AND POPULATION STRUCTURE OF TWO DOMINANT PLANT SPECIES OF THE HIGH ANDEAN WETLANDS OF CHILE'S NORTE CHICO

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High Andean wetlands are important reservoirs of biodiversity and providers of ecosystem services. *Patosia clandestina* (Juncaceae) and *Carex gayana* (Cyperaceae) are two dominant species of these ecosystems in Chile's Norte Chico. In this study, we aimed to reveal their genetic structure over the latitudinal range of this region. Plant samples were collected in 21 high Andean wetlands spanning all Chile's Norte Chico (between 26°S 69°W and 32°S 71°W) during summer 2011, and we used the *rbcL* gene and AFLP markers to detect population genetic structure in both species. Our results demonstrate that both *C. gayana* and *P. clandestina* are spatially and genetically structured but the two plants species show different patterns of variation. In *C. gayana*, genetic structure is hierarchically ordered: the first hierarchical level separates three wetlands from the north and one wetland from the south from the rest (N=17), while the second hierarchical level follows a latitudinal stepping-stone pattern. In *P. clandestina*, a clear-cut genetic barrier in the north of the Limarí basin separates the northern and southern wetlands of Chile's Norte Chico, the southern group being more structured than the northern group. Our findings are discussed in terms of the orogenic history of the basins and current landscape connectivity. Knowledge on the genetic connectivity of these two dominant plant species provides insight into the patterns and processes influencing gene flow in wetland plant communities. Such understanding is necessary for adequate management of these ecosystems, which are facing high anthropogenic disturbance and climatic instability.

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OSVII24

FUNCTIONAL CHARACTERIZATION OF SALICYLIC ACID-INDUCIBLE GENES CODING FOR GLUTATHIONE *S*-TRANSFERASES AND GLUTAREDOXINS IN THE DEFENSE RESPONSE TO STRESS IN *Arabidopsis thaliana*

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Plants are organisms constantly exposed to several biotic and abiotic stress conditions that increase the production of reactive oxygen species (ROS) and alters the cellular redox state. Survival of plants depends on a complex balance between the production and detoxification of ROS. Salicylic acid (SA) is a key phytohormone in the establishment of the defense response to stress, being essential for the production and also for the contention of the oxidative burst needed to establish the defense responses. SA induces the expression of genes coding for proteins with antioxidant and detoxifying function; among them glutathione s-transferases (GSTs) and glutaredoxins (GRXs). In this work, we performed an analysis of microarray databases to determine the expression patterns of GSTs and GRXs under different stress conditions where SA is involved. We identified 8 GST and 2 GRX genes and we confirmed their expression patterns induced by stress conditions using real-time PCR. We selected mutant plants for GSTU7, GSTU8, GRXC9 and GRXS13 and evaluated their relevance to overcome different stress conditions such as treatments with methyl viologen, UV-B radiation and avirulent bacteria. Our results indicate that SA induces the expression of a set of GST and GRX genes in a temporal specific manner and that these genes are important in the contention of oxidative damage produced by different types of stress, suggesting a particular role for them in controlling ROS accumulation in the defense response.

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OSVII25

RESISTANCE *LOCI RUN1* AND *REN1* IN *Vitis vinifera* ARE ASSOCIATED TO THE ACTIVATION OF AN ETI-LIKE MEDIATED IMMUNE RESPONSE AGAINST *Erysiphe necator*.

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Despite its vast genetic diversity, most grapevine (*Vitis vinifera* L.) cultivars are susceptible to powdery mildew, a disease caused by the filamentous biotrophic fungi *Erysiphe necator*. Through many years, breeding programs have aimed to introduce resistance against this pathogen in commercial cultivars. Dominant *loci* conferring resistance against *E. necator* have been mapped, where *Run1* and *Ren1* have been the most studied. Within these regions it has been found clusters of resistance gene analogs, which could code to resistance proteins able to recognize the pathogen and induce a robust immune response, termed effector-triggered immunity (ETI). Well is known that *Run1* and *Ren1* confer resistance to *E. necator*, but it remains unclear if an ETI-mediated immune response is activated. Thus, the aim of this work was to evaluate cellular and molecular events associated to these *loci* in order to characterize the response given by the presence of *Run1* and/or *Ren1* in *Vitis vinifera* against the infection of *Erysiphe necator*. First, selection of double *locus* and single *locus* plants in an interspecific grapevine population were performed through molecular markers. Once selected, we observed that the presence of both *loci* in the same plant reduces the pathogen ability to proliferate in its host earlier than in plants carrying a single resistance *locus*. Moreover, the presence of at least one of these *loci* is required to induce locally ROS accumulation, papillae formation in the infection site, changes in gene expression and the induction of a hypersensitive-like response (HR-like), which are important defense responses against this type of pathogen. Taking all together, these results suggest the activation of an ETI response mediated by the *loci Run1* and *Ren1*.

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OSVII26

VVNAC1, A TRANSCRIPTIONAL REGULATOR INDUCED UNDER A VIRAL COMPATIBLE INTERACTION IN *Vitis vinifera*

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Grapevine (V*itis vinifera)* is affected by several viral infections; among them the infection caused by GLRaV-3 is one of the most widespread. The disease produced by this virus (GLR) causes an incomplete maturation of the berry. Previous studies of our group identified a putative gene induced in both leaves and berries infected by GLRaV-3. This gene is predicted to belong to the NAC family of transcription factors (NACTFs). Recent studies have linked NACTFs with viral compatible interactions, in which some NAC proteins seem to be induced as part of the defense mechanismsof the plant, while others are cellular factors needed by the virus in order to replicate and spread to different tissues. On the other hand, NAC transcription factors can lead the transcriptional activation or transcriptional repression of certain genes. Recently, a repressor domain in the NACTFs was described and named NACRD (NAC Repression Domain). The aim of this work is to characterize the putative transcription factor *VvNAC1* to determine their functionality as a regulator of gene expression. We have cloned the *VvNAC1* gene, and validated its induction under viral infection. The modeling of its NAC domain showed high structural conservation among other NAC proteins. Additionally *VvNAC1* was found to contain a NACRD-like domain. In order to address its role as transcriptional regulator, we performed reporter analysis in protoplasts. From our results we concluded that VvNAC-1 acts as a transcriptional repressor *in planta*. In this work we described the first NACTF that is related to viral infections in *Vitis vinifera*. Functional studies of this gene under viral infections will help to determine the role of *VvNAC1* in this plant-pathogen interaction

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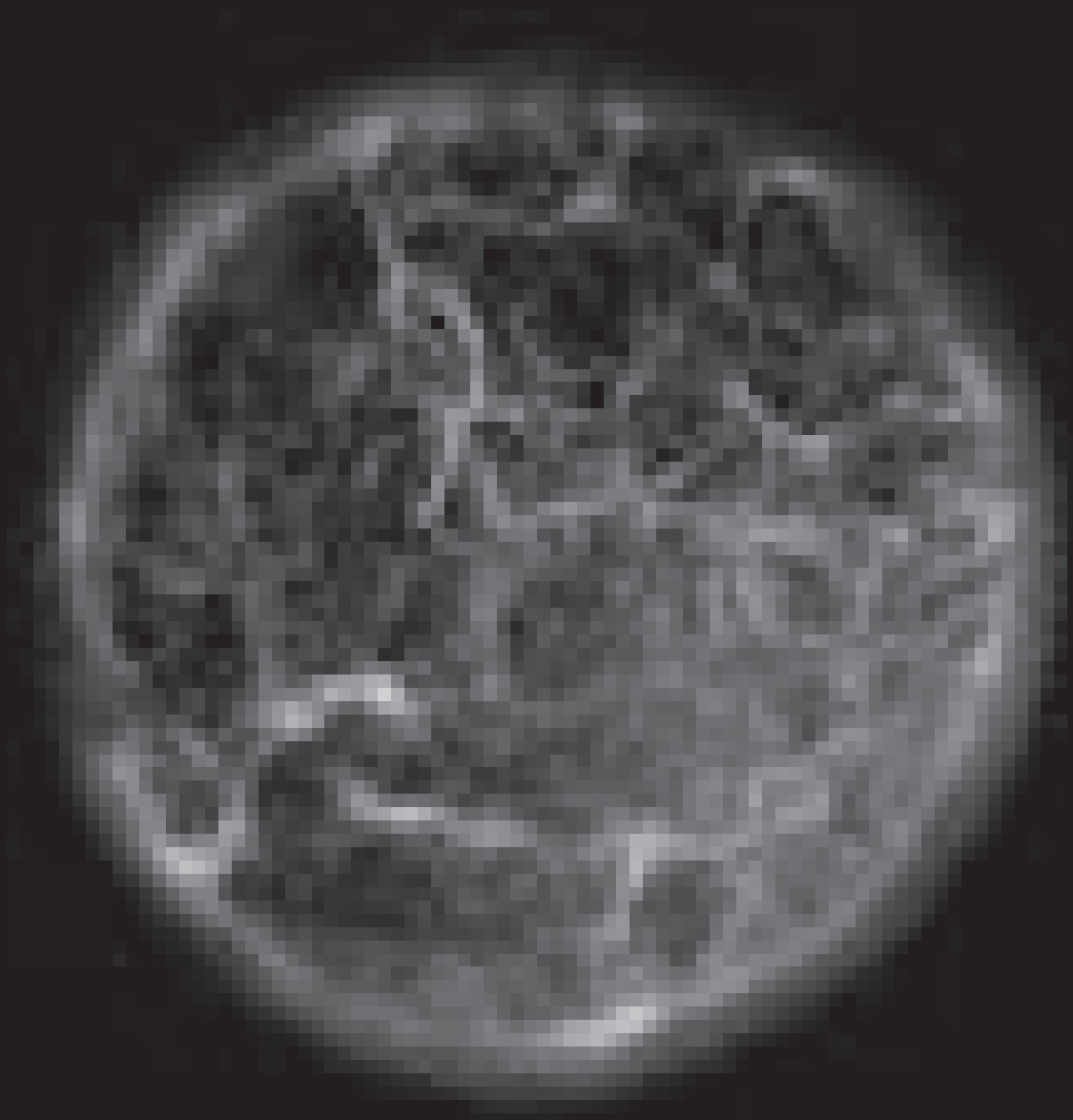

Panel Sessions

Fotografía: Gentileza de Carlos Flores PhD. Student

PS1

IDENTIFICATION AND CHARACTERIZATION OF INHIBITOR PROTEASES DURING DEVELOPMENT OF *Fragaria chiloensis* L. (DUCH.) FRUITS

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Phytocystatins are proteins that specifically inhibit the papain family C1A cysteine proteases. These proteins have been implicated in two functions; firstly in the endogenous regulation of storage proteins turnover in seeds. Secondly, in a defensive role, based on their capacity to inhibit the growth of fungi. *Fragaria chiloensis* the native Chilean strawberry is more tolerant to fungal attack than the commercial strawberry *F*. x *ananassa*. In suppression subtractive hybridization libraries from different stages of fruit development, a putative cystatin gene (*FcCYS1*) was found. According to the intron number, *FcCYS1* belongs to the second group of phytocystatins. Expression analysis by qRT-PCR showed that *FcCYS1* displayed a higher transcript level in fruits with red achenes and green receptacle, suggesting that this gene could be involved in the degradation delay of seed storage proteins at early stage fruit development. In the same fruit stage, methyl-jasmonate application increased the transcript levels of *FcCYS1*. This hormonal response suggests that *FcCYS1* could be implicated in responses to wounding and biotic stress. This work is an initial approach to the characterization of the protein, in order to establish the molecular function of FcCYS1 that is probably involved in the inhibition of cysteine-proteases in *F. chiloensis*.

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PS2

OPTIMIZATION OF *in vitro* PROPAGATION PROTOCOLS IN CHILEAN POPULATIONS OF *Colobanthus quitensis*.

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Colobanthus quitensis **(**Kunth) Bartl. (Caryophyllaceae) is distributed from southern Mexico to northern Antarctic Peninsula and from 0 to 4200 m.a.s.l. It is a species with high scientific interest due to its extreme habitat and distribution. Because of its small plant size and inaccessibility of its habitat, efficient methods for *ex situ* propagation are required. In this work, physical (culture flask cover, glass or polypropylene flask and light intensity) and chemical (silver thiosulfate and seven hormone combinations) parameters were evaluated for its *in vitro* propagation, in order to reduce negative effects such as yellowing and death of explants, and to improve the conditioning of the new seedlings. Seedlings from three different *C. quitensis* populations, previously established *in vitro* were used as explants. The physical parameters evaluated stimulated the emergence of new shoots and roots, and reduced yellowing and death of seedlings. The double foil coverage, glass bottles and light intensity between 28 to 45 µmol m^{-2} s^{-1}, showed the best results. The application of 10 uM STS inhibited around 50% and 25% yellowing and the death of shoots, respectively. Based on the different hormonal combinations tested, was possible to establish the most favorable for *in vitro* propagation of the three populations evaluated. The medium supplemented with IAA (0.25 mg L^{-1}) + BAP (0.5 mg L^{-1}) and pH 5.7 showed better results for pPA and pC, whereas for pPar was the medium supplemented with kinetin (2 mg L^{-1}, pH 4.5). More studies are still needed to establish whether different *C. quitensis* populations that displayed differential response to hormonal combinations are related to genetic or ecotypic variability.

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PS3

DEVELOPMENT AND CHARACTERIZATION OF THE DEFENSE RESPONSE OF NEW TABLE GRAPE CULTIVARS RESISTANT TO *Erysiphe necator*, CARRYING *RUN1* AND *REN1* DOMINANT RESISTANCE LOCI

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The grapevine (*Vitis vinifera*) is the fruit species with the major national production, being Chile the world's largest exporter of table grapes. One of the most economically important diseases that attack the grapevine is powdery mildew. Its etiological agent is the biotrophic fungus *Erysiphe necator*, an obligate pathogen of the Vitaceae family that affects plant green tissues by using its nutrients, leading to important detrimental effects in photosynthesis, growth and yield. Nowadays, there is a global need to reduce or even avoid chemical control of diseases affecting vegetables and fruit production. In this context, this work aims to the development of potential new *V. vinifera* cultivars, with natural long lasting resistance to grape powdery mildew, and characterize its defense response. For this, we selected five segregant plants carrying *RUN1* and *REN1* dominant resistance loci, by using four molecular markers that cosegregate with the resistance. We also used two commercial table grape cultivars, as parental lines in controlled crosses. The obtained progenies were assessed to direct *E. necator* infection by inoculating leaves to identify resistant phenotypes. After the marker-assisted selection, several *RUN1REN1* genotypes were identified. In these new resistant cultivars, we studied some aspects of the resistance mechanism given by *RUN1* and *REN1* loci.

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PS4

GYPSUM EFFECT ON METABOLITES OF *Vaccinium corymbosum* L. GROWN UNDER TOXIC-ALUMINUM

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Highbush blueberry (*Vaccinium corymbosum* L.) is an important crop cultivated in Chile, principally on acid soils (Andisols). This crop is well adapted to acid soils but it is sensitive to toxic aluminum (Al^{3+}). This toxicity affects negatively the plant metabolism, resulting finally in crop yield reduction. Gypsum amendments (calcium sulphate, $CaSO_4$) are frequently used to mitigate Al^{3+} toxicity. We study $CaSO_4$ application effect on amino acids, starch, aluminum (Al), calcium (Ca) and sulphur (S) concentration on roots and leaves of blueberry cultivars (Brigitta, Legacy and Bluegold). They were grown in pots with peat (vermiculite, perlite and acid bark), watered with Hoagland solution and amended with $CaSO_4$ as follow: Control (Hoagland without amendment); 1000µM Al; 1000 µM Al + 2000 kg ha^{-1} $CaSO_4$ and 2000 kg ha^{-1} of $CaSO_4$, during 30 days. Results showed a differential response in leaf-starch concentrations among cultivars under $CaSO_4$ application and aluminum toxicity, decreasing leaf-starch concentration in Bluegold by Al toxicity. In roots, starch decreased with Al-toxicity and increased by $CaSO_4$ in all cultivars. Amino acids concentration in leaves and roots of all cultivars also decreased under Al-toxicity, but increased under $CaSO_4$ application. The amendment reduced Al and elevated Ca and S concentrations mainly in leaves of all cultivars. In conclusion, the $CaSO_4$ application reduces Al concentration in plant tissues and improves the concentration of starch and amino acid in *V. corymbosum* cultivars grown under Al-toxicity.

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PS5

MOLECULAR CHARACTERIZATION OF *WRKY-LIKE* GENES IN STONE FRUIT TREE SPECIES (*Prunus* L.) UNDER ROOT HYPOXIA

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Root hypoxia limits stone fruit tree (SFTs) development. To overcome this problem, SFTs are grafted on clonal rootstocks from different *Prunus* species. Therefore, the stone fruit tree tolerance to hypoxia and other environmental stresses is mainly mediated by the performance of the rootstock. The high variability in the physiological responses to hypoxia in *Prunus* species suggests that different molecular mechanisms could evolve within the genus for dealing with this stress. However, the molecular bases of hypoxia responses are still largely unknown. Molecular analysis of angiosperm responses to the root asphyxia, suggests an important role of WRKY transcriptions factors, but such studies have not been done in *Prunus* species used as rootstocks. In this study, we identified 61 *WRKY*-like genes in *P. persica*genome by *in silico* analyses. Phylogenetic studies revealed their classification into 3 groups. On the other hand, expressionanalyses of 9*WRKY*-like genes in response to root hypoxia revealed that they aredifferentially regulated in *Prunus* rootstocks with different degree of tolerance to thisstress. Furthermore, transient expression studiesshowed thatPcxPmWRKY14-GFP and PcxPmWRKY37-GFP are localized in the nucleus. The resulting groups classification, the identification of putative functionalmotifs, the subcellular localization andthe expression patterns in response root hypoxia should be useful in selecting*WRKY*candidate genes from specific groups for functional analysis.

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PS6

OPTIMIZATION OF *in vitro* MASS CLONAL PROPAGATION PROTOCOLS IN THE *Leucocoryne* GENUS

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Leucocoryne (Alliaceae) is a genus of geophyte plants endemic to Chile, nationally known by the common name “Huilli” and internationally as “Glory of the Sun”. This genus has exceptional qualities to be used as cut flower, potted plant and in landscaping, because it has a long vase life and wide variety of shapes, designs, colors and aromas. There are about 15-20 species distributed throughout the country, with its major center of diversity in Coquimbo and Valparaiso regions. Plants of this genus have small tunicate bulbs and umbel inflorescence type with 3-12 flowers. The life cycle of *Leucocoryne* is slow and it varies between different species. Usually takes 3-4 years from seed to floral bulb production, which hinders its commercial propagation. Due to its attractiveness and the threat of some of their natural habitats, a Chilean breeding program has been established for the conservation and commercial production, which up to date has patented three *Leucocoryne* cultivars. This research focuses on the development of *in vitro* techniques to support *Leucocoryne* breeding programs because one of the main challenges still pending is to develop and to optimize protocols for mass clonal propagation for future commercialization of new cultivars. Therefore, we are testing different *in vitro* culture systems, media, growth regulators and the response of different types of explants on several *Leucocoryne* genotypes to fulfill such goals. To date, by an adequate disinfection process it has been possible to successfully establish *in vitro Leucocoryne* material and different multiplication rates of the bulbs have been observed.

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PS7

GENE EXPRESSION ANALYSIS OF VOLTAGE DEPENDENT ANION CHANNEL AND ITS RELATION TO COLD ACCLIMATION IN *Eucalyptus nitens*

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Cold is one of the most critical stresses limiting geographical distribution, affecting growth and quality of crops and forest plantations. *Eucalyptus nitens* is an important species in Chile because it has a higher tolerance to low temperatures than *Eucalyptus globulus.* Cold acclimation increases freezing tolerance by involving physical and biochemical changes in the cell, such as induction of the expression of cold responsive (COR) genes, accumulation of osmoprotectant compounds and changes in the physical properties of the membrane. The main objective of this work was to study the relative expression of two voltage-dependent anion channel genes (*VDAC1* and *VDAC2*) related to cold acclimation in *E. nitens* showing differences in freezing damage and survival. These genes participate in the exchange of ions and metabolites between the mitochondria and cytosol, which have been involved in cold tolerance. A cold acclimation assay was established in a chamber, using young plants from four different families (pedigrees) of half-sibs plants (F1-F4) of *E. nitens,* the conditions used were: non-acclimated (NA, 12/20 °C day/night), cold acclimated to non-freezing temperature (CAC, 4/8 °C day/night), acclimated to freezing temperature (CAF, 6/12 °C day/night), and de-acclimated (DA, 6/12 °C day/night). A night frost of -6 °C during DA was applied to determine survival and damage percentage for each family to assess their freezing tolerance. Plant material from leaves of three plants per family at NA and CAF conditions was collected for gene expression analysis. The results of survival and damage indicated that F2 and F1 were the most tolerant and F4 the most sensitive family. Only *VDAC2* was differentially expressed at CAF condition, compared to NA for the F1. This result suggests that *VDAC2* could be involved in the cold acclimation process associated to signaling the response to freezing in *E. nitens*.

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PS8

SOURCE-SINK BALANCE AND ITS IMPACT ON THE PHOTOSYNTHETIC RATE AND TRANSPORT OF SUGARS IN TWO VARIETIES OF *Prunus persica*

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Production yield and fruit qualitydepends onsustained photosynthesisto provide carbohydrates for fruit growth. The objective of this workwas to studythe effect of thinning at sink/source balance, and how this impacts photosynthetic rate and sugar exportation to the fruits. Magique, a mid-season variety that takes 100 days after blooming (DAB) to reach harvest time and Red Pearl, a late-season variety that takes 160 DAB to reach harvest time were used. Photosynthetic rate and fluorescence parameters were analyzed in trees with different thinning levels: unthinned, commercial thinning 34:1 leaves/fruit and total thinning. Leaf samples were taken from different branches and three pools were usedfor chlorophyll and activity measurements of various enzymes related to the phloem load and unload. It was observed an increase in photosynthesis in unthinned trees of both varieties during the second exponential fruit growth phase. The same pattern was observed for the activities of enzymes related to phloem loading and unloading. The significant differences in the photosynthetic rate among the thinning treatments were more pronouncedin the S3phase for the variety Magique. Fluorescence parameters and chlorophyll content didn't show variation among the thinning treatments on both varieties. The results showed that the sugar demand of fruits (sink) harbored by the tree control photosynthetic rate and sugar export by the leaves (source), it seems that in mid-season varieties the sink strength affect more the source activity than in late season varieties that possess more time to reach maturity.

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PS9

In vitro ESTABLISHMENT OF ANTARCTIC *Juncus bufonius* L.

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Juncus bufonius L. var. *bufonius* (Juncaceae) is a cosmopolitan species that has shown a wide flexibility of adaptation to different environments. Recently, it has been found in the maritime Antarctic sharing niche with the only two native vascular plants of the region. The conservation and controlled multiplication of individuals from Antarctica are necessary for current and future research on their arrival and ability to adapt to this extreme environment. *In vitro* conservation is an efficient method because it prevents contamination and it can control the tissue growth according to the needs. This work describes two protocols for disinfection and *in vitro* establishment of plant material collected from Antarctica, which is propagated under controlled conditions in the laboratory. For both protocols, the plant material was previously washed with water and commercial detergent to remove all soil traces. For treatment 1 (T1) a disinfection with antifungal solution (1.5 g L^{-1} Hongos and 0.5 g L^{-1} Dithane) was applied, and then with commercial bleach (NaOCl 7%), post-disinfecting explants were placed on MS medium containing salts and vitamin, 3% sucrose, 0.5 mg L^{-1}or 1 mg L^{-1} BAP and 0.145 g L^{-1} Vitrofural, pH 5.8. For treatment 2 (T2) after washing, disinfection was performed with commercial bleach and then with 5% v/v PPM, the explants were placed on the same medium but Vitrofural was replaced by 0.2% PPM. The evaluated parameters were contamination rate and tissue necrosis. Seedlings in T1 showed 0% contamination but up to 78% of necrotic tissues. In contrast, in T2 contamination was 0% and necrosis reached only 10%. Based on these results, nowadays, we are evaluating hormonal combinations for efficient micro-propagation as well as for *in vitro* conservation.

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PS10

GENETIC VARIATION AND POPULATION STRUCTURE IN QUINOA (*Chenopodium quinoa* Willd.) USING MICROSATELLITE MARKERS

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Quinoa (*Chenopodium quinoa* Willd.) is an important seed crop originated in the Andean region of South America andit is a primary protein source for many of the indigenous inhabitants of this area. Its nutritional properties are exceptional because of perfect balance among lipids, carbohydrates and amino acids. The genetic variability of quinoa allows adapting to different ecological environments (salinity, drought, frost andhigh temperatures) and also can display tolerance to biotic and abiotic stress. Due to its potential, Quinoa breeding programsare being carried out in Chile and other South American countries. The objective of this work is to characterize the genetic diversity and population structure of the Quinoa germplasm bank of the breeding program at INIA Intihuasi. Twenty-one microsatellites from public database were assessed for genotyping 96 accessions of quinoa using capillary electrophoresis. The genotypic information will be used to determine the genetic diversity through UPGMA cluster analysis and two-dimensional PCA analysis using Xlstat, which will be displayed on phylogenetic dendrogram. Furthermore, population structure will be determined using Structure v2.3 software. This information will be the first stage to characterize the germplasm bank in order to determine diversity in the breeding program and to select accessions as inbred linesto finallygenerate new commercial cultivars.

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PS11

IMPROVING B-CAROTENE CONTENT IN FRUITS: OVEREXPRESSION OF A CAROTENOID MINI PATHWAY IN TOMATO

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Carotenoids are colored pigments synthesized in plants, algae, yeast and bacteria. Most of them possess high antioxidant properties, which can retard aging and prevent some diseases such as cancer. Moreover, β-carotene, the main carotenoid of carrots, is precursor for vitamin A. Animalsare unable tosynthesizethese pigments, therefore these compounds must be incorporated in the diet. During this decade, metabolic engineering of the carotenoid pathway has successfully enhanced the carotenoid content in crops. Actually, it is a well-defined strategy to develop carotenoids enriched functional foods. In this study, key genes of the carotenoid pathway phytoene synthase (*Psy)* and lycopene cyclase (*Lcyb)* from plants, and carotene desaturase (*crtI)* from yeast*,* were cloned under a fruit specific promoter in an own binary vector. Combinations of the carotenoid genes were expressed in tomato (*Solanum lycopersicum*) cv.microtom, and the effects on carotenoid production were revealed. Optimization of tomato transformation yields a 25% efficiency of *calli* generation, from which 35 lines of transgenic plants were obtained. Molecular analyses for the gene expression and carotenoid quantification by HPLC were performed in tomato lines. Transgenic fruits expressing *Psy* showed a significant 25% of increment in total carotenoids and lycopene respect to wild type. Plants expressing the carotenoid mini pathway (*Psy, crtI* and *Lcyb*) produced an accelerated development in plants and fruits, and the generation of orange tomatoes, which was also noticed by a 3-fold increment in β-carotene in the fruit mesocarp. These results indicate that the presence of the mini pathway is required to redirect the production of lycopene to β-carotene in tomato. Moreover, the effectiveness of these results let us to propose that these carotenoid genes can be used to improve carotenoids and β-carotene content in commercial valuable fruits. Currently, transformation of apples with these genes is on course.

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PS12

BREEDING OF *Vitis vinifera* VARIETIES TO INTROGRESS RESISTANCE AGAINST *Botrytis cinerea* OR *Erysiphe necator*, AND MOLECULAR CHARACTERIZATION OF THEIR DEFENSE RESPONSE

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Biotic stress is one of the major adverse conditions to which a plant is exposed during its life cycle. Pathogenic microorganisms are the principal biotic factors, which can be classified as necrotrophicsif they obtain nutrients from dead tissue, biotrophics if they feed on nutrients obtained from living tissue and hemibiotrophics if they develop a biotrophic phase and a final necrotrophic phase. The grapevine (*Vitis vinifera* L.) is highly susceptible to the necrotrophic fungus *Botrytis cinerea* and the biotrophic fungus *Erysiphe necator*. Due to its agronomic importance is essential to introgress resistant traits in grapevines against these pathogens and to understand how they respond to the infection. The aim of this work is to generate and evaluate *V. vinifera* plants with greater resistance to *B. cinerea* or *E. necator* by traditional breeding and to characterize molecularly the defense responses against these pathogens. For doing this, experimental crosses using plants with greater level of resistance but less commercial interest were made and thus varieties with lower susceptibility to infection by *B. cinerea* or *E. necator* were selected by phenotypic analysis. We are currently evaluating the resistance of selected plants through biochemical or histological strategies. Later, most resistant lines will be characterized at molecular level to analyze the type of the defense strategy against each pathogen. This work will contribute to the study of plant-pathogen interactions in no model but agronomically important crops.

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PS13

Alstroemeria FRAGRANT X NON FRAGRANT HYBRIDIZATION: INVESTIGATING THE CHARACTER OF SCENT

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The *Alstroemeria* genus is native to South America with Chile and Brazil as the main diversity centers. These species have been very attractive for breeders as an ornamental crop. Interspecific hybridization has been the most common technique used as breeding method because of the high level of variability obtained. *Alstroemeria* breeding programs have been focused on many different characters, although the scent has not been well developed. In this study, 5 fragrant and 8 non-fragrant *Alstroemeria* genotypes from the Breeding program at Cornell University were cross pollinated during two seasons. Embryo rescue was performed at 14 days after pollination and embryos were cultured under dark conditions in petri dishes on ¼ MS medium supplemented with 7 $g \cdot L^{-1}$ agar and 30 $g \cdot L^{-1}$ sucrose. Oneto 3 months after germination embryos were transferred to test tubes using MS medium supplemented with 7 $g \cdot L^{-1}$ agar and 30 $g \cdot L^{-1}$ sucrose, and kept under a 16/8 photoperiod. After 4 to 6 weeks seedlings were transferred to fresh test tubes using the same medium previously described supplemented with 2 mg L^{-1} de BAP. For inducing roots, seedlings were transferred to the same MS medium supplemented with 1 mg L^{-1} de IBA. Finally seedlings were transferred to pots using peat moss and perlite (1:1) andacclimated to greenhouse conditions. The first season (2013) 20 cross pollinations were performed and 142 embryos were rescued from which 20 plants have been already acclimated. These new hybrids are starting to flower. During the second season (2014) 23 cross pollinations were performed and 280 embryos were rescued from which 182 have germinated. The new seedlings obtained will be phenotyped and a transcriptomic analysis will be performed in order to discover candidate genes involved in the biosynthesis of volatile compounds in *Alstroemeria*.

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PS14

CHEMICAL MUTAGENESIS OF *Pasithea coerulea* USING ETHYL METHANE-SULFONATE (EMS): DETERMINATION OF DOSAGE FOR AN APPROPIATE SEED GERMINATION

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A high diversity of native and endemic species with a considerable ornamental value are observed in Chile. *Pasithea coerulea* (Azulillo) is a geophyte native to Chile distributed from Antofagasta to Valdivia. This species shows six tepals of blue colour, which is highly appreciated in the ornamental market. *Pasithea coerulea* belongs to a monotypic genus therefore the using of mutagenesis as breeding technique is a suitable method to induce variability in this species. In this study seeds of *Pasithea coerulea* were collected and submitted to a pre germinative treatment consisting of rinsing under water for 72 h and stratification, for three weeks at 4°C. Seeds were disinfected with NaOCl (2.5%) for 20 min and then rinsed in sterile water. In order to evaluate the effect of ethyl methanesulfonate (EMS) the treated seeds were exposed for 24 h to seven concentrations of EMS: (T_1) 0.05; (T_2) 0.1; (T_3) 0.15; (T_4) 0.2; (T_5) 0.25; (T_6) 0.3 y (T_7) 0.35% (v/v), plus a control (T0). After this treatment the seeds were rinsed six times with water and sown in Petri dishes with MS medium under a dark conditions and 21 °C. Three replicates per treatment and seven seeds per replicate were performed. After six weeks, T2 and T3 were significantly different to the rest of the treatments, showing the best results of germination (76.2 y 66.7% respectively). The higher results in T2 and T3 compared to the control (57.1%) could be explained because of a scarification effect caused by the EMS in low concentrations. As expected, the lowest germination (19%) was found with the highest concentration of EMS (T_7). Observation of plumule was also evaluated and T2 showed the highest result (47.6%). This study is undergoing and further analysis will include calculation of the optimum dosage of EMS and phenotyping of the mutant seedlings.

PS15

PRELIMINARY STUDY OF DROUGHT STRESS IN *Vaccinium corymbosum* L. (ERICACEAE)

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In many cultivated species, one of the most important factors limiting production is water deficiency. Nonetheless, plants exhibit a variety of strategies to reduce or avoid desiccation, such as osmolyte accumulation, stomatal closure and reduced photosynthetic activity, among others, which in themselves reflect changes in gene expression. Blueberry is a fruit with high antioxidant capacity that is widely cultivated in Chile mostly for export. So far, most stress research in this species has focused on cold acclimation, and little information exists on physiological and molecular responses to drought stress. In order to evaluate the responses of blueberry under severe drought stress conditions, a rapid water shock assay was performed with the cultivar Elliott. Leaf tissue was sampled at different time points and the leaf relative water content, proline level and malondialdehyde content were determined. In parallel, using the database for the cold acclimation transcriptome, drought stress response genes were identified and primers designed, which were used to evaluate expression profiles by qPCR. The results showed that water relative content was decreased while proline and malondialdehyde content was increased in stressing conditions. Moreover, the qPCR results evidence induction of genes involved in drought stress response (dehydrine coding genes and transcription factors such as COR11). The experimental approach presented here illustrates an effective strategy to search for variants of candidate genes involved in water stress response and their potential exploitation in breeding programs.

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PS16

IDENTIFICATION OF CYTOKININ BIOSYNTHETIC PATHWAY GENES EXPRESSED DURING FRUIT DEVELOPMENT IN *Prunus persica*

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Fruits are an important part of a well balance diet, providing benefits not only in basic nutrition, but also improving overall human health and well-being. A better understanding of the mechanisms by which fruits grow and develop, may provide information associated with desirable commercial characteristics such as fruit size, flesh firmness, stone lignification, sugar content and anthocyanin production. Fruit size has been attributed to two factors: the increase in the number of cells (cell division) and the increase in the size of the cells (cell expansion) during fruit development. It has been demonstrated that phytohormones such as auxins and cytokinins may play a key role during these processes. However, the molecular mechanisms by which these hormones are acting on the fruits are poorly understood. RNA-seq analyses have enabled us to identify specific cytokinin biosynthetic pathway genes that are differentially expressed during peach fruit development. Many of these genes are members of large gene families, such as families Hybrid histine kinase (*AHK*), HPt protein (*AHP*) and Response regulators (*ARR*). The expression analyses of these gene family members reveal that not all members are expressed in a similar manner. These analyses are enabling us to identify gene family members of the cytokinin biosynthetic pathway that may be playing a role in cytokinin synthesis and cytokinin action on peach fruit development.

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PS17

REGULATORS OF VEGETATIVE PHASE CHANGE IN TWO GENOTYPES OF *Prunus*.

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Plants experience several changes during their life cycle. In trees, the period of juvenility can last several decades. The juvenile to adult vegetative phase change is marked by an increase in reproductive potential. It is during the adult phase when the flower induction begins. In model plants, the molecular mechanism of vegetative phase change involves the microRNAs 156 and 172 families and their targets SQUAMOSA PROMOTER BINDING PROTEIN LIKE genes (SPL) and a set of APETALA 2 LIKE genes (AP2), respectively. This work shows the expression profile of microRNAs 156 and 172 and their target genes in leaves of two genotypes of *Prunus* sp. with contrasting periods of juvenility: the precocious flowering genotype 'Garnem' (*P. amygdalus* (L.) Batsch x *P. persica*) and the late flowering genotype 'Colt' (*P. avium* x *P. pseudocerasus* Lindl.) during three growing seasons. The major differences were found at the third growing season, where the plants of 'Garnem' genotype flowered while the plants of 'Colt' genotype remained in juvenile phase. Our results suggest that the aging gene pathway seem to be conserved in *Prunus sp*. and could play a key role in vegetative and reproductive phase change transitions.

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PS18

IDENTIFICATION OF MICROSATELLITE LOCI IN MAQUI (*Aristotelia chilensis*) USING NEXT-GENERATION SEQUENCING (NGS).

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Maqui (*Aristotelia chilensis*) is a native evergreen tree from Chile. Their height varies among 3 to 4 m, growing from the Coquimbo Region to the Aysén Region, at altitudes up to 2500 meters oversea level. The fruit is a shiny black berry, 3-5 mm diameter, which is used as food and dyer. Maqui fruit has analgesic, anti-inflammatory and antioxidant properties. Maqui fruit is characterized by a higher antioxidant activity due to their high anthocyanin and phenol contents. The objective of this work is to develop microsatellite or simple sequence repeat (SSR) markers from genome shotgun sequencing of maqui. We have generated and characterized a total of 165,043 genome shotgun sequences with the average read length of 387 bases covering 64 Mb of the maqui genome using 454 sequencing technology. Assembly of the obtained nucleotide sequence reads was performed using the GS De Novo Assembler (v 2.9) software. Redundant reads were reduced to 43,660 contigs with the average contig length of 1075 bases. The average GC content of maqui genomic DNA generated in this study is 38.94%. Besides, we identified SSR motifs that could be used as potential molecular markers. In this work, we provided evidence of generating levels of diverse microsatellite markers and gene content from high throughput next generation sequencing of the maqui genomic DNA. The markers could be used in germplasm analysis, accessing genetic diversityand linkage mapping of maqui.

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PS19

THE EFFECT OF THINNING IN SUGAR COMPOSITION OF A MID-SEASON NECTARIN VARIETY (CV MAGIQUE)

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Fruit quality in peaches and nectarines is composed of a number of traits such as acidity, size and sweetness. The last two are mainly managed by agronomical practices such as thinning, which consist in lowering the fruit load to strengthen the sink/source ratio. In this work trees from the mid-seasonnectarine Magique were managed with differential thinning treatments: unthinned, 20:1 (leaves:fruit), 40:1, and 60:1. Fruits at two developmental stages, stone hardening and harvest maturity were sampled from one branch and made into a sample pool, for stone hardening and independent fruits for harvest maturity the ripening parameter was firmness close to 10 pounds. Metabolite extraction was performed from freeze-dried tissue using miliQ water as a solvent. Neutral sugars were analyzed by HPAE-PAD (High Performance Anion Exchange - Pulsed Amperometry Detection). The results showed a significant increase in sucrose content in fruits at stone hardening stage as the intensity of thinning increase. At this stagefruit metabolic machinery shifts to lignin synthesis, however in individuals that suffered intensive thinning the high leaves:fruit proportion can sustain the concomitant accumulation of sucrose. At harvest maturity stage fruits of all treatments presented a boost in their sucrose levels. This increase was less pronounced in fruits from the unthinned trees. The sucrose accumulated in this stage probably is hydrolyzed in glucose and fructose during ripening. Therefore, we can conclude that thinning intensity not only affects fruit size, but also alter fruit sugar composition of this variety, causing a positive impact in the fruit, at least in the sugars that most contribute to quality.

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PS20

POSSIBLE ROLE OF AUXIN DURING DEVELOPMENT AND RIPENING OF RASPBERRY FRUIT (*Rubus idaeus*) cv HERITAGE.

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Auxin plays an important key role in development of berry fruit. However, little is known about the indol-3-acetic acid (IAA) production, transport and regulation by conjugation of this hormone during development and ripening of raspberry. In particular, the indole-3-acetic acid-amido synthetase has been reported as key enzyme involved on regulation of auxin homeostasis by conjugation to amino acid such as aspartic acid and tryptophan. To understand the role of this hormone during berry development and ripening, IAA content and related transcripts were evaluated. Therefore, half-ripe fruits showed higher levels of IAA content. In addition, a RNA-Seq approach showed a total of 2,409 transcripts identified as differentially expressed, including transcripts related to auxin. In particular, we found six transcripts related to auxin transporter, one of them showed high expression levels on development stages and other in the ripe stage of raspberry fruit. In a similar way, we found two putative auxin response factors in *R. idaeus*: *RiARF1-like* and *RiARF19-like* with different expression pattern during ripening; observing major levels of *RiARF19-like* during development. Interestingly, we reported other three putative transcripts in *R. idaeus* codifying Indole-3-Acetic acid-amido synthetase, one *RiGH3.1* and two *RiGH3.5* with different expression patterns. These results suggest an important role of auxin during development and ripening of raspberry. Further studies are ongoing to elucidate the role of auxin on development and ripening of this fruit and the mechanisms involved on regulation of auxin response by conjugation.

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PS21

IDENTIFICATION AND CHARACTERIZATION OF PHYTOHORMONE-REGULATED GENES DURING FRUIT RIPENING OF *Fragaria chiloensis*.

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Fragaria chiloensis is a non-climateric fruit. The fruit of this Chilean species has a characteristic white-pinkish color, an intense aroma and is particularly sweet. The ripening of non-climacteric fruits is under the control of phytohormones like abscisic acid (ABA) and auxin. During fruit development, ABA levels gradually increase while auxin levels decrease. Given the economic potential of the Chilean strawberry, studying the ripening process of this endemic fruit and its regulation is a potentially powerful tool for the development of biotechnological strategies. The impact of hormonal regulation on fruit development is one of the focuses of our research. We have taken information from suppression subtractive hybridization (SSH) libraries, developed and published by Pimentel et al (2010), where the progression of fruit development was classified in: C1, small green fruit; C2, large green fruit; C3, turning stage; and C4, ripe fruit. Of the differentially expressed genes during fruit development, we selected three genes: 1, the ABA receptor encoded by *FcLANC-LIKE*2, which has highest levels in C2 and C3; 2, a gene from the family of the *FcSAUR* genes, with highest levels in C3 and C4; and 3, a gene codifying an Auxin Repressed Protein (*FcARP*), which has highest levels in C1 and C2. To evaluate whether these genes are regulated by phytohormones, fruits were treated with ABA or auxin. We found that *FcLANC-LIKE*2 has an early response to ABA and auxin treatments, *FcARP* has an early response to auxin, but not to ABA, while *FcSAUR* responds differentially to the two hormones, showing an early response to auxin, and a late response to ABA. Overall the results suggest that the three genes could be regulated by phytohormones such as ABA and auxin.

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PS22

RNA-SEQ BASED *in silico* ANALYSIS: *S. lycopersicum* AND *S. peruvianum* RESPONSE UNDER WATER STRESS CONDITIONS

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Tomatoes are the most cultivatedvegetables in the world with an important economic value. This crop is very sensitive to water deficit affecting severely its productivity and fruit size. Differing from the cultivated tomatoes certain wild species such as *Solanumchilense* y *S. peruvianum* possess certain traits that allow them to tolerate a severe water deficit. Thus, both species have a high genetic variability, which simultaneously is related to different character combination associated to biotic and abiotic stress tolerance that allow them to adapt to a specific micro-habitat. In order to understand the genetic factors that control the adaptive mechanism activation found in these wild species, bothtranscriptomes have been analysed under contrasting conditions of water availability. Therefore, in this research we present the analysis process of 32 RNA-seq libraries, pre-processed with a Truseq Kit and sequenced through paired-endsIlumina Hi-Seq2000 platform. Such libraries consisted of two biological repeats for control treatments, PEG 5% and PEG12% in the MoneyMaker genotypes (*S. lycopersicum*) and SP395 (*S. peruvianum*). The bioinformatic analysis consisted in a pre-process ofdata through Fastx-toolkit and FastQC softwares for adaptors elimination, quality filtering and visualization. Tophat software was used for reads alignment to the reference genome, while assembling was done with Cufflinks tool. Finally, the gene expression results were obtained through statistic packages Cuffdiff and edgeR. The results are discussed in function of methodology used for analyse them and obtain optimal assembling, gene ontology assignment and gene expression values during drought stress and between the species *S. lycopersicum and S. peruvianum*.

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PS23

ELUCIDATING MOLECULAR INTERACTIONS AND DNA-BINDING SITES IN *Arabidopsis* NAC042 TRANSCRIPTION FACTOR

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In plants, the survival to exposure to different kind of biotic and abiotic stresses such as insects, drought, high salinity, and low temperature involve hormonal, metabolic, and physiological process mainly mediated by transcription factors (TF) to regulate gene expression. The NAC (NAM/ATAF/CUC) proteins constitute one of the largest families of plant-specific TF and have an important role in plant development related to nutrient distribution and stresses responses making them relevant in the context of crop optimization. However, knowledge on the DNA-binding properties of this family is limited. In this sense, the aim of this study is to generate deep understanding of the binding mode between NAC042 (a NAC TF) and 18 DNA *cis*-elements containing a TGCCGT core sequence, by means of *in-silico* approach. In the present report, the tridimensional structure model of NAC042 homo-dimer was built by homology modeling. The model revealed a β–fold structure where two intermolecular salt-bridges were found between R23 and E30, which plays a key role in the formation of the dimer. Subsequently docking, molecular dynamic simulations and MM-GBSA methods were employed in order to obtain a numerical correlation with the experimental evidence of the relative binding affinity (RBA) between NAC042 and DNA-sequences. Moreover, an analysis of the intermolecular interactions allowed the identification of key residues inserting into the mayor groove of DNA that govern the affinity and specific recognition of DNA-bases at the molecular level.

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PS24

FUNGI BIODIVERSITY IN THE RIZOSPHERE OF A HYDROPHILIC FOREST IN CHILE ASSESSED BY MOLECULAR MARKERS

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Chilean native forests hold a huge potential for social, cultural and economic development. Molecular techniques to analyze soil samples have opened the possibility to study in more detail microbial communities. Genetic diversity studies based on CAPS markers from known genes or non-codifying regions are advantageous since they can focus the study on specific microorganisms within the community. It has also been demonstrated that microbial communities play a key role in the development of plant communities. This study was aimed to estimate fungi genetic diversity in soil where different tree species are established. Fungi DNA was obtained from the rizhosphere of five native species: *Myrceugenia exsucca* (Pitra), *Blepharocalyx cruckshanksii* (Temu), *Luma chequen* (Chequen), *Drimys winteri* (Canelo), *Crinodendro patagua* (Patagua) inhabiting in an unprotected native forest in the O`Higgins Region (33º 51' and 35º 01' S; 70º 02' W). Rizospheric samples from soils planted with corn and soybean near the forest patch were also analyzed. CAPS makers showed high degree of molecular polymorphism indicanting a high fungi biodiversity at rizosphere level of all the species. *D. winteri* holds the highest molecular polymorphism (85%), which contrasted with the cultivated soils samples that only reached 40% of molecular polymorphism. Molecular Variance Analysis (AMOVA), based on CAPS polymorphisms, showed a medium degree of biodiversity differentiation among different tree species in the forest stand. Principal Components Analysis (PCA) showed that fungi biodiversity is widely distributed all over the different native species in the forest, but is significant different to cultivated soils near the forest stand, indicating that the agricultural activities can reduce the amount of rizospheric fungi. These results support the use of CAPS molecular markers as biosensors to detect soil microbiological quality. Also they can generate useful information to be applied in projects for ecological restoration and reforestation of degraded native forest.

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PS25

SYNTHESIS OF EXPANSIN PROTEINS AND COMPARISON WITH PUTATIVE EXPANSINS EXTRACTED FROM WHEAT TISSUES

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Expansins proteins are key regulators of plant cell wall extension during the growth of plant organs. They are also involved in several other plant processes such as softening during fruit ripening, pollination, germination and abscission. The objective of this work was to evaluate the synthesis of plant expansins in heterologous systems and its comparison with putative expansins extracted from wheat tissues. An expansin from *Bacillus subtilis* was subcloned into a P22 vector and recombinant DNA was introduced into *Escherichia coli* BL21 host. The presence of the expansin sequence in the expression vector was evaluated by PCR using specific primers. On the other hand, native expansin proteins were extracted from leaves of wheat following the Bradford´s methodology. The assessment of the expansin concentration in transformed *Escherichia coli* colonies and extracted from wheat tissues was performed by SDS-Page. Thereafter, the expression level of the expansin was assessed in the supernatant of the culture medium using polyclonal antibodies and compared with the expression of the native protein from wheat plants. PCR results showed that the expansin sequence was inserted into the plasmid at different ferment volumes (3 and 5L). SDS-PAGE showed that recombinant *E. coli* expressed a single band of 28 kDa as expected, corresponding to the size of the *Bacillus´*s expansin. Polyclonal antibodies raised against the expansin showed different levels of expression in plant extracts (as control) and supernatants of recombinant *E. coli*. Although low levels of expression were detected in the culture supernatants of transformed bacteria, the protein was detected, thus it seem promising the use of this methodology for the synthesis of expansins with potential for plants.

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PS26

SNPS, SSR, ISSR AND PHENOTYPIC EVALUATION OF JAPANESE PLUM (*Prunus salicina* L.) CULTIVARS

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Single Nucleotide Polymorphisms (SNPs), Simple Sequence Repeat (SSR), Inter Simple Sequence (ISSR) and morphological and phenological descriptors were evaluated in order to analyze intraspecific variation of 29 commercially important Japanese plum (*Prunus salicina* L.) cultivars. We analyzed 57 thousands SNPs, 17 SSR loci, 3 EST-SSR related to the flavonoid biosynthetic pathway (structural genes and putative transcription factors). The number of putative alleles revealed by SSR primer pairs ranged from two to eight. Three to six alleles per locus were observed for EST-SSR. The average of heterozygosity was superior to 0.6. We used 11 ISSR primers, which reveled 427 ISSR bands. High level of SNPs diversity was found. We also studied 35 phenotypic characteristics. The cultivars were established in the field following a Randomized Complete Block Design (RCB), with three replications per cultivar. The experimental orchard was established in the Experimental Station of Pontificia Universidad Católica de Chile, located at Pirque, Santiago. ANOVA and multivariate analyses were carried out. An important level of genetic and phenotypic variability was found for three types of molecular markers and 35 phenotypic characteristics among the Japanese plum cultivars.

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PS27

GENETIC AND MORPHOLOGICAL ANALYSIS OF THE ENDANGERED AUSTRAL PAPAYA (*Vasconcellea chilensis* (Planch. ex A. DC.) Solms)

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The Austral papaya is an endangered species that is found growing naturally in Chile only as fragmented populations between Coquimbo and Atacama regions. It is a species that grows under extreme environmental conditions of drought, salinity and temperature. We collected 111 samples of *Vasconcellea chilensis* from three natural populations. We evaluated 86 ISSR bands and five fruit traits (equatorial diameter, longitudinal diameter, soluble solids, number of seeds and fruit weight). The main results suggest a relatively recent fragmentation. This implies that the fragmentation has not yet had its full effect on the genetic variation and it will be urgent to develop conservation strategies to preserve the remaining genetic variation, particularly for the most northern populations, which are not currently protected.

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PS28

STRUCTURAL GENOMIC COMPARISON OF WHOLE GENOMES IN *Prunus persica*: 'VENUS' COMMERCIAL VARIETY AGAINST REFERENCE GENOME

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At present, several whole genome sequences are available for plants of economic importance such as rice, corn, apple, tomato and grape. These reference genomes are key to perform genomic studies and to develop biotechnology tools such as molecular markers. However, these reference genomes contain information of only one genotype. In the case of peach reference genome, 'Lovell' was sequenced because it is a natural double-haploid, nevertheless this genotype is not representative of peach commercial varieties. For this reason, the objective for this work was to compare the whole genome sequence of 'Venus' against the peach reference genome 'Lovell' V1.0. Towards this end, DNA was extracted from leaves of 'Venus' variety, using the DNeasy Plant MiniKit (Quiagen, Germany). A gDNA Illumina library was constructed using the Tru-Seq DNA kit (Illumina, USA) and was sequenced on MiSeq plataform (Illumina Inc). Three paired ended (2z300bp) runs were performed. Reads were filtered using Flexbar scripts and were mapped by Botiew2 against 'Lovell' V1.0. SNP and indels markers were detected using GATK tools to compare 'Venus' with 'Lovell' considering deep sequencing equal or greater than 20 reads. Deletions of 1 kb or more were detected using Perl custom script filtering for deep >50. We have obtained a depth of 93X for 'Venus' and 598.316 SNP and 11.724 Indels were detected. Detected structural variants were characterized (type, frequency/chromosome, position, coding or non-coding region, etc) and were plotting with Circos software. This work is one of the first steps to reveal a comprehensive catalog of structural variants in peach.

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PS29

EFFECTS OF SALINITY ON GERMINATION AND *IN VITRO* MULTIPLICATION IN *Colobanthus quitensis*

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Colobanthus quitensis **(**Kunth) Bartl. (Caryophyllaceae), must withstand saline stress across its distribution, including Antarctica. Mainly because several of its habitats are in moist sites with brackish water, the same for flood tides, through direct waves or constant sea spray due to winds. This may suggest that this species has biochemical, physiological and even morphological mechanisms that could allow tolerate saline stress. In order to investigate these possible mechanisms, in this work, we studied the response to salinity in germination and *in vitro* propagation of *C. quitensis* in presence of four NaCl concentrations (50, 100, 150 and 200 mM). The germination percentage was only affected from the 150 mM NaCl (50,7%), while seedling survival decreased from the 100 mM treatment (20,8%). However, during the propagation of *in vitro* seedlings, despite the appearance of new shoots decreased from 100 mM NaCl; root development was not affected except at 200 mM NaCl. Whereas undesirable symptoms of *in vitro* tissue culture, such as occurrence of reproductive tissues and chlorosis, were observed at 100 and 200 mM NaCl, respectively. This first approach to salinity tolerance in *C. quitensis* would allow to preliminarily considering it as a moderately tolerant species.

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PS30

DAILY TIME-COURSE OF EXPANSINS EXPRESSION IN FLOWERS AND GROWING KERNEL OF SUNFLOWER

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Taking into account that the ovary of flowers develop into the pericarp of grains in grasses and dicots such as sunflower, it has been proposed that the pericarp imposes a physical restriction to growing kernels. The physiological processes through which the pericarp controls kernel weight (KW) are only starting to be understood. Expansins are proteins that play a key role in plant growth by inducing the loosening of cell walls, which determines cellular growth rate. Recently, it has been reported the association between length, water content and expansin expression dynamics in growing kernels of wheat, but the expression of expansins in carpels, pericarp and embryo of dicots is unknown. Moreover, the dynamic of expansin expression through the day is key to accurately evaluate the expansin dynamic of growing kernels, and has not been assessed. The objective of this research was to evaluate the daily time-course of expansin expression in flowers and growing kernels of sunflower. Two sunflower hybrids adapted to the South of Chile were sown in a Completely Randomized Block Design with three replicates at the “Estación Experimental Agropecuaria Austral” of the Universidad Austral de Chile in Valdivia. For daily dynamics the samples were taken 6 times within 24hs at R3 (flowers) and R5.5 (kernels) developmental stages. RNA was extracted from sampled ovaries, pericarp and embryo of plants. Strand cDNA was synthesized by reverse transcription and six novel expansin sequences were found by PCR.

The analysis of results showed different expression of expansins across the day at both phenological stages, i.e. R3 and R5.5. In R3 (flowers) an increase of expansin expression was recorded from 8 am to 4 pm. In R5.5 the expression was also variable through the day in both pericap and embryo tissues.

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PS31

CALLUS INDUCTION IN *Deschampsia antarctica* DESV.

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Deschampsia antarctica Desv. (Poaceae) is known for being the only native grass that has colonized Antarctica maritime. Because of their ability to survive in abiotic extreme conditions such as high UV radiation, salt stress, drought stress, and low temperature, it has become a very interesting species in the search for genes that confer tolerance to abiotic stress, as well as in the production of secondary metabolites, such as antioxidants, which have become increasingly important in the pharmaceutical, food and cosmetic industries. Callogenesis is a type of plant tissue culture, which consists of inducing callus formation (an undifferentiated cell mass) in a differentiated tissue, through growth regulators addition to the culture medium. In this study we have established a protocol to induce callus formation in *D. antarctica*, since these callus can be used both as massive micropropagation method and a biotechnological tool to obtain greater concentration of secondary metabolites, and in studies of genetic variability. For this purpose, four concentrations of 2,4-dichlorophenoxyacetic acid (2,4-D), a synthetic auxin promoting cell division (0.5 mg L^{-1}, 1.0 mg L -1, 2.0 mg L-1 and 3.0 mg L^{-1}) and a control treatment containing 6-benzylaminopurine (BAP) instead of 2,4-D were assessed. The parameters evaluated were: callus color and friability, number of dedifferentiated callus, and organogenic capacity. Also, a morphological analysis was carried out using plantlets obtained from callus. The concentrations of 0.5 mg L^{-1} of 2,4D were the optimal concentration for inducing callus in *D. Antarctica,* because it exhibited the highest number of friable callus and highest callus with more organogenic capacity.

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PS32

SHORT-TERM ASSESSMENT OF Mn TOLERANCE OF RYEGRASS CULTIVARS UNDER ACIDIC CONDITIONS.

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In south-central Chile, the main forage species is perennial ryegrass (*Lolium perenne* L.), which is mainly cultivated in ash-derived soils like Andisols. One of the major problems for plant growth in these soils is the high acidity (pH≤5) that release toxic aluminum (Al) and toxic manganese (Mn). Although Mn is an essential micronutrient for plants, in acid conditions an excess of available Mn^{2+} is generated, which is toxic for plants. Thus, an excess of Mn^{2+} is an important limiting factor for crop production. We studied the response of ryegrass cultivars recently introduced in south-central Chile (One-50, Halo, Banquet and Nui) to increasing concentrations of Mn (control 2.4 µM Mn until 750 µM Mn) in a Taylor-Foy nutrient solution at pH=4.8 by four days, to determine their tolerance or sensitivity to Mn (supplied as $MnCl_2$). As indicators of Mn-tolerance or sensitivity, relative growth rate (RGR) of shoots and roots and relative chlorophyll (Chl) in shoots were used. Additionally, antioxidant activity (AA) by DPPH method was determined. At the highest Mn treatment, greater reductions in RGR were exhibited in roots than shoots in all cultivars respect to control. One-50, Halo and Nui had ~50-60% root reduction, whereas Banquet showed the lowest RGR of roots. In shoots RGR of Nui had the highest reduction (35%). Contrarily, Banquet did not exhibited changes either in RGR or relative chlorophyll in shoots. Nonetheless, this cultivar increased gradually its AA reaching the biggest values at the highest Mn treatment. The results suggest that according the evaluated parameters and conditions used in this study, ryegrass cultivar Banquet was the most tolerant to Mn excess.

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PS33

IDENTIFICATION OF THE GENE RESPONSIBLE FOR THE SLOW RIPENING TRAIT IN *Prunus persica*

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Fruit ripening is a highly coordinated and genetically programmed event characterized by physiological and biochemical changes. Fruit softening is one of the most important phenomena that determine quality and postharvest performance. In peach, slow ripening (*sr*) individuals have been identified, which are a good model to fruit ripening studies. These individuals show slow rates of ethylene production and flesh softening tends to zero. The aim of this work is to characterize the slow ripening phenotype and to identify the major gene(s) associated with it. Twenty five percent of the ´Venus` x ´Venus' progeny showed the slow ripening trait, which was mapped on LG4 as a morphological marker. Harvest and postharvest characterization for slow and normal ripening siblings were carried out and we observed that the flesh firmness in slow ripening siblings did not change significantly during cold storage and the shelf life period. The estimated cell size and cell number in fruit flesh samples were lower in slow ripening fruits compared to melting fruits. Our results show a deletion of 26 Kb in the genomic region associated to the slow ripening phenotype. PCR and whole sequencing confirmed the structural variant on the slow ripening siblings. Two genes were identified in this region of which one is related to ripening (NAC transcription factor). Nuclear sub-cellular localization of the NAC protein was established by confocal microscopy. This work suggests that a NAC transcription factor plays an essential role in the fruit ripening signaling pathway and the slow ripening phenotype is due to a deletion of the gene.

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PS34

EFFECT OF DEFICIT IRRIGATION THE PHYSIOLOGICAL PERFORMANCE OF FOUR GENOTYPES OF QUINOA UNDER FIELD CONDITIONS

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Water availability is one of the principal limiting resources for cropproductivity worldwide. Quinoa (*Chenopodium quinoa*) is a grain staple with a high nutritional value and high drought resilience, which constitutes a great alternative to contribute to food security. Four genotypes (R49, PRJ, PRP, and UdeC9) provenancesfrom differentChilean climatic conditions were grown in a randomized complete block design. Plants were restricted to 50% (50%DI) and 25% (75%DI) respect their optimal irrigation. Physiological traits related withspecific leaf area (SLA), net photosynthesis (A_{max}), relative water content (RWC) and Chlorophyll amount were assessed after flowering onset (2 weeks). All genotypes presented similar RWC under control conditions; however, under both DI treatments PRJ and PRPgenotypes were able to maintain RWC, which was related witha strong reduction in individual area that not affected significantly SLA. R49 showed lower plasticity, respect the other genotypes and showed higherA_{max} reduction during both DI treatments. These results were correlated toa higherincrement of temperature and stronger decrease of *gs* under drought.On the other hand, DIdid not affectpanicles nitrogen content in any of the genotypes. Nevertheless, initial results of glutamine synthase inmunoblotsshowed an enzyme incrementon UDEC9 and R49 with drought treatment, which could have a role controlling ammonium toxicity produced by drought. These results will be linked togene expression analysis, currently in progress. Altogether, genotypic responses indicated differential tolerance mechanisms to cope with water deficit among the Chilean quinoa genotypes.

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PS35

PARTICIPATION OF TRANSCRIPTION FACTOR BZIP17 IN RESPONSE TO ABIOTIC STRESS IN *Arabidopsis thaliana.*

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Plants are exposed to the action of biotic an abiotic stress, which affect plant growth, limiting production of economically important species. Of these factors, drought and salinity represent a serious agricultural problem especially related to climate change in our planet. AtbZIP17 is an endoplasmic reticulum bound transcription factor implicated in the response to salt stress and in the unfolded protein response in *Arabidopsis thaliana*. Nevertheless, its role in abiotic stress is not completely clear. Recently, some authors have shown that AtbZIP17 regulates the expression of genes associated to salt and drought stress such as NAM-LIKE, ATHB7, PP2C-LIKE, RD20 and RD29A. In order to get insights about the role of AtbZIP17 under abiotic stress, we analyzed by means of RT-qPCR, if this transcription factor acts by regulating the expression of several genes involved in the plant response to abiotic stress like *PP2C, bHLH96, ABI3* and *RD29B* during salt and osmotic stress conditions. Our results showed that the expression of these genes is altered in *bzip17* line compared to the wild type plants under salt and mannitol treatment. Moreover, physiological experiments in this line showed that different concentrations of mannitol treatments produced changes in root length as well as in the germination rate but NaCl treatments didn't have any effect in plant growth. These results suggest that AtbZIP17 participate in the network that regulates the response to salt and osmotic stress although an independent regulation of both responses is observed at physiological level.

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PS36

OCCURRENCE AND GENETIC DISTANCE OF *TOMATO RINGSPOT VIRUS* (ToRSV) IN *Rubus idaeus* FROM THE MAULE REGION ORCHARDS, CHILE.

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Rubus idaeus is one of agronomic and commercially important species that outstands in Maule Region, because concentrates 57% of the whole country's surface. Its production is mainly exported. In Chile, *Rubus idaeus* is propagated by etiolated buds, which facilitates the spreading of diseases and potentially decreases productivity as well as the quality of the fruits. In this study, presence of *Tomato Ringspot Virus* (ToRSV) and the genetic distance of the virus from different varieties of *Rubus idaeus* collected in the Maule Region were determined. The Results indicates that Chilliwack, Amity and Heritage varieties presented high incidences of ToRSV at percentages about 71%, 83.6% and 43% respectively, while Coho variety, showed a viral incidence of 37%. The varieties first group, were collected at Linares Province, while the second was at Curicó Province. The viral sequence analysis, indicated that 89% to 98% of its sequence was similar to partial sequences of ToRSV found in Rubus *idaeus* and *Vaccinum* sp deposited in GenBank. The observed genetic distance indicates that there are three different clusters. The first cluster includes the sequences ToRSV, isolated in the Linares Province with the AF135410, AF135409, L9655 and AF135408 (Genbank accessions). The second cluster is composed by virus sequences detected, in orchards of Linares and San Clemente. While, the third cluster include the viral sequences located from Linares, San Clemente, Parral, Molina with accessions GQ141525, GQ141527, GQ141528 (from *Vaccinum* sp) and DQ641947 (from *Rubus idaeus*). Our results suggest a need to test routinely in *Rubus idaeus* orchards, since there is an increase of the virus in Maule Region from past studies. Furthermore, sequence analysis of ToRSV indicated that exist differences in some isolated found in Chile, with other ToRSV of the world.

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PS37

MOLECULAR MODELING AND STRUCTURAL ANALYSIS OF AQUAPORINS NIP SUBFAMILY OF *Prunus* ROOTSTOCKS UNDER HYPOXIA STRESS

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Aquaporins are structural membrane proteins that have been characterized as carriers of water and/or solutes being involved in plant responses to abiotic stresses. NIPs (Nodulin 26-like intrinsic proteins) represent a large, 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 varied sizes depending of residues composition of the ar/R filter. In this work, we have characterized structurally 7 NIPs that were identified in the re-sequenced genomes of two *Prunus* rootstocks with contrasting responses to hypoxia stress. Computational methods were used to construct structural models based on comparative modeling of the putative pore regions of 3 NIPs with contrasting responses to hypoxia stress between both genotypes evaluated by qPCR analyses. Ar/R regions were analyzed and compared with AtNIP2;1 as a model, an anaerobic-induced gene that encodes a lactic acid transporter and may play a role in adaptation under anaerobic stress. Upon homology modeling and structural comparison we could see that the residues surrounding the pores remained conserved across the subgroups. The aromatic/arginine (ar/R) constriction is most important for solute selection, but the exact pore requirements for efficient conduction of small solutes remain difficult to predict. The purpose of this study was to investigate by molecular simulations, which are potential substrates of these selected aquaporin NIPs, and identify structural differences between genotypes studied.

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PS38

ROOT PHENOTYPING OF CHILEAN ACCESSIONS OF QUINOA

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Quinoa (*Chenopodium quinoa* Willd.) is a crop cultivated for centuries in the Andes. During the last decades it has received an increasing attention because of its nutritional value and for its adaptability to different environmental constraints. Root architecture has an important role in determining the ability of a plant to explore the soil. These aspects linked to root architecture are not well known in quinoa. According to that, two experiments were carried out to evaluate the applicability of the rhizotron system for root assessment in quinoa. The first one was focused in establish whether the traits obtained by images analysis are representative of the plant development and the second one to analyze the effect of water stress on root architectural parameters. Six Chilean ecotypes of quinoa were used. The plants were grown under greenhouse conditions in rhizotrons in Forschungszentrum Jülich, Germany. Plants grew until the roots reached the bottom of rhizotrons. During the second experiment a water stress treatments were practiced: a half of the plants were only watered to enable seedlings establishment. The following traits were measured: the length of primary, lateral and tertiary roots; root system depth, width and area; and root dry weight. Significant correlations were found among traits and there was variation among ecotypes in terms of the root architectural parameters. There was a significant effect of water stress on root traits. In conclusion, there are co-relationships between traits measured in rhizotrons and traits of the plant/root system; and traits measured in rhizotrons represent the variation observed in the plant/root system and provide details about the effect of water stress on roots.

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PS39

MODULATION OF RELATIVE GROWTH RATE AND ITS COMPONENTS BY WATER STRESS IN ANTARCTIC PLANTS FROM TWO POPULATIONS IN THE ANTARCTICA

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Global warming and changes in water availability are two of the most important characteristics of climate change. Antarctic Peninsula is one of the regions most affected due this change. The plants that grow there have developed a series of mechanisms that allow them to cope with the hard Antarctic climate. However, the effect that water availability could have on the growth rate of these species is unknown. Because that, plants from different populations in Antarctica were collected and growth in room chamber at 16°C (optimal photosynthetic temperature) under two irrigation treatment: field capacity and 25% of field capacity. *Colobanthus quitensis*, regardless of their provenance, significantly decreased its relative growth rate (RGR) under water stress; this decrease was mainly determined by decreases of the relative contribution of the leaf mass ratio (LMR), specific leaf area (SLA) and the net assimilation rate (NAR). In contrast, differences between populations of *Deschampsia antarctica* were observed only at field capacity. Under water stress, the decrease in RGR was independent of the provenance and was mainly determined by NAR. The contribution of each component varied between provenance and specie, for each hydric condition. This different response may reflect differences in plants adaptation and surviving strategies to drought periods, which can determine different responses to climate change.

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PS40

BIOTECHNOLOGY TOOLS FOR CHARACTERIZING AND MAINTENANCE GERMPLASM OF *Pinus pinea* TREE FROM CASABLANCA VALLEY (panel)

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The Stone Pine (*Pinus pinea* L. family *Pinaceae*) is native species to the Mediterranean region that covers a global area of 600.000 hectares. It´s considered a vigorous and versatile tree with many applications ranging from useful in soils recover programs and landscape architecture modification. But also is well know their high nutritional potential of their edible seeds and the capacity of their essential oil as a weeds control and crops control diseases. The present work reports the results of the application of two biotechnological techniques: one is a molecular analysis using Inter-SSR markers and the other is *in vitro* culture. Together both techniques help in the study and characterization of putative ecotypes of *Pinus pinea* native from different European regions and currently located in the Casablanca Valley. For molecular analysis, a set of inter-SSR molecular markers was selected to determine the existence of different ecotypes. For this purpose DNA sample was obtained from pine needles representative of each ecotype of the Casablanca Valley, and by utilizing the PCR reaction proceeded to amplify these samples with different ISSR oligos. For *in vitro* culture, a plant regeneration method for producing clone from mature tree of *P. pinea* via adventitious buds was developed. The first stage (introduction) was the definition of an efficient *in vitro* protocol for disinfection and germination of zygotic embryos, using different salt media and growth regulators. The shoots obtained in the first stage were transferred to the stage of induction media containing various combinations of cytokinins, the growth medium, which favored a greater number of side shoots and length, was selected for germplasm maintenance. At present part of this collection is successfully maintained under *in vitro* conditions and will provide us with elite of non-traditional species, with high potential in Chilean agro-forestry systems.

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PS41

CHARACTERISING AtA6PR1 AND AtA6PR2, PUTATIVE ALDOSE 6-PHOSPHATE REDUCTASES IN *Arabidopsis thaliana*

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Polyols or sugar alcohols, such as mannitol, xylitol and sorbitol, are widely distributed among angiosperms. They are transported in the phloem, and in some families constitute the main form of translocated carbon. Several studies have determined that polyols, as primary photosynthetic products, allow more efficient use of carbon, act as compatible solutes in abiotic stress, protect against hydroxyl radicals, facilitate the mobilization of boron and are involved in plant-pathogen interactions. Sorbitol is present in most species of the Plantaginaceae and Rosaceae families, and its synthesis has been well-studied. The key enzyme in sorbitol synthesis in source leaves is aldose-6-phosphate reductase (A6PR), which reduces a primary product of photosynthesis, glucose-6-phosphate to sorbitol-6-phosphate, which is subsequently dephosphorylated to sorbitol. The A6PR protein has been expressed in plants that do not accumulate sorbitol naturally, obtaining lines with increased resistance to abiotic stress and improved mobility of boron. A6PR-like enzymes have been found in non-Plantagineaceae and non-Rosaceae species that accumulate sucrose, whose expression is mainly associated with osmotic stress tolerance. In *Arabidopsis thaliana* (a sucrose-translocating Brassicaceae), we have identified two proteins which contain the structural features and share ~70% amino acid identity with known plant A6PRs; we call these proteins AtA6PR1 and AtA6PR2. We have determined by qPCR that *AtA6PR1* and *2* are differentially expressed in different organs of *Arabidopsis*. Moreover, using specific anti-AtA6PR1 antisera, we determined that this protein is localised in the cytosol of the cell. We are working towards determining the subcellular localisation of AtA6PR2 by transient transformation of *Nicotiana tabacum* leaves and we are also genotyping potential *ata6pr2*- mutants, which will be compared with previously studied *ata6pr1*- mutants. These results are the first steps in the characterization of AtA6PR1 and AtA6PR2, and will be useful in determining the physiological role of these enzymes in a non-sorbitol translocating species.

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PS42

A SIMPLE METHOD FOR EVALUATION OF COLD TOLERANCE IN TEMPERATE RICE (*Oryza sativa* L.) AT SEEDLING STAGE

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Low temperature is the most important abiotic factor that affectsrice (*Oryza sativa* L.) developmentin Chile. Temperatures below 10°C can be occurring at seedling stage in the field, affect rice growth. Accordingly, the aim of the present study was to finda simple method for evaluation of cold tolerance in temperate rice at seedling stage. Thus, 90 genotypes from Breeding Program Rice from INIA Quilamapu, Chile, were evaluated. Chlorophyll concentration, atLEAFvalues (Chlorophyll meter), carotenoids concentration, proline concentration, and visual damage weremeasuredten days after cold treatment, at 5 °C for 72 hours under completely dark. The classification of genotypes was performed using BLUP predictors calculated for each trait evaluated, and principal componentsanalysis. Quila 126058, Quila 126057 and Quila 126062, were considered as cold tolerant, whereas Quila 126097, Quila 126103 and Quila 126100 were considered susceptible genotypes. Low heritability was observed for chlorophyll and carotenoid content. Furthermore, we foundthat proline content did not allowfinding differences among genotypes with intermediate cold tolerance. Finally, the best trait related with cold tolerance was atLEAFvalue, with good heritability and normal distribution. This is a nondestructive, easy and objective methodology.

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PS43

TRANSCRIPTIONAL AND GENETIC CHARACTERIZATION OF MONOTERPENE BIOSYNTHETIC PATHWAY INVOLVED IN MUSCAT FLAVOR OF *Vitis vinifera*

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Aroma and flavor are attractive quality attributes in fruits. Muscat aroma is common in spirits like *Pisco* and some wine grapes such as Muscat of Alexandria, however it is rarely found in table grapes varieties due to a negative correlation between Muscat aroma and quality at harvest or postharvest. Although this attribute has an environmental component, it is defined by the genetic background of each variety. It is known that a single nucleotide polymorphism in 1-deoxy-d-xylulose-5-phosphate synthase (DXS) gene increases dramatically its enzymatic activity, allowing the accumulation of monoterpene precursors and enabling the accumulation of Muscat aroma components. However, the genetic or molecular causes of the organoleptic differences within Muscat varieties are still unknown. It is believed that differential expression or structural variations in coding regions of genes involved in the biosynthesis of monoterpenes such as geraniol and linalool might be responsible for the organoleptic differences between different Muscat varieties. With the aim to test this hypothesis we analyzed the relative expression of DXS, geraniol synthase and linalool synthase in a collection of grape varieties that have different Muscat content levels. Full cDNA sequences were isolated for these genes looking for structural variations. Several structural variations and differential expression patterns were identified between varieties and require further validation analyses to determine their role in aroma variation, generating basic knowledge to unlink Muscat aroma and fruit quality problems.

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PS44

IDENTIFICATION AND CHARACTERIZATION OF GENES ASSOCIATED WITH VASCULAR DEVELOPMENT IN *Fragaria chiloensis*

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The native white Chilean strawberry (*Fragaria chiloensis*) has great commercial potential due to its distinctive organoleptic characteristics. Strawberries are accessory fruits, consisting of many small individual fruits embedded in a fleshy receptacle, connected by vascular tissue. Previously, a suppression subtractive hybridization library from four different developmental stages of the Chilean strawberry was performed (C1, small green fruit; C2, large green fruit; C3, turning stage; and C4, ripe fruit) and transcripts of three genes, which are associated with vascular development in *Arabidopsis*, were found. These genes are anthocyanidin synthetase (ANS), membrane steroid-binding protein 1 (MSBP1) and syntaxin-like 24 (SYP-24), which could participate in vascularization during fruit formation. To initiate the functional characterization of these genes, their coding and genomic sequences were isolated. Furthermore, transcript levels were determined from C1 to C4. *FcANS* levels increase as the fruit develops; *FcMSBP1* levels are highest in C2, whilst *FcSYP-24* shows the lowest level in C2 and rises to stage C4. Additionally, we are evaluating the effect of abscisic acid, brassinosteroids, ethylene and auxin on the gene expression, hormones known to be involved in vascular development. In parallel, to evaluate the function of these genes in the fruit, we are developing the stable genetic transformation of *F. vesca,* which has the advantage over *F. chiloensis* of being diploid, more-easily transformed and with a shorter lifecycle. We have implemented the *in vitro* propagation of *F. vesca* from explants, attaining 50% regeneration efficiency. Therefore, this system is a powerful tool to address the molecular function of our selected genes in vascular development in *F. chiloensis*.

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PS45

TRANSCRIPTOME PROFILING DURING A DESICCATION-REHYDRATION CYCLE IN *Hymenoglossum cruentum* A DESICCATION TOLERANT FILMY FERN.

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Hymenoglosum cruentum (Cav.) Presl. (Hymenophylleceae) is a desiccation tolerant filmy fern characterized by a single-cell, without stomata laminated fronds, with a rudimentary water loss control. It is able to survive weeks under 5% water content. Our goal is to study the molecular mechanisms involved in desiccation tolerance of *H. cruentum*. To achieve this goal, RNA from *H. cruentum* during three stages of desiccation-rehydration cycle was sequenced by Illumina MiSeq platform. Results from transcriptome analyses have revealed that *H. cruentum* gene products can be classified within the following functional categories of dehydration-induced genes: (I) genes encoding protective proteins including Late Embryogenesis Abundant (LEA) and detoxifying enzymes, (II) genes encoding products with regulatory functions (RNAs and proteins), (III) proteins involved in transport of water, (IV) genes encoding enzymes related to protein, lipid and carbohydrate metabolism and other molecules. These groups are expressed principally constitutively, except by the overexpressed group of LEA genes. LEA proteins and soluble sugars are considered critical in the acquisition of cellular desiccation tolerance. The genes encoding LEA, are induced in response to water deficits in *Craterostigma plantagineum*, a desiccation-tolerant angiosperm, as it was observed in *H. cruentum*. In contrast *Tortula ruralis*, a desiccation-tolerant moss, dehydrins are apparently constitutively expressed. On the other hand, accumulation of soluble sugars has long been correlated with the acquisition of desiccation tolerance. In *H. cruentum* expression of genes encoding sugar metabolism enzymes are down regulated during rehydration as reported in *T. ruralis*. The lack of desiccation–induced sugar accumulation appears to be a common feature of tolerant filmy ferns and mosses but not in *C. plantagineum.* This probably indicates that gene expression associated to desiccation tolerance in Hymenophylleceae is constitutive, similar to mosses and lichens, remarking the primitive origin of filmy ferns.

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PS46

MOLECULAR CHARACTERIZATION OF *FCMT2* AND *FCMT3*, PUTATIVE METALLOTHIONEIN GENES FROM CHILEAN STRAWBERRY (*Fragaria chiloensis*)

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Metallothioneins (MTs) are characterized as low molecular weight heavy metal-binding cysteine-rich proteins. Their role in plants is unknown, but the evidence suggests their participation in copper and zinc homeostasis, as well as in ROS scavenging. Based on the cysteine residues arrangement, plant MTs have been classified into four types (I-IV). Even though MTs are expressed throughout the plant, some have been found to be expressed in a tissue-specific manner. Previously, two MTs were found as differentially expressed sequence tags (ESTs) during *Fragaria chiloensis* fruit development. In this work, we report the molecular characterization of these two MTs from *F. chiloensis*. With this aim, fruits at four different developmental stages were collected. Both genomic and cDNA sequences for each MT were cloned and sequenced. The predicted polypeptides show similarity to class II and III MTs, and were thus named *FcMT2* and *FcMT3,* respectively. The transcript levels for each MT are different during *F. chiloensis* fruit development, validating the previous EST screen. However, the expression patterns are not identical. *FcMT2* transcripts accumulate in the early fruit stages. At a later stage the transcript level decays three-fold, which correlates with the loss of firmness reported during fruit development, suggesting a role for *FcMT2* in this process. On the other hand, *FcMT3* transcripts accumulate in the middle stages of fruit development, similar to a pattern described previously for cell wall remodeling enzymes, which are regulated by ethylene. Therefore, treatments with ethylene were performed in order to establish its effect on the expression of *FcMT*s. These experiments showed a dual role for ethylene, as an inhibitor or promoter of *FcMTs* expression, which depends of the fruit developmental stage.

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PS47

ROLE OF MBW COMPLEXES ON PROANTHOCYANIDINS AND ANTHOCYANINS BIOSYNTHESIS DURING STRAWBERRY (*Fragaria* x *ananassa* CV. AROMAS) FRUIT RIPENING: PRELIMINARY RESULTS

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In *Arabidopsis*, three transcriptional factors (TFs) are necessary for proanthocyanidins (PAs) biosynthesis, acting together in a ternary regulatory MYB-bHLH-WD40 (MBW) protein complex. Functional homologues of those transcriptional regulators were characterized in strawberry fruits: FaMYB9/FaMYB11, FabHLH3 and FaTTG1. However their expression patterns during ripening have not been described. Moreover, other TFs like EGL3 (R/b-like bHLH) and PAP1 (R2R3-MYB) are components of transcription activation complexes that control anthocyanin biosynthesis and are conserved in plants, and whose expression profiles are not been studied in *F.* x *ananassa.* Besides, a probable negative regulation mechanism of MBW complexes could be represented by FaMYB5 and FaMYB1. We are currently analyzing the expression profiles of 9 genes codifying for the MBW protein complex and others proteins that interact with this complex during strawberry fruits ripening. During strawberry fruit ripening FaMYB9, FaMYB11, FaEGL3, FaTTG1 and FaPAP1 genes showed a decrease in transcript levels, while FaMYB5 and FabHLH3 genes showed a relatively constant expression. On the other hand, FaMYB1 gene exhibited a gradual increase in expression levels, whereas FaMYB10 gene showed a remarkable increment between turning stage and fully ripe stage. Additionally, a qualitative and quantitative characterization on content of PAs and anthocyanins is being performed by HPLC analysis.

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PS48

THE MALE S-DETERMINANT PrpS FROM *Papaver rhoeas* (POPPY) FUNCTIONS IN MAMMALIAN HeLa CELLS

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Self-incompatibility (SI) is an important genetic mechanism that flowering plants utilize to reject "self" pollen, increasing genetic diversity by preventing self-pollination. SI is controlled in an allele-specific manner by a single locus with multiple haplotypes; each haplotype encodes both male and female *S*-determinants. The S-determinants of *Papaver rhoeas* (poppy) are PrsS (Papaver *rhoeas s*tigma S) and PrpS (*Papaver rhoeas* pollen S). PrsS is a small cysteine-rich protein. It interacts with its cognate pollen S-determinant PrpS, a small novel transmembrane protein (so not a "classic" receptor). Interaction of PrsS with incompatible pollen stimulates increases in cytosolic free Ca^{2+} ($[Ca^{2+}]_{cyt}$), prompting the hypothesis that PrsS isa signaling ligand. Downstream, striking alterations to the actin cytoskeletonand initiation of programmed cell death involving caspase-like activities are major targets for SI in pollen. We recently demonstrated functional expression of PrpS in *Arabidopsis thaliana* pollen. This study was remarkable, as *A. thaliana* is not only self-compatible, but is highly diverged from the *Papaver* lineage (~140 Mya), yet can nevertheless initiate a response similar to that seen in *Papaver* when exposed to PrsS. This finding is important, as it suggests that the *Papaver* SI system must be accessing a highly conserved set of responses. This prompts the question: how far can we take this? We will describe current attempts to assess whether the poppy SI *S*-determinants are functional in mammalian HeLa cells. Imaging of HeLa cells stably expressingPrpS have revealed transient increases in $[Ca^{2+}]_{cyt}$ after addition of cognatePrsS. Moreover, striking alterations in both the morphologyand actin organization were observed in these cells. Together, this provides the first evidence that the poppy S-determinants may be functional in mammalian HeLa cells.

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PS49

PLOIDY DETERMINATION BYFLOW CYTOMETRY IN *Prunus* SPECIES USED AS ROOTSTOCKS

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Knowledge of nuclear DNA content and genome size estimates are fundamental parameters in many genetic and molecular studies. This information is particularly useful inevaluatingsomatic and reproductive compatibility for breeding programs that are based on interspecific crosses. Differences in ploidy level lead to genetic barriers to obtain interspecific hybrids. Thejoint *Prunus* rootstock breeding program between EEAD-CSIC and CEAF includes inter-specific hybrids betweendifferent species belonging to different *Prunus*subgenera (Euamygdalus and Prunophora). The determination of the ploidy level inparental lines and elite candidates under selection is a priority tobe used in our breeding programs. Therefore, this study aimed to determine the ploidy level of different accessions of *Prunus* rootstocks included in the germplasm bank and the breeding programs of EEAD-CSIC and CEAF.We have characterized inter-specific hybrids of the genus *Prunus* using as reference standards of well-knownploidy level (commercial cultivars). Leaf samples were collected early in the summerfrom mature orchard trees.Ploidy levels were determined byflow cytometry(PAS, PARTEC). For isolation of nuclei, leaf tissue (approx. 0.5 cm^2) was chopped with a scalpel using the UV CyStainploidy (DAPI) solution. Data were displayed as histograms of the number of nuclei vs. the relative fluorescent intensity using a logarithmic scalealong the y-axis. We have obtained various ploidy levels.In general, most Myrobalan plums (*P. cerasifera*) were diploidswhilecommon plums (*P. domestica*) were hexaploids. The inter-specific hybrids showed different ploidy levels, according to thoseobserved in their parental genotypes. These results will be corroborated by counting chromosomes (karyotype) and with the molecular markers characterization by SSRs.

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PS50

PROTEOMIC ANALYSIS OF *Deschampsia antarctica* DESV. IN RESPONSE TO COLD STRESS

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Temperature-induced stress has important implications for agriculture. Considerable efforts have been directed to understand its effects in plants. Plants native to cold climates acquire increased freezing tolerance during exposure to low nonfreezing temperatures in a process known as cold acclimation. This involves many adaptive responses, including massive changes in the accumulation of cold-regulated proteins, whose functions are largely unknown. *Deschampsia antarctica*, is the only natural grass species in the maritime Antarctic. Its singular physiological responses attract the interest of many specialists, represented an invaluable resource for the identification of genes and proteins related to abiotic stress. This work focused on the analysis of protein accumulation after 6, 12, 24 h of cold treatment (4 ºC) *in vitro*, and field Antarctic conditions using 2D SDS-PAGE. Finally, differentially accumulated proteins in *Deschampsia antarctica* were identified by mass spectrometry. The analyses of approximately 800 spots revealed qualitative and quantitative differences between the samples evaluated. These differentially accumulated proteins were related to various functional categories including energy, protein synthesis/degradation and stress responses. Several proteins identified here have not previously been reported differentially accumulated during cold conditions. These proteins could be relevant to understand the mechanisms by which this extremophile survives in its environment and contribute to the development of biotechnology in Antarctic species.

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PS51

TRANSCRIPTIONAL AND TRANSLATIONAL INHIBITION OF *Hymenophyllum caudiculatum* DURING A DEHYDRATION/REHYDRATION CYCLE, PHYSIOLOGICAL AND DIGE ANALYSIS

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The Hymenophyllaceae fern family presents poikilohydric behavior, with a rudimentary control of water loss. One of the most outstanding features of this family of ferns is the presence of fronds with one of few cell layers (hence the name of filmy ferns) and therefore the absence of stomata. For this reason they present poikilohydric behavior, with a rudimentary control of water lost. *Hymenophyllum caudiculatum* is able to lose more than 80% of water content, remain dry for some time and survive upon rehydration. Previous experiments have showed that *Hymenophyllum caudiculatum* resist fast dehydration/ rehydration by constitutive and not inducible mechanisms, more similar to bryophytes that to angiosperms. This research is meant to understand the importance of translational regulation during the dehydration/rehydration cycle. Using optical, confocal and electronic microscopy, chloroplast movement and cell ultrastructure were characterized during a dehydration/rehydration cycle. Proteomics 2D DIGE techniques using fluorescent dyes and IPG strips pH4-7 were used to analyze the effect of treatment with a transcriptional (Actinomicyn D) or translational (Cycloheximide) inhibitor. During dehydration chloroplast avoidance movement to reduce photo-damage was extensive and reversible. The use of inhibitors treatments showed differential accumulation of proteins. Protein characterized by MS/MS will be analyzed in terms of functional categories identified. The recovery time during rehydration showed a dependence on time of dehydration.

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PS52

JASMONATE SIGNALING PATHWAY DURING DEVELOPMENT AND RIPENING OF STRAWBERRY FRUIT: PRELIMINARY RESULTS

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Ripening of the non-climacteric strawberry fruit is regulated in part by hormones such as jasmonic acid (JA), whose biological function is exercised by the bioactive molecule (+)-7-iso-jasmonoyl-L-isoleucine (JA-Ile). We hypothesize that JA could regulate certain ripening traits in strawberry fruit through signaling and repressor mechanisms. In *Arabidopsis thaliana* the JA-dependent responses require degradation of Jasmonate Zim-domain (JAZ) through Skp-Cullin-F-box-type E3 ubiquitin ligase complex (SCF^{COI1}). The JAZ proteins act as transcriptional repressors in the repressor complex TOPLESS-NINJA-JAZ. This complex represses the transcription of early JA-responsive genes through the binding to MYC transcription factors (MYC2, MYC3 and MYC4). Furthermore, the histones deacetylases HDA19 and HDA6 had been described as regulators of JA-dependent transcription. To decipher the regulation of strawberry fruit ripening by JA at the molecular level we start to design specific primers for the above genes. After a search of orthologous genes of *Arabidopsis* genes in the transcriptome of *Fragaria vesca*, 16 predicted sequences were analyzed: COI1 (1), TOPLESS (4), NINJA (1), JAZ (5), MYC (1), HDA6 (3) and HDA19 (1). Gene expression analyses and JA-Ile determination are underway to characterize the role of JA during development and ripening of strawberry fruit.

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PS53

QUANTIFICATION OF ANTIOXIDANTS (LYCOPENE AND BETALAIN) IN TOMATO (*Solanum lycopersicum* L.) AND SUGARBEET (*Beta vulgaris*) IN RESPONSE TO SALT AND BORON STRESS CONDITIONS PRESENT IN FIELD CONDITIONS IN THE LLUTA VALLEY.

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The development of the study aims to quantify the pigments of vegetables tomato (*Solanum lycopersicum* L.) "Poncho Negro" and sugarbeet (*Beta vulgaris*) varieties Detroit and Larka, in response to salinity conditions and boron excess in the Lluta Valley. Plants were grown in soil with EC_S: 8,2 mS/cm and EC_W: 2,56 mS/cm; Na: 687,45 mg/L, Cl: 1.312,43 mg/L, B: 27,62 mg/L and the experiment was performed under field conditions and located at kilometer 19 in the experimental plots of the University of Tarapacá, Arica, Chile. Lycopene and betalains antioxidant content in various stages of physiological development of tomato and sugarbeet were analyzed. The amount of extractable or synthesis of both pigments lycopene (tomato) and betalains (sugarbeet) it will be obtained under stress. The extraction will be made with the Soxhlet extractor; this process will take place in the Laboratory of Chemistry of water-soil and vegetal-tissues. The crops were grown under in soil and irrigation water stressed conditions because possibly the increased synthesis of these antioxidants may serve as tolerance mechanisms in both crops, suggesting a new alternative of productivity in this valley, a situation that due the effect of climate change on agriculture is increasing the adverse conditions and decreasing crop surfaces.

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PS54

CHARACTERIZATION OF A SEPALLATA LIKE TRANSCRIPTION FACTOR DURING FRUIT DEVELOPMENT OF *Fragaria vesca*

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Fruit export is an important activity for Chilean economy. Fresh fruit generates high revenues, and its export requires a delicate preservation process closely related to the ripening process of each fruit. Ripening involves biochemical, structural and physiological changes mainly controlled by hormones and transcription factors (TF). Commercial strawberry, *Fragaria x ananassa*, is world wide produced and exported by Chile. *Fragaria vesca* is the plant model for *Fragaria* genus, useful for genetic and functional studies to understand and characterize the molecular mechanisms associated to ripening. Previous studies indicate that TFs, specifically the MADS-box SEPALLATA subfamily, could control or influence the ripening process of fleshy fruits by binding to CArG-box regions present in the promoter regions of genes associated with this process, such as cell wall degrading enzymes. To provide new information regarding the role of MADS-box TF during ripening of the *Fragaria* genus, we determined the expression profile of SEPALLATTA like genes in *Fragaria vesca* fruits, using qRT-PCR. One TF was highly expressed at some developmental stages of *F. vesca* fruit, and named as FvSEP1. The structural model of FvSEP1 was built by comparative modeling. Furthermore, molecular docking was used to understand the interaction of FvSEP1 and CArG-box sequences present in the promoter region of a Xyloglucan endotransglycosilase/hydrolase gene (FvXTH1), described in previous studies as an XTH highly expressed in ripening fruit. This approach shall contribute to elucidate the role of these TFs as regulators during ripening of *F. vesca* fruit.

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PS55

EVALUATION OF THE ANTIOXIDANT ACTIVITY AND PHENOLIC COMPOUNDS IN THE METHANOL EXTRACT OF *Empetrum rubrum* (Vahl ex Willd.)

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Plants, for their biodiversity and abundance in secondary metabolites, provide a rich source of antioxidants and in a search for new compounds with this activity, we focused on shrub species *Empetrum rubrum* (Vahl ex Willd.), commonly known as brecillo, which is characterized by tolerate harsh conditions, dryland environments, temperatures as low as –15 °C, high winds, and direct sun exposure. The habitat of *Empetrum rubrum* suggests the development of a chemical metabolism as an adaptation strategy to environmental conditions. By spectrophotometric analysis of the methanol extract, the content of total polyphenols and antioxidant activity *in vitro* was measured using capture techniques of radical 2,2-diphenyl-1-picrylhidrazyl ($DPPH^{\bullet}$) and 2,2'-azino-bis(3-ethylbenzthiazoline-6-sulfonic acid) diammonium salt ($ABTS^{\bullet+}$). Antioxidant effect results were expressed as (±)-6-Hydroxy-2,5,7,8-tetramethyl-chromane-2-carboxylic acid (Trolox) equivalents, and gallic acid. The presence of secondary metabolites was determined using staining reagents and precipitation. For assays with $DPPH^{\bullet}$ and $ABTS^{\bullet+}$, the IC_{50} values measured were 0.41 and 0.11mg/mL, respectively, and the IC_{50} extract concentration required to inhibit 50% the absorbance of the radical. The content of polyphenols in gallic acid equivalents was 22.47±0.91 mg/g of extract; this corresponded to a 2.25±0.09%. The results of the inhibitory activity equivalent to ABTS were 153.51± 2.44 mg of Trolox/g of extract and 30.00±1.50 of gallic/gr acid extract in the case of DPPH. The observed results concerning the antioxidant effect confirmed the presence of phenolic compounds. Qualitative phytochemicals assays revealed the presence of tannins and flavonoids as well.

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PS56

GAMETOPHYTIC CONTROL OF LATE FLOWER MATURATION: EVALUATION OF AUXIN ACCUMULATION IN POLLEN AND TAPETUM AND ITS ROLE ON STAMEN MATURATION IN *Arabidopsis thaliana*

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In *Arabidopsis*, early phase of stamen development involves establishment of anther morphology and cell and tissue differentiation. The late phase consists in three well-coordinated developmental processes: pollen grain maturation, stamen filament elongation and anther dehiscence. These three processes are essential for sexual plant reproduction. We recently generated a model of male sterile plants through the genetic ablation of pollen, expressing the bacterial RNase Barnase under the transcriptional control of pollen specific promoters. The transgenic plants were male sterile and 100% of pollen grains dies in the late phase of development. Surprisingly, stamen development was also affected, and absence of anther dehiscence and anther filament elongation was observed. Interestingly, these sporophytic defects are reverted when flowers are treated with jasmonic acid or the auxin IAA, and anther dehiscence and filament elongation is restored. Previous studies suggest that pollen and possibly tapetum are involved in the signaling processes regulating late stamen development through auxin polar transport and accumulation. To study if the auxin accumulation in pollen and/or tapetum is controlling the stamen maturation through a time-dependent process, we will generate *Arabidopsis thaliana* transgenic plants expressing the bacterial auxin inactivator iaaL under the control of temporal and tissue specific promoters. Also, expression analyses of stamen-specific genes involved in the maturation process will be analyzed in male sterile plants with or without hormone treatment. We propose that pollen is involved in an auxin-dependent signal transduction pathway that regulates the coordinated events that take place during stamen maturation.

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PS57

CHANGES IN FATTY ACIDS METABOLISM DURING FRUIT DEVELOPMENT AS A TOOL FOR PREDICTING POSTHARVEST POTENTIAL IN AVOCADO CV 'HASS'

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Avocado cv. Hass *(Persea americana)* is distinguished for long fruit development. Texture and flavor have very important effects in determining fruit postharvest quality, and even more at consumer arrival after a long period of storage. Even though flavor is a mixture of compounds, lipids are the most important, which are accumulated since the beginning of development until harvest time (with a minimum of 9%). The objective of this study was to analyze and compare the lipid profile during fruit development, and the expression of genes related with enzymes involved in fatty acids metabolism, with the final goal of understanding if these changes determine the postharvest potential of the fruit. Fatty acids profile of Hass avocado was characterized at different stages of development from two commercial orchards from the central area of Chile. Results showed that oleic acid accumulates quickly in early stages of development and remains constant along harvest and post-harvest; palmitic, palmitolenic and linolenic acids rise slowly to harvest. We also analyzed the expression profile of delta 12 fatty Acid desaturase (*pamdFAD)*, omega-3 and omega-6 fatty Acid desaturases (*pamw3FAD*, *pamw6FAD),* which showed a little rise in harvest; acetyl-CoA carboxylase (*pamAco-AC)* showed a peak only during post-harvest; subunit BC of acetyl-CoA carboxylase (*pamAco-BC)* and acyl-ACP desaturase (*pamSAD)* rises from development to harvest, and showed a decrease in post-harvest. Finally, subunit BCCP of acetyl-CoA carboxylase *(pamAco-BCCP)* increased only during development, and three acyl-CoA synthetases (*pamAco-AS1, pamAco-AS2* and *pamAco-AS3*) exhibited a rise only during post-harvest. The relationship between these changes and the postharvest potential is under study.

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PS58

GLOBAL CHANGES IN THE *Prunus persica* TRANSCRIPTOME IN RESPONSE TO CYTOKININ TREATMENTS DURING FRUIT DEVELOPMENT

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Cytokinin is a phytohormone that plays a critical role in many plant growth and developmental processes, including organogenesis, leaf senescence, vascular differentiation, and nutrient acquisition. To better understand the effects of cytokinin in peach fruit development, fruits were treated with t-zeatin at pre-lignification, lignification and post-lignification stages of development. Stage-specific global changes in the transcriptome of peach fruits treated with cytokinin were determined by RNA-Seq analysis. These differentially expressed transcripts were annotated using Gene Ontology (GO). Additionally, the metabolic processes affected by the exogenous cytokinin treatment were visualized using Mapman software. Our results suggest a stage specific response to cytokinin treatment during peach fruit development, with the lignification stage showing the greatest variation in the expression of genes of multiple metabolic processes.

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PS59

FUNCTIONAL CHARACTERIZATION OF THE POLLEN SPECIFIC GENES *PSK3* AND *PSK4* TROUGH THE GENERATION OF KNOCK-DOWN TRANSGENIC PLANTS EXPRESSING ARTIFICIAL microRNAs (amiRNA)

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Pollen development starts inside the anther, where the sporogenous initial cells undergo meiosis to form a tetrad of cells that are enclosed in a thick callose wall. Each microspore enlarges and goes through an asymmetric mitosis that results in two cells, the larger cell called vegetative cell –that will form the pollen tube– and a smaller cell called generative cell, which is engulfed inside the cytoplasm of the vegetative cell. Later, this generative cell undergoes a second mitosis to form two sperm cells. During fertilization, the pollen tube transports directionally the sperm cells to the ovule to produce the double fertilization event. Little is known about signal transduction pathways and molecular components involved in these processes. Using microarray data, we identified 2 genes that encode for protein kinases and were named *PSK3* and *4* (for *POLLEN SPECIFIC KINASE*). To functionally characterize these genes, we have generated transgenic plants expressing artificial microRNAs using a pollen specific promoter (LAT52). amiRNAs has been successfully used in plants to silence endogenous genes and they are generated by exchanging the miRNA sequence of endogenous precursors with artificial sequences to create constructs targeting the gene of interest. Analysis of pollen development, germination and tube elongation was performed to establish the physiological role of these genes. Our results indicate that *PSK3* is not necessary for pollen tube germination or elongation. On the other hand, *PSK4* could be required for the callose plugs formation into the pollen tube of *Arabidopsis thaliana*, as transgenic lines show a lower number of callose plugs in pollen tubes. Additionally, all the transgenic lines analyzed posses low quantity of pollen grains compared with a wild-type plant, a phenotype that may be linked to the methodology used to silence these genes.

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PS60

A METABOLOMIC APPROACH TO STUDY THE NATIVE POTATOES (*Solanum tuberosum* Spp. *tuberosum*) GROWN IN SOUTHERN CHILE

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Wild potatoes are native from America, having a wide geographical distribution, which could affect the genotype metabolic composition. Cultivated genotypes in Chiloé Island show high variability in tuber shape, flesh and skin color. We studied the metabolic composition of eleven native potatoes varieties of *Solanum tuberosum* ssp. *tuberosum* L. Concentration of polyphenols, flavonoids, anthocyanins, antioxidant activity (AA) and metabolic profile in skin and pulp were determined, using two cultivars as control. Our results showed significant differences ($P \leq 0.05$) between skin and pulp of all potato varieties analyzed. The skin had a higher polyphenol concentration than pulp in all varieties studied and showed higher AA than pulp in all the varieties analyzed. While the skin polyphenols ranged from 1200 to 3000 μg g^{-1} FW of chlorogenic acid. Flavonoids were 6-fold higher in skin than in pulp in all the varieties. In some native varieties this concentration exceeded 6000 Eq. Rutin mg g^{-1} FW. The anthocyanins concentration showed minor differences between both tissues; however, “Guicoña”, “Tonta” and “Clavela” exhibited significant differences. “Lengua” and “Clavela” varieties have the highest concentrations in skin (ranging between 16.5±0.83 and 16.15±0.35 μmol g^{-1}trolox eq FW, respectively) compared to the other potato varieties analyzed. The metabolic profile showed differences in the concentration and distribution of the primary metabolites between tissues. Varieties with red or darker skin are associated in the hierarchical clustering with precursors of antioxidant metabolites such as phenylalanine, glutamine, valine, asparagine and others, correlating with the pulp in some varieties. In varieties with light skin (white or yellow) more associated metabolites to sugar metabolism (maltose, xylose, glucose, sorbitol and others) were observed. The specific metabolites content could be explored in Chiloé Island germplasm to improve characteristics in breeding programs, developing potato varieties with best nutritional value.

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PS61

GENETIC IMPROVEMENT OF *Vitis vinifera* TO CONFER RESISTANCE TO THE FUNGUS *Botrytis cinerea*

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Grapevine is one of the most cultivated crops worldwide and is the most economically relevant in Chile. Fungal diseases are known to cause substantial crop losses in grape. Most qualitative and quantitative grape losses in Chile are caused by *Botrytis cinerea*, a necrotrophic fungus that kills the plant tissues to grow and develop, resulting in a deep damage to the plant and its fruits. For many years conventional breeding has approached the development of cultivars with resistance to pathogens, but some disadvantages are the amount of years that take to develop a new cultivar and the negative traits acquired in conventional crosses that need to get eliminated. Limitations to the use of transgenic plants have prompted the development of new technologies in genetic manipulation, enabling transformation of desired genes/ traits into plants by a marker free technology that uses native genes to improve crop properties. This work aims the identification and overexpression of the grapevine gene *STS* (stilbene synthase), that codifies to an enzyme involved in the biosynthesis of the phytoalexine resveratrol, under the control of the grapevine pathogen inducible promoter of *PR10* (Pathogen Related 10 gene) in order to increase resistance of *Vitis vinifera* to *Botrytis cinerea*. For doing this, the promoter and codifying regions were amplified and cloned in an expression vector for further *Agrobacterium tumefaciens* transformation of *Arabidopsis thaliana* and *Solanum lycopersicum* as study models, and subsequently transformation of *Vitis vinifera* embryonic tissue for future biotechnological applications. In parallel, *in vitro* assays with resveratrol were done to evaluate the inhibitory effect of the biomolecule on *Botrytis* development, as an approximation to the resistance that might have the transformed plants. Finally, is important to highlight that increased levels of resveratrol also raise antioxidant effect of grape, widely described as stimulating human good health.

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PS62

THE ER-CALCIUM DYNAMICS ARE INVOLVED IN THE TRANSCRIPTIONAL REPRESSION OF UPR-GENES DURING THE DEFENSE RESPONSE TO BACTERIAL INFECTION IN *Arabidopsis thaliana*

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Plants are potential hosts for diverse groups of pathogens, including bacteria. However, plants are able to mount a defense response against the infection. Bacterial challenge triggers the Unfolded Protein Response (UPR), in a salicylic acid (SA) dependent manner and leads to the establishment of plant immunity. A fine tuning of the UPR-genes is necessary to avoid the programmed cell death generated in this response. It has been described the role of WRKY IId transcription factors as repressors during the bacterial infection. To evaluate the role of these factors during the defense response, we analyzed the expression of UPR-genes in wild type and WRKY-mutant plants treated with SA. We observed an up-regulation of the UPR-genes in the mutant plants suggesting that WRKY TF negatively regulates the expression of these genes. This family group of WRKY TF has a calmodulin (CaM) binding site and we analyzed the *in vivo* interaction between these proteins by experiments of bimolecular fluorescence complementation (BiFC) in tobacco leaves. Our data suggest that Ca^{2+} could activate WRKY IId family group in a CaM dependent manner uncovering a connection between calcium dynamics and UPR during the establishment of plant immunity. To test this hypothesis we evaluated the expression of UPR-genes after the treatment with SA in plants affected in the ER Ca^{2+} efflux, blocking three different calcium channel receptors (NAADP, IP3 and cADPR) and the ER calcium influx using four Ca^{2+}/ATPases mutant plants (*aca1, aca2, eca1* and *eca 4*). Taken together we propose that WRKY11 and -17 are negative regulators of the UPR genes that are involved in the programmed cell death by a complex mechanism involving the ER Ca^{2+} dynamics.

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PS63

PHYTOENE SYNTHASE 2 (*DCPSY2*) OF *Daucus carota* INDUCES MORPHOLOGICAL AND DEVELOPMENTAL CHANGES IN TRANSGENIC CARROTS

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Daucus carota is a biennial plant that produces high amounts of carotenoids on its storage roots that develops exclusively in darkness. Carotenoids are colored isoprenoid pigments derived from the secondary metabolism. They are synthesized in plastids where they act as accessory pigments in light harvesting and protect cells against photooxidation. Carotenoids are precursors of hormones such as abscisic acid and provide attractive color to flowers and fruits. Significant human health benefits are attributed to carotenes, because of their antioxidant and provitamin-A activity. Even though, carotenoids, gibberellins and chlorophylls derived from isopentenyl diphosphate (IPP), the production of phytoene, catalyzed by phytoene synthase (PSY), is the first committed step and a key regulatory point in the biosynthesis of carotenoids. In *Daucus carota*, two *PSY* genes have been reported. Both genes are expressed in leaves and root during development, being *DcPSY2* mostly expressed in the storage root and *DcPSY*1 in leaves. *DcPSY2* produce an increment in total carotenoid and β-carotene when expressed in *Nicotiana tabacum* and transgenic *DcPSY2* tobacco plants showed significant tolerance to NaCl stress. Here we show, that transgenic carrot plants overexpressing *DcPSY2* present and increment in total carotenoids. Surprisingly, transgenic seedlings have an orange phenotype and develop a storage root when cultured *in vitro* in the presence of light, whereas in wild-type plants light acts as inhibitor of the storage root formation. Moreover, some transgenic plants showed accelerated flowering and seed production in less than a year. These results suggest that the over-expression of *DcPSY2* not only increases the carotenoid content, but also exert an effect on plant development maybe thorough a feedback effect on hormone synthesis.

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PS64

ASSESSMENT OF ANTIMICROBIAL ACTIVITY IN THE LEAVES OF ENDEMIC LUCUMILLO (*Myrcianthes coquimbensis*) SHRUB

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Lucumillo (*Myrcianthes coquimbensis*, Myrtaceae) is an endemic Chilean shrub that grows exclusively in the coast of Elqui Province (Coquimbo Region). This leaf-aromatic shrub has been poorly studied at the chemical level, and some local people attribute antiseptic properties in their leaves, especially those related to oral and stomach infections. Our aim was investigate the antimicrobial activity of eight extracts obtained from leaves of *M. coquimbensis* and tested in *Escherichia coli* (gram -) and *Staphylococcus aureus* (gram +) bacteria. Among the eight extract evaluated, the extract macerated with water (EMW) showed the better antimicrobial activity, with a minimum inhibitory concentration (MIC) of 9400 mcg/mL for *E. coli* and 1500 mcg/ml for *S. aereus*. Using a thin layer chromatography (TLC), a mobile phase of ethanol:ethyl acetate (3:1), and a stationary phase of silica gel chromatolayers, high content of terpenes, flavonoids, coumarins and hydrolysable tannins were identified. Interplay between these chemical compounds and the antimicrobial activity detected was performed using a direct bioautography method, which showed two fractions putatively involved in the antibacterial activity. Hydrolysable tannins were identified in the polar fraction, whereas terpenes were the most abundant compound in the other fraction. Our results indicated that secondary metabolites of *M. coquimbensis* might be acting as antibacterial against *E. coli* and *S. aureus*, and that both, hydrolyzable tannins and terpenes might be involved in such inhibition.

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PS65

TOLERANCE TO COPPER (II) IONS ON GERMINATION AND *in vitro* PROPAGATION OF *Colobanthus quitensis*

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Along its wide latitudinal distribution, *Colobanthus quitensis* **(**Kunth) Bartl. (Caryophyllaceae) is described as a species that must withstand conditions that would be adverse for any other type of plant. For example, several of its habitats have evidenced high concentrations of copper ions. This situation is originated primarily by the runoff from the Andes, which are deposited in bogs where this species lives. This condition suggests that the Antarctic pearlwort could have mechanisms of morphological, physiological and biochemical tolerance to endure these conditions. In this study, copper tolerance was evaluated during germination and *in vitro* propagation of *C. quitensis*, using two $CuSO_4$ concentrations: a minimum one (100 µM) and a maximum one (500 µM). The germination and survival percentages were sensitive to the maximum concentration of $CuSO_4$. Generally, there were no significant differences between the control (0 µM) and the lowest concentration of the contaminant. During *in vitro* propagation, a marked reduction in the appearance and development of roots to 500 µM $CuSO_4$ was observed. Also, stress symptoms as chlorosis and floral tissue appearance were identified. Regarding the conditions tested, this is one of the first studies showing evidence about the effect of metal ions Cu (II) on the germination and *in vitro* tissue culture of *Colobanthus quitensis.*

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PS66

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

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The gravitropic response in trees is a widely studied phenomenon, but the molecular mechanism that involves the response to loss of verticality remains unclear. RNA-Seq strategy was used to identify differentially expressed genes in response to inclination. Young seedlings of radiata pine were inclined at 45°, and total RNA was extracted from a stem bulk after 2,5 hours of inclination. As control total RNA from vertical radiata pine plants were considered. The stem was cut longitudinally and two samples were collected from a single tree, the upper side and the lower side of the stem. The transcriptome of *Pine radiata* D. Don was based in the Ilumina sequencing. A total of 248.350 contigs were obtained for the three libraries, having each library a contigs length of N50 1.300 bp. Contigs redundancy was clustered by CD-hit. A re-entry of the transcripts was performed after using blastx against NR database to get annotations. These annotated sequences were submitted to Blast-2GO to visualize the functional annotation and the reconstruction of metabolic pathways. Differences in transcript accumulation of genes involved in lignin, terpens and the synthesis of flavonoids were detected as differentially expressed. Transcripts differentially expressed from the library was determined by FPKM and validated by qRT-PCR.

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PS67

CHARACTERIZATION OF *VvMYB24*, A PUTATIVE *AtMYB24* ORTHOLOGUE AND ITS ROLE IN STAMEN DEVELOPMENT

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In *Arabidopsis thaliana, AtMYB21* and *AtMYB24* are two members of the R2R3-MYB family of transcription factors, which are mainly expressed in reproductive organs. Both genes have been associated with stamen development. *AtMYB24* mutants do not show any phenotype due to its redundancy with *AtMYB21,* but transgenic plants over-expressing (OE) *AtMYB24* present dwarf flowers, non-dehiscent anthers, abnormal pollen grains, male sterility and altered expression of genes related to the phenylpropanoid pathway. Previously, in our lab we have characterized the R2R3-MYB family in grapevine (*Vitis vinifera*) and identified a gene with high sequence identity respect to *AtMYB24,* thus referred now as *VvMYB24*. In this work we aim to characterize the function of *VvMYB24*. For doing this, its coding region was cloned from *Vitis vinifera* cv. Cabernet Sauvignon flowers, identifying the conserved signatures of the R2R3-MYB family. Ectopic expression of *VvMYB24* fused to *GFP* in tobacco plants revealed its nuclear localization. To assess its function *in planta*, *VvMYB24* OE Arabidopsis plants were generated. OE lines with similar vegetative growth to wild-type plants were selected according to the number of rosette leaves when the floral primordium appeared. Despite this, reproductive growth was compromised in these lines showing reduced filament elongation and presence of senescent ovules. Also we observed that the overexpression of *VvMYB24* in Arabidopsis affects the expression of phenylpropanoid pathway-related genes. Together, these results suggest that *VvMYB24* could be the *AtMYB24* orthologous in grapevine.

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PS68

IDENTIFICATION OF REFERENCE GENES FOR QUANTITATIVE GENE EXPRESSION ANALYSES DURING PEACH FRUIT DEVELOPMENT USING A BIOINFORMATIC APPROACH

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Quantitative analysis of gene expression requires reference genes that do not alter expression levels under the conditions being analyzed, such that the data associated with genes of interest may be normalized. It is a daunting task to identify reference genes, whose expression does not change under all experimental conditions being analyzed. Physiological conditions, experimental treatments, tissue and/or organ specificity, as well as developmental stages can alter the expression of genes, which have been previous reported as reference genes in other experimental conditions. In order to study gene expression during peach fruit development, we have analyzed the expression of genes that have been reported previously as reference genes in peach. However, under our experimental conditions, many of these genes did not demonstrate expression stability under all stages and/or treatments being analyzed. For this reason, we used a bioinformatic approach in order to identify potential peach candidate reference genes during peach fruit development. We analyzed published microarray data as well as our RNA-Seq database for genes that maintained a stable expression level. These analyses revealed 266 candidate reference genes that maintained stable expression levels in the microarray analyses. Of these candidate reference genes, only 11 candidates showed a stable expression level in RNA-Seq analysis in all stages of peach fruit developmental. Four of these candidate reference genes were selected for quantitative PCR confirmation. Primer-pairs for each candidate reference gene were used to optimize quantitative PCR conditions. Quantitative PCR analyses using two of these candidate reference genes, have confirmed that they are expressed stably during peach fruit development, thereby validating our bioinformatic approach.

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PS69

FIELD-DROUGHT RESPONSES OF FIVE NATURALIZED GRAPEVINE GENOTYPES (*Vitis vinifera*) AS TOLERANT ROOTSTOCKS FOR NORTHERN CHILE

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One of the main problems that affect grapevine productivity is seasonal drought occurring in most of the world's producing regions, a situation that is worsen in arid and semiarid regions, which have experienced severe declines in rainfall. The aim was to analyze morpho-physiological responses of grapevine genotypes exposed to water stress and to determine their tolerance for developing tolerant rootstocks. Plant architectural traits and gene expression were evaluated in genotypes G25 and G32 (Copiapó valley); G57, G65 and G70 (Huasco valley), from the latitudinal gradient collection "GermoVidNor" (18 ° SL to 32 ° SL). Plant materials were evaluated in a complete random block design, with five replicates and two treatments: moderate stress (50% of control irrigation) and severe stress (25% of control irrigation), including a control treatment using full commercial irrigation. All treatments were evaluated at field conditions in Experimental Station INIA Vicuña. To evaluate the effects of treatments on plant architecture, shoot growth and size, cluster weight and number, and pruning weight, measurements were performed throughout 2013/2014 season. Furthermore, using composite samples, gene expression of target genes related to adaptive responses and effectors for hormones such as aquaporins, proline, glutamate, auxin and ABA were measured by RT-qPCR. Significant differences were obtained at both genotype and treatments levels. Interestingly, there was no significant difference between control and moderate stress. Among genotypes, G65 displayed the best performance in severe stress, with greater vigor and yield; this was correlated with up-regulation of *VvNaC1, APETALA2,* and *Auxin induced-regulated-responsive-activated* (VIT_19s0014g03130) genes. Genotype G70 also exhibited good responses, but up-regulating others genes, including *TIP2.1* (aquaporin) and *NCED1* (ABA biosynthesis) genes. Following this combined approach, we will select best genotypes at field conditions to fully exploit their potential as rootstocks for arid and semiarid regions, as well as emphasizing the fundamental role of exploring the grapevine genetic variability.

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PS70

SALICYLIC ACID PROMOTES AN ADAPTIVE RESPONSE TO SALT STRESS THROUGH THE INTERACTION BETWEEN NPR1 AND bZIP17.

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In response to salt stress, bZIP17, a membrane-associated transcription factor that reside in the endoplasmic reticulum (ER) is activated by intramembrane proteolysis catalyzed by site-1 protease (S1P) and site-2 protease (S2P). The N-terminal bZIP component (bZIP17ΔC) is translocated to the nucleus, where it activates the expression of salt stress response genes. bZIP17 is homologous to the tobacco transcription factor TGA1b, which interact with the transcriptional coactivator NPR1. NPR1 is the master regulator of salicylic acid (SA) signaling pathways during the establishment of plant defense response. Upon pathogen infection, SA triggers a biphasic redox change in the cytosol that allows NPR1 to translocate to the nucleus, where it mediates the expression of SA-responsive genes. In this work we found that low concentrations of SA promote the maintenance of membrane fluidity, seeds germination and chlorophyll contend in Col-0 plants treated with 100mM NaCl. In contrast, the protective effect of SA under salt stress conditions disappears in *bzip17* and *npr1* mutants. Furthermore, using qRT-PCR we found that induction levels of salt stress response genes in both mutants decreased after salt treatment suggesting that NPR1 and bZIP17 are required for the transcriptional regulation of salt stress response genes during salt treatment. Additionally, Bimolecular Fluorescence Complementation (BiFC) assays in Tobacco leaves reveal that NPR1 interacts with bZIP17ΔC. Taken together, our results suggest that SA promotes an adaptive response to salt stress in *A. thaliana* through the interaction between NPR1 and bZIP17, which modulate the expression of salt stress response genes to increase the probability of plant population adapts to unfavorable conditions such as salinity.

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PS71

FUNCTIONAL ANALYSIS OF LIPID TRANSFER PROTEIN (nsLTPs) IN *Solanum* SPP.

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The plant cuticle is a hydrophobic extracellular layer covering the aerial organs of plants, providing protection against desiccation and environmental stress. The cuticle's protective capacity is based on the physical and biochemical properties of the two main components, cutin and waxes. Nowadays, lipid biosynthesis enzymes and several lipid transporters have been identified and characterized; however, the process of intra and extracellular trafficking remains entirely unclear. Nonetheless, the lipid transfer proteins (nsLTPs) have been proposed to transport compounds from the endoplasmic reticulum to the plasma membrane and then to the apoplast. In Arabidopsis it has been probed that mutants for LTPG1, showed a 25% of reduction in waxes deposition and levels of alkanes were diminished. In order to study these proteins, we initially used as model tomato fruit, where the cuticle plays an important role in the integrity of the market value of this vegetable. We identified two genes coding for LTPG that were overexpressed in tomato fruit peels. qRT-PCR analysis showed different levels of expression during the development of tomato fruits, suggesting a putative role in peel development during the growth of tomato fruit. We identified and lined all the tomato nsLTPs based on its genome and were grouped into clades. Also we compared to others *LTP* genes previously described in other species such as *Arabidopsis thaliana*. Additionally, genes coding for *nsLTPs* were selected from RNAseq datasets obtained from leaves of *S. peruvianum*, *S. chilense* and *S. lycopersicum* var. Money Maker under normal conditions and water stress. These results were contrasted and compared for previously genes found in fruits. From these trials, insertion mutant plants were generated in var. Money Maker, for two of the most important *nsLTPs*.

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PS72

DETERMINATION OF ANTHOCYANIN PRODUCTION IN RESPONSE TO RADIATION AND DROUGHT ON *Solanum peruvianum*

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Anthocyanins are plant pigments synthetized in leaves, flowers, fruits, stems and roots. In photosynthetic tissues they participate in protection from the photo-inhibition induced by high light and UV radiation. Also, the addition of others stresses, such as cold or drought can enhance the production of anthocyanin. *Solanum peruvianum* fruits are green and they have not capacity to accumulate carotenoids. However, in late development states, these fruits accumulate naturally anthocyanins in the peel. Synthesis regulation of this pigment in wild tomato is unknown and propose interesting prospect to breeding uses in cultivated tomato. Previously studies realized in us laboratory included the expression analysis of genes *DFR*, *5GT* and *ANT1* that encode for dihydroflavonolreductase, glycosyltransferase and the transcription factor Anthocyanin 2, respectively. These genes, related with anthocyanin biosynthesis pathway and regulation were overexpressed by drought and high radiation in *Solanum peruvianum* genotypes. From this preliminary study we selected a particular genotype characterized by larger fruit and high level of anthocyanin accumulation. In order to quantify anthocyanin and regulation of gene expression for *DFR*, *5GT* and *ANT1* by different environmental conditions we established an experiment that consisted in treatments of drought and UV radiation. For the last, we separate in 3 different treatments: greenhouse, field and artificial light plus UV-B. The results show a relation of drought and UV radiation in the regulation of these genes and the timing for anthocyanin accumulation. The details are discussed in this research.

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PS73

FUNCTIONAL ANALYSIS OF *Vitis vinifera AGAMOUS-like 11* IN FLOWER AND BERRY DEVELOPMENT IN TOMATO

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Previous work enabled us to identify and propose *Vitis vinifera AGL11* (*VvAGL11*) as the best candidate gene responsible of the genetic control of seedlessness in grapevine. *VvAGL11* is a transcription factor that belongs to the MADS-box family of genes and, besides its role in seedlessness, it appears to affect berry size, firmness and harvest date; as well as flower organs, ovule and berry development. It is not clear if *VvAGL11* affects these traits directly or through the pleiotropic effect mediated by hormones produced by the seed. With the purpose to further characterize the functionality of *VvAGL11*, we introduced *VvAGL11* in wild type tomatoes and in genotypes where endogenous gene *Solanum lycopersicum AGL11 (SlAGL11)* was knocked down. Expression of *VvAGL11* in wild type tomato (cv Micro-Tom) under control of CaMV 35S promoter has shown significant changes in flower morphology and development. Some transgenic lines present a large number of reproductive structures, changes in sepal morphology, overdeveloped stigma at early stages of flower development and coiled petals. A co-transformation experiment, designed to evaluate the function of *VvAGL11* without the effects of the endogenous gene *SlAGL11* in tomato, is in course and will provide additional supporting evidence for the putative role of *VvAGL11* in flower, berry, ovule and seed development. The role of *AGL11* in ovule development seems to be conserved across flowering plants, however, specific functions might have evolved in different crop species and its characterization may help to improve quality traits of agronomical interest.

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PS74

DETERMINATION OF THE ANTIOXIDANT EFFECT OF THE LICHENS *Pseudocyphellaria dissimilis* (NYL.) D. GALLOWAY & P. JAMES AND *Flavoparmelia caperata* (L.) HALE.

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The lichens are organisms that present symbiotic association that involves at least one fungus who protects it from excessive radiation and an algae or *cyanobacterium* that performs photosynthesis. They are known as the living beings best adapted of the land because they support extreme unfavorable conditions. In this way, they produce a great variety of secondary metabolites that guard the liquens of oxidation caused for free radicals and also they are used widely in biologic actions such as antifungal, antimicrobials, among others. In this research we compared the antioxidant activity between two foliose species of lichens, *Pseudocyphellaria dissimilis* and *Flavoparmelia caperata* that compete by a same ecological niche. Thin layer chromatography was performed, where it was possible determine that these species present differences in their chemical composition, and also an analysis of polyphenols by means of the technician of Folin-Ciocalteau. Furthermore, it was measured the antioxidant capacity through tests with free radicals 1,1-diphenyl-2-picryl-hidrazyl ($DPPH^{\cdot}$) and 2,2'-azinobis (3-ethylbenzothiazoline)-6-sulfonic acid ($ABTS^{\cdot+}$). The IC_{50} corresponds to the concentration of necessary extract to produce 50% of decrease of the absorbance of both radicals. The value IC_{50}, in the methanolic extract of *P. dissimilis* was of 0,094 mg/mL, obtained by means of DPPH and of 0,360 mg/mL, obtained by means of $ABTS^{+}$. Whereas for the methanolic extract of *F. caperata,* the values of IC_{50} were of 0,214 mg/mL and 0,108 mg/mL through $DPPH^{\cdot}$ and $ABTS^{+}$, respectively. Both lichen extracts have antioxidant capacity, presenting a potential for further studies of secondary metabolites and antioxidant enzymes.

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PS75

MODULATION OF ETHYLENE ON METABOLIC AND GENETIC CHANGES OF FLAVOR-RELATED COMPOUNDS IN AVOCADO CV. HASS.

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One of the most important quality traits in avocado is flavor, which is defined by a combination of compounds including sugars, organic acids, volatile compounds and fatty acids. In some climacteric fruits, production of determined flavour-associated metabolites, and the expression of genes involved with synthesis and degradation, are modulated by ethylene; however, this situation remains unknown for avocado. The goal of this study was to characterize the variation in these flavour-associated metabolites in avocado cv. Hass, and the differences in expression profile of some genes involved specifically with volatile compounds biosynthesis. This study was performed by considering both the effect of temperature and the ethylene inhibition/stimulation response. Avocados with 11% of oil content were harvested and stored at 5ºC for 30 days and then were ripen at 20ºC up to reach the ready to eat stage. Ethylene inhibition was performed by applying 300 nLL^{-1} of 1-MCP, while stimulation was performed with 100 uLL^{-1} ethylene. Results showed that hexanal was the predominant volatile compound, which decreased its concentration when fruits were treated with 1-MCP. Genes of lipoxygenase and alcohol dehydrogenase showed ethylene response, but this one was dependent on stage of maturity/ripening. The main sugars were mannoheptulose and perseitol, while the organic acids with the greatest concentration were malic and citric acid. Both sugars and organic acids were not affected by stimulation or inhibition of ethylene, obtaining the same final concentration in both non-treated and treated fruits. We are currently studying the effects of ethylene on aldehyde synthesis and other important groups involved in defining aroma.

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PS76

ROLE OF ETHYLENE DURING DROUGHT STRESS IN *Solanum lycopersicum L.* AND *Solanum peruvianum L.*

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Tomato (*Solanum lycopersicum* L.) is one of the most important and consumed vegetable in the world. Different stress conditions affect their productivity, between them, drought is the most relevant. Some wild tomato species are adapted to desert habitat and possess specific mechanisms to tolerate water deficit. Ethylene has been described as a hormone involved in acclimation to drought in plants and also in induction of morphological changes of aerial organs in *A. thaliana*. In this research, we explored the effect of ethylene in leaf development and the expression of genes coding for several ERF transcription factors in plants of *S.peruvianum* and *S. lycopersicum*. To respond to this aim we performed treatments with Etherfon 400mM (chemical that release ethylene) or PEG8000 3% and 5% under hydroponic condition. Treatments with Etherfon produced a deformity of the apical buds in both species, suggesting a toxical effect of the product under this concentration. Treatment with PEG8000 showed a medium reduction of foliar area after 15 days in both species and was proportionally to the level of stress (considering 3% and 5% PEG). Also we measured the water consume in both treatments. Drought stress treatment induced a reduction of water use, while Etherfon did not show to induce any change compared with the control. These results suggest that ethylene has no effect on water consumption levels in both tomato species, but could be involved in plant growth height.

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PS77

REGENERATION AND MICROPROPAGATION OF *Jatropha curcas IN VITRO* PLANTS THROUGH DIRECT AND INDIRECT ORGANOGENESIS

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Jatropha curcas is an important oilseed crop, used for the production of second-generation biodiesel. Its low adaptability to climatic conditions present in Chile has led to the development of technologies for the production of hybrid varieties with productive and commercial interest. The totipotency of plant cells to regenerate whole plants, has positioned the *in vitro* culture techniques of plants as the main tool in the development of technologies for obtaining plants in short-time together with the preservation of the genetic identity. The objective of the present work was developing protocols for the *in vitro* plant regeneration of *Jatropha curcas.* Two methodologies were established; 1) direct organogenesis: multiplication of axillary shoots from nodal segments established in Murashige-Skoog (MS), Woody-Plant-Medium (WPM) and Gamborg-B5 basal mediums, supplemented with kinetin (Kn), 6-*benzylaminopurine (BA), indole*-3-butyric *acid* (IBA), gibberellic *acid (*GA_3*)* and hemisulfate adenine; 2) indirect organogenesis: adventitious shoots regeneration from callus formed from explants of young and mature leaves, established in MS and Gamborg-B5 basal mediums, with different concentrations and combinations of 1-naphthaleneacetic acid *(*NAA), 2,4-dichlorophenoxyacetic acid (2,4-D), IBA, BA and Kn. The best medium for multiplication and development of axillary shoots in nodal explants was MS containing 1.0 mg/L Kn, 0.5 mg/L BA, 1.5 mg/L IBA, 0.5 mg/L GA_3 and 80 mg/L adenine hemisulfate, being obtained in average 4.03 shoots per explant and an average height of 3.2 cm of length. Morphogenetic callus were obtained from young leaf explants in MS medium, with combinations 1.0 – 2.0 mg/L NAA and 5.0 – 1.0 mg/L BA, respectively. The best medium for the regeneration of shoots from callus obtained was MS containing 0.25 – 0.5 mg/L IBA in combination with 1.0 mg/L BA, initially obtaining nodular structures, which then differentiate in shoots. Nowadays, elongation and rooting of shoots obtained by both organogenic pathways are being evaluated.

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PS78

FT-IR MICROSPECTROSCOPY AND MULTIVARIATE ANALYSIS IN *Eucalyptus nitens* CUTICLE AND EXPRESSION *ABCC2* AND *KCS10* GENES IN RESPONSE TO COLD ACCLIMATION

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Most plants can acquire freezing tolerance if they are previously exposed to cold temperature, but nonfreezing, a phenomenon known as cold acclimation. *Eucalyptus nitens* shows tolerance to cold temperatures, allowing its establishment in areas where other species have growth limitations like *Eucalyptus globulus.* However, the mechanisms involved in cold-acclimation are not well known. *Eucalyptus* species have a hydrophobic layer, which gives a glaucous appearance to leaves and is known to play an important role in protecting aerial organs to the effects of environmental stress. In this work, the main functional groups deposited on the leaf cuticle of *E. nitens* in response to cold acclimation by FTIR microspectroscopy and multivariate analysis were identified. Additionally, the expression of *KCS10* and *ABCC2,* genes participating in the biosynthesis of the cuticle were assessed. A cold chamber assay was established to acclimate young plants from four different families (F1-F4) of *E. nitens*, under the following conditions: non-acclimated (NA, 12/20 °C day/night), cold acclimated to non-freezing temperature (CAC, 4/8 °C day/night), acclimated to freezing temperature (CAF, 6/12 °C day/night), and de-acclimated (DA, 6/12 °C day/night). A night frost of -6 °C during DA was applied to determine survival and damage percentage for each family to assess their frost tolerance. Leaves from three plants per family at NA and CAF were collected. FTIR analysis was applied in different areas of the leaf, without sample preparation. The results showed that family F1 was the most sensitive and F2 the most tolerant. The principal component analysis showed the presence of fatty acids, esters cutin and polysaccharides compounds in the lamina of leaves at CAF condition. *KCS10* gene expression showed significant differences in the transcript accumulation only. Accordingly, content of fatty acids and *KCS10* contributed to the tolerance of *E. nitens* to low temperature.

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PS79

MOLECULAR DYNAMICS SIMULATIONS OF LEA TYPE PROTEINS OF *Arabidopsis thaliana* DURING CELLULAR DEHYDRATION

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Cold has a major influence on plant growth. Considerable effort has, therefore, been directed towards understanding how plants adapt to low temperature. However, freezing damage is not a consequence of low temperatures, but rather the result of cellular dehydration generated by extracellular ice crystallization. Genetic approaches have defined some of the key regulatory components of cold acclimation in *Arabidopsis thaliana*. A central role is played by the *C-repeat binding factors (CBF)*. These transcription factors are rapidly induced in response to cold and in turn activate the expression of a set of target genes including a number of COR/LEA (Late Embryogenesis Abundant) protein-encoding genes. COR/LEA proteins play a crucial role by improving cell resistance during cellular dehydration. According to experimental evidence, COR/LEA proteins are intrinsically disordered proteins (IDP) on water, but can acquire secondary structure during cellular dehydration. Based on Circular Dichroism (CD) spectroscopy analysis, it has been seen that the proteins COR15A (At2g42540) and COR15B (At2g42530) of *Arabidopsis thaliana* on solvent are mostly unstructured, but after dehydration the unstructured content decreased significantly, acquiring secondary structure (mostly α-helix) during cellular dehydration. On that concern, we aim to explain the structural changes of both COR15 proteins during cellular dehydration by performing *all-atom* molecular dynamics (MD) simulations on glycerol-water mixtures solvents in order to represent the peculiar behavior of these proteins in response to water loose. Accordantly to our MD simulations, both COR15 proteins are largely unstructured in a fully hydrated state and gradually folded into a hairpin-like, double-bundled, α-helical conformation with the loss of water molecules as the experimental data suggested. This behavior can be explained by the fact that glycerol molecules stabilize the COR15 proteins by compacting its movement and reducing protein flexibility during the MD simulations, concluding that our theoretical approach was able to predict what occurs in nature.

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PS80

TRANSCRIPTOME-BASED METABOLIC PATHWAY DATABASES TO DISSECT MOLECULAR MECHANISMS IMPLICATED IN ADAPTATION TO EXTREME ARID CONDITIONS IN ATACAMA DESERT FLORA.

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The arable land desertification in this century has been increasing. In parallel, an explosive rise in the world population over the next 50 years has been predicted. This scenario implies the need to improve plant productivity in arid soils, where water and nutrients are scarce, and temperatures are often high, all factors that have a significant impact on plant productivity. The Atacama Desert, the oldest and most arid desert in the world, is an attractive reservoir of species that can become excellent models for studying the molecular level response of plants to aridity. We have characterized and collected samples from sixty three Atacama Desert plant species. Subsets of fourteen species have had the transcriptome sequenced using Illumina technology. Metabolic pathways databases for these fourteen species were generated using Pathway_Tools software v18.0. Here we show the results from our initial evaluation of these fourteen databases in order to identify biochemical mechanisms that could allow these plants to survive the extreme arid conditions of their natural environment.

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PS81

TRANSFERABILITY OF SSR MARKERS FROM *Fragaria x ananassa* TO *Fragaria chiloensis*

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Codominant microsatellite markers have been widely used in the *Fragaria* genus, for different studies. The ease to identify homologous Simple Sequence Repeats (SSR) between related species or genera is a powerful tool to develop markers for using them on unstudied species. *F. chiloensis* is a close relative to *F.* x *ananassa*, and there are just a few genetic studies in the species. In order to transfer markers from *F.* x *ananassa* to *F. chiloensis*, 10 landraces were selected to test 95 SSR markers that have been previously described in the commercial strawberry. A successful transferability was achieved since markers can be amplified through PCR in at least six out of 10 landraces, with good band intensities and a similar size to the reported in the donor species. PCR products were assessed through electrophoresis in 3% agarose gel. Seventy-eight out of 95 markers were successfully transferred. Finally, 39 polymorphic markers were selected for further assessment on capillary electrophoresis in order to determine the exact size of the fragments.

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PS82

IDENTIFICATION OF HOUSEKEEPING GENES FOR GENE EXPRESSION STUDIES IN ROOTS OF *Prunus sp*. USING RT-qPCR.

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RT-qPCR is the technique most used for detecting and quantification of mRNA transcription due to its high sensitivity, specificity, and reproducibility. In studies of gene expression, many experimental variations should be taken into account, such as quality and amount of starting material, presence of inhibitors in sample materials, primer design, RNA extraction and enzymatic efficiencies, among others. Therefore, selection of a suitable normalization strategy is important for the acquisition of biological meaningful data. Among several methods proposed, the housekeeping, reference or constitutive genes are the most frequently used to normalize RT-qPCR data and to control the experimental possible errors generated in the quantification of gene expressions, since the reference genes are exposed to the same preparation steps as the gene of interest. There are not universal reference gene for all the assays, genotypes and tissues. Thus, the identification of reliable reference gene(s) is an important criterion for the interpretation of data generated by qPCR. Our study was conducted to identify suitable reference gene(s) for normalization of gene expression studies in different genotypes of *Prunus sp*. The information of putative housekeeping genes were generated from a previous RNA-seq experiment from roots of the rootstocks Mariana 2624 (*P. cerasifera* Ehrh x *P. munsoniana* W. Wight & Hedrick) and Mazzard F-12 (*P. avium* L.). These housekeeping genes will be validated with samples of *Prunus sp*. from different tissues and stress treatments such as drought, salinity and nutrient deficiency.

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PS83

ALTERING THE *AtA6PR1* CONTENT AFFECTS THE GROWTH OF *Arabidopsis thaliana*

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In most plant species, the primary photosynthate is sucrose, which is translocated through the phloem from source to sink organs. However, in several plant families (including Rosaceae and Plantaginaceae), polyols such as sorbitol and mannitol are the predominant photosynthates translocated. The presence of polyols in these families has various advantages related to the tolerance to abiotic stress. For this reason, plants such as tobacco, persimmon and wheat have been engineered to synthesise and accumulate polyols. Once transformed, accumulation of sorbitol or mannitol provided greater protection against salt stress, but was accompanied by changes in the levels of soluble sugars (sucrose, glucose and fructose), and a harmful effect on the growth of some transformants (dwarfism and various types of lesions), related to a high accumulation of the polyols and an inability to degrade them. *Arabidopsis thaliana* has the enzymes necessary for the synthesis (aldose-6-phosphate reductase, AtA6PR) and degradation of sorbitol (sorbitol dehydrogenase, AtSDH). High concentrations of this polyol in this species have not been reported, and its main photosynthate is sucrose, which makes it ideal for studying the effect of an accumulation of sorbitol in the plant. Wild-type and *atsdh-* mutants were transformed with the cDNA of FLAG-AtA6PR1. Different behaviours between the transformed lines were obtained; exogenous and native *AtA6PR1* accumulation was detected in some, but not all plants, suggesting that some were silenced. However, in lines where high presence of the protein was detected, a delay in growth relative to control plants transformed with the empty vector was evident. These results are correlated with, but do not completely explain, a significant decrease in the levels of sucrose. Subsequent studies evaluating concentrations of sorbitol, starch, myo-inositol and other metabolites will enable us to fully elucidate the effect of the over-accumulation of *A6PR1* in *Arabidopsis*.

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PS84

TRANSCRIPTIONAL CONTROL OF FOUR POLLEN SPECIFIC KINASES DURING LATE POLLEN DEVELOPMENT AND POLLEN TUBE GROWTH.

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In most land plants successful reproduction relies on the correct growth and development of a pollen tube through the female reproductive tissues. This process requires the correct temporal and spatial expression of gene subsets specifically dedicated to this feature, from sensing the receptive stigma, grow and guidance of the pollen tube to the release of the sperm cells in the embryo sac. Several pollen specific genes have been characterized and even though their promoters confer pollen specific transcription in different plant species, there isn't a comprehensive transcriptional mechanism yet reported that regulate this process. Using the available transcriptomic datasets, we selected four *Arabidopsis* pollen specific genes coding for putative receptor like cytoplasmic kinases proteins named *PSK* (for *POLLEN SPECIFIC KINASES1-4*), which transcripts accumulate during the final stages of pollen development and/or during pollen tube growth. To characterize the transcriptional regulation involved in the pollen specific expression of *PSK*s, we cloned their full intergenic upstream region and also 5' deletions of these promoter regions to the *uidA* gene. We identified relevant *cis*-elements based on GUS activity in Arabidopsis transgenic lines. On the other hand, we identified *GT-4* gene as a putative positive regulator of pollen specific transcription, and RBP31 as a transcriptional repressor candidate of pollen specific genes in sporophytic tissues. Analyzing the expression profiles of PSK genes in RBP31 T-DNA mutant lines we have found ectopic expression of these pollen specific kinases in sporophytic tissues, suggesting that RBP31 has a role in the negative regulation of pollen specific genes in sporophytic tissues.

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PS85

SUBCELLULAR LOCALIZATION OF POLLEN SPECIFIC KINASES PSK1-4 IN *Arabidopsis thaliana*

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In our laboratory we have identified 4 genes encoding kinase proteins (*PSK1-4*) that are expressed exclusively during late pollen development. In order to get more information regarding the physiological relevance of these proteinswe decide to analyze the sub-cellular localization of the encoded proteins. According to previous bioinformatics analysis, based on amino acid sequences, PSK1 (At2g41979) and PSK3 (At5g26150) would be found in the cytoplasm, while PSK2 (At5g18910) and PSK4 (At5g12000) in the nucleus. To experimentally verify this data, we generated translational fusions of the PSKs ORF to GFP under control of three different promoters: the pollen specific promoter *LeLAT52,* the native promoter of each *PSK* or the constitutive promoter 35S. Once obtained the constructions, wild type *Arabidopsis thaliana* plants were stably transformed by floral dip method (*LeLAT52* and endogenous promoters) and tobacco leaves (35S promoter) were transiently transformed by agroinfiltration, for subsequent analysis of GFP fluorescence using confocal microscopy. Preliminary analyzes in tobacco leaves indicate that PSK1 would be located in the cell wall, PSK2 in the nucleus, PSK3 in the plasma membrane and PSK4 in plasmodesmatas. Analyses in the pollen tube suggest that PSK2 is localized in the nucleus of the vegetative cell –according to the heterologous expression analysis observed in tobacco leaves– but also is detected in the tip of pollen tube. Taking into account that mutants in PSK2 display abnormal phenotypes in pollen tube guidance this tip localization of PSK2 could be important for their biological role.

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PS86

FUNCTIONAL ANALYSIS OF THE POLLEN SPECIFIC GENES *PSK1* AND *PSK2* USING ARTIFICIAL MICRORNAS IN *Arabidopsis thaliana*

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In flowering plants, mature and dehydrated pollen grains are released from the anthers to the surface of a receptive stigma, where it is rehydrated and germinates to form a pollen tube. It has been shown that alterations in the development of the pollen tube can significantly affect the fertility of plants. Based on transcriptome analyses, we identified four genes encoding protein kinases (*POLLEN SPECIFIC KINASE 1-4*). These genes are specifically expressed during the last stages of pollen development but their physiological role remains elusive. One way to characterize these genes is by means of post-transcriptional silencing via artificial microRNAs (amiRNAs). The amiRNAs can silence genes of interest in plants and have been used in functional analyses of genes in Arabidopsis and *Oryza sativa*, among other plants. amiRNAs were designed for *PSK1* and *PSK2* genes, commanded by a pollen-specific promoter (*LeLAT52*). Transgenic lines silenced in *PSK1* showed lower pollen viability compared to wild type plants and very low germination rate *in vitro*, which is reflected in a decrease in their seed set. For *PSK2* we also detected lower pollen viability; however, we did not detected alterations in pollen germination and tube growth*invitro*. Our results suggest that both genes are required for pollen viability in Arabidopsis

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PS87

GENETIC DIVERSITY IN *Gaultheria pumila*, (L.F.) D.J. MIDDLETON (ERICACEAE) THROUGH INTER SIMPLE SEQUENCE REPEAT (ISSR)

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Gaultheria pumila is a native Chilean species from the Ericaceae family, commonly known as Chaura. It grows as a low bush that can reach up to 80 cm height, depending on the environmental conditions. Its distribution ranges from Metropolitana to Magallanes regions. Descriptions mostly note the fruit morphometric characteristics, such as their color (red, pink and white) as well as for different shapes and diameters. Besides, this species grows even under extreme temperature and soil conditions. *G. pumila* accessions show a variable phytochemical composition, even among individuals from the same population. Such variation could indicate the potentiality of using this species as a commercial plant. Inter-simple sequence repeats (ISSR) have been proven as a useful tool for studying genetic diversity in a wide range of species. The objective is therefore to use ISSR'smarkers to assess rapidlythe genetic diversity and structure of the species.For this study 6 ISSR markers in 15 populations, comprising some 501 entries were used. 61% of the genetic variability was detected within populations and 39 % between populations, according *GenAlex* software. Within the 15 populations, 74% of the loci were polymorphic.

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PS88

EXPRESSION PATTERN OF GENE INVOLVED IN ABA BIOSYNTHESIS IN TWO *PRUNUS* ROOTSTOCKS UNDER WATERLOGGING STRESS.

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In heavy soils, poor aeration in the rhizosphere is an important problem for the cultivation of *Prunus* species. In these soils, heavy rain or excessive irrigation can cause waterlogging and root hypoxia. In fruit trees, the tolerance to oxygen deficiency in roots is mediated by the characteristics of the rootstock. *Prunus* rootstocks are classified as hypoxia-sensitive, although differences among genotypes have been reported. An early physiological response to soil waterlogging is reduction of root permeability. Aquaporins play a key role in root water uptake capacity, which would provide a molecular basis for fast and reversible regulation of transmembrane water transport. Under abiotic stress, plant hormones play a crucial role in the whole plant responses. Abscisic acid (ABA) is the most important hormoneinvolve in the plant responses to abiotic stresses, among them, root permeability. Exogenous ABA alters the expression pattern of different aquaporins genes. We evaluated the expression pattern of six key genes involved in ABA biosynthesis and three ABA signaling downstream markergenesin two *Prunus* rootstocks with contrasting responses to waterlogging stress. qPCR analyses evidenced differences in the transcript levels of these genesbetween both genotypes under waterlogging stress. These results provide new information about ABA role in *Prunus* rootstocks response under hypoxic stress.

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PS89

MECHANISMS ASSOCIATED TO DROUGHT TOLERANCE IN THREE LOWLAND QUINOA GENOTYPES.

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Drought is one of the most important abiotic stress producing economiclosses and social disasters. One of the biggest challengesfor this decade is to found new crops highly droughttolerant to ensure the world's food. Quinoa (*Chenopodium quinoa*) is atraditional Andean crop with abalance content of aminoacids and high level of drought tolerance. In Chile, genetic characterizations have allowed the grouping ofdifferent genotypes into two broad ecotypes: Salaresand lowlands. In Central Chile, lowlands genotypes present high yields, even under extreme drought conditions. Nevertheless, poor information is known about the mechanisms involved. In order to have a better understanding of the mechanisms involved, threelowlands genotypes from central (Faro and UDEC) and south of Chile (B078) were exposed, for three weeks,to a 30% of water restriction treatment during the grain filling period. Physiological performance, including chlorophyll content, PSII performance through chlorophyll *a* fluorescence and relative water content (RWC), were assessed. Chlorophyll *a* and *b* content tended to decrease in Faro and UDEC9, but it was maintained in BO78. These chlorophyll changes in Faro and UDEC9 were related to a decrease on PSII efficiency and to an increase on non-photochemical energy dissipation along the stressing time. In contrast, BO78 tended to maintain the photochemical process without changes in non-photochemical energy dissipation, with the highest RWC throughout the treatment. These preliminary results show the differential mechanisms used by these lowlands genotypes to cope with drought stress. Nevertheless, relationships between the physiological traits and crop productivity are necessary for a deep understanding of the performance of these genotypes under drought conditions.

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PS90

ANALYSIS OF TRANSCRIPTION FACTORS IN EARLY STAGES OF BERRY AND SEED DEVELOPMENT IN GRAPEVINE

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Grapevine is one of the most economically important horticultural crops worldwide. One of the most desirable features in the berries used for the consumption of table grapes is seedlessness. In nature, seedless berries may develop due to parthenocarpy or stenoespermocarpy mechanisms generating berries without seeds or with rudimentary seeds, respectively. Despite considerable efforts to understand the molecular basis of seedlessness, the phenomenon is not completely understood in grapevine. Previous studies developed in our laboratory focused on analyzing the segregating plants from a cross between a seeded maternal line and seedless paternal line. The progeny showed phenotypes of normal seeds and seedless berries, which were used to assess global gene expression in early stages of fruit development, using the *Vitis vinifera Genechip* ® from Affymetrix. From this analysis, we found new candidate genes whose expression changes could be responsible for the seedlessness phenotype. Candidate genes are putative transcription factors such as *VvAIL5*, *VvAGL6*, *VvERF19* and transcriptional co-repressors like *VvLUG3* and *VvLUG7*. The aim of this study is to evaluate the expression profiles of some of the transcription factors found in the Affymetrix microarray analysis in early stages of berry development. For this, seeded and seedless plants of the last season were used, in stages of closed flower, open flower and fruit set and expression analysis of these genes were performed using real time PCR. Subsequently, tissue specific gene expression will be determined using *in situ hybridization* and the function of these genes during seed development will be evaluated by transformation of model plants. Thus, this investigation will contribute to elucidate part of the complex mechanism of seedlessness in grapevine.

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PS91

STUDYING THE SNAREs GENE EXPRESSION IN PHOTOMIXOTROPHIC CULTURES OF POPLAR AND RASPBERRY UNDER OXIDATIVE STRESS

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Both the phenylpropanoids and products of peroxidation reactions (oxidative burst) comprise signal molecules, which induce the plant defense mechanisms, even though other functions/applications could be shortly identified. In this context, to understand the transport cell mechanisms for plant metabolites remains a crucial task for biotechnologists. To increase the basic knowledge, differential expression of gene related to transport (SNAREs), photosynthesis, phenylpropanoids, and the oxidative burst has been studied in photomixotropic TIBs cultures of poplar (*Populus spp*) and raspberry (*Rubus spp*) treated with H_2O_2. As novelty, during 30 days the differential gene expression for *SYP111*, *SYP121*, *SYp125* and *SYP131* was revealed in H_2O_2-stressed plants. Specific role associated to an increase of metabolites releasing in stressed plants to the oxidative burst was evidenced for genes *SPY121*, *SPY125* and *SPY131*. The expression increase of *SYP111* and *SYP121* may be also related to TIBs culture, which enhanced the whole plant functioning including the production of phenylpropanoid metabolites. Results also corroborated the effect of TIBs cultures to improve the physiological machinery, in this case, through the increased activity of photosynthesis and phenylpropanoids paths. Additionally, in the sucrose-reduced treatments a consistent photomixotrophic stage has been evidenced in parallel with an augment in both PAL and RUBISCO activities; in the meantime, a significant increase of *SOD* transcripts was determined in plants treated with H_2O_2.

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PS92

QUANTITATIVE DETERMINATION OF EXTRACELLULAR AND INTRACELLULAR PROTEIC POLYSACCHARIDES COMPLEXES IN MYCELIAL BIOMASS OF EDIBLE FUNGI

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Edible fungi are widely consumed due to their good flavor, aroma, and texture. However, their potential as functional food with nutritious and medicinal properties is largely understudied. It has been shown that fungal compounds can positively or negatively modulate the biological response of immune cells. These compounds are mainly carbohydrates, usually polysaccharides or glycoproteins, constituting 50-90% of the dry weight of the carpophore. We isolated and mass-produced mycelia of *Agaricus bisporus, Lentinus edodes*, and *Pleurotus ostreatus* in EMA (enriched malt extract) and PDA (potato-agar-dextrose) media under controlled laboratory conditions. We obtained mycelia biomass that when treated with distilled water at 90°C and ethanol precipitated extra- and intracellular proteic polysaccharides (EPS and IPS respectively). These polysaccharides were quantified in a spectrophotometer at 490 nm using the phenol-sulphuric acid method, with D-glucose as standard. For all species EPS and IPS weight were greater in PDA compared to EMA. We recovered the highest levels of EPS and IPS in *A. bisporus* biomass compared to the other two edible fungi. In *P. ostreatus* we found 4.3 and 1.8 mg of glucose per g of polysaccharide in PDA and EMA respectively. In *L. edodes* had 8.2 and 6.9, and *A. bisporus* 4.9 and 6.7 mg of glucose per g of polysaccharide in PDA and EMA, respectively. The quantified glucose contents were not directly proportional to the precipitated EPS and IPS complexes and the total biomass in each studied culture media. Our results allow quantitative comparisons in bioactive polysaccharides with medicinal potential in edible fungal species.

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PS93

PHOTOCHEMICAL AND PHOTOINHIBITION IN RESPONSE TO DIFFERENT TEMPERATURES IN *Colobanthus quitensis* FROM TWO ANTARCTIC POPULATIONS

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The Antarctic Peninsula has one of the fastest warming rates on earth, with increases about 1-2°C per decade. This warming trend is higher in some areas, so its effect on plants can be non-uniform. *Colobanthus quitensis*is the only dicot that has colonized the Antarctic.Sincethe warming isnot uniform, we have assessed the physiological changes in plants from two Antarctic populations. Specifically, changes in the photochemical activity and photoinhibition in response to the temperature increase. Plants from King George Island, near to the Arctowski Station (62° 09' S, 58° 28' W) and Lagotellerie Island (67° 52'S, 68° 42'W) were grown at 5°C (maximum temperature observed during summer in Antarctica) and 16°C (optimal photosynthetic temperature of this species). Independent of the growth temperature, photosynthetic efficiency was higher in plants from the most austral population (Lagotellerie). The same occurred in the electron transportrate (ETR). Thus, these plants conducted a greater proportion of energy through photochemical processes and a lesser extent towards thermal dissipation (NPQ), contrary to what was observed in plants from Arctowski. In both temperatures, plants of both populations showed nophotoinhibition, maintaining anFv/Fm close to 0.8, against different predarkness periods. We conclude that differences in photochemical activity of *C. quitensis*between populations help to cope with different climate conditions within Antarctic.

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PS94

DETERMINATION OF PLOIDY LEVEL AND DNA CONTENT OF DIFFERENT ACCESSIONS OF CHILEAN STRAWBERRY THROUGH FLOW CYTOMETRY

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The Chilean strawberry (*Fragaria chiloensis*) is a cultivated species for indigenous people of Chile since over 1000 years ago. Ecotypes of the species can be found in diverse climatic conditions between latitudes 35º and 45º S. Actually, a germplasm collection of Chilean strawberry from these latitudes is maintained and characterized at University of Concepcion. The aim of this study was to determine the ploidy level and DNA content of different accessions of *F. chiloensis* by mean of flow cytometry using propidium iodide as fluorochrome. Fifty three accessions were evaluated according to the protocol described by Galbraith et al. (1983). Marie buffer (1993) was used, with modifications. *Fragaria vesca*, *Fragaria* x *ananassa* and *Hordeum vulgare* plants were used as control for diploidy, octoploid level, and DNA content, respectively. The results indicate that the most of the accesions are octoploids. However, the MEN accession, Mentue (39°19'50.91"S 71°43'11.49"O) would be a diploid *Fragaria* species probably a wild *F. vesca*.

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PS95

STUDY OF THE ROLE OF At5g11230, A PUTATIVE NUCLEOTIDE SUGAR TRANSPORTER, IN THE SYNTHESIS OF MUCILAGE IN *Arabidopsis thaliana.*

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The cell wall is mainly composed by cellulose, hemicellulose and pectins. Among them, it is known that pectins are composed predominantly by three types: homogalacturonan (HG), rhamnogalacturonan I (RGI) and rhamnogalacturonan II (RGII). The synthesis of pectins occurs in the lumen of the Golgi apparatus and it is mediated by glycosiltransferases that use nucleotide sugar as substrate. These nucleotide sugars are synthesized in the cytosol and should be incorporated into the Golgi lumen and it has been shown that nucleotide sugar transporters (NSTs) perform this function. In *Arabidopsis thaliana* there are approximately 50 NST, however the role that each plays in the biosynthesis of pectin and other cell wall polymers is still under study. At5g11230 codified for a putative nucleotide sugar transporter that is highly expressed in seed coat. Seed coat is a good model because it synthesizes and accumulates a large amount of pectin that forms the mucilage. For this work, knockout lines for At5g11230 were isolated and immunofluorescence techniques were used to analyze the structure of mucilage. By comparing the At5g11230 knock out lines with wild type plants, we were able to determine cell wall epitopes that are affected in this mutant and suggest a role of this NST in pectin biosynthesis.

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PS96

FUNCTIONAL CHARACTERIZATION OF THE BIOSYNTHESIS OF EICOSAPENTAENOIC ACID IN *Nannochloropsis*

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A great deal of interest hasgenerated the long chain polyunsaturated fatty acids (PUFA or omega-3 fatty acids) due to its beneficial characteristics associated to human consumption. Moreover, studies have suggested that humans evolved with an omega-3/omega-6 relation of 1, nevertheless, actual diets have a relation close to 1/15. Human diet obtains omega-3 fatty acids mostly from fish, but overfishing and reduction of natural stocks have raised the number of fish produced through aquaculture. These fish present a low content of omega-3 fatty acids, due to the restrictions of this type of culture. The latter can be explained because fish obtain omega-3 fatty acids from the primary producers, microalgae. But these organisms are poorly present in this type of culture. The industry has adopted the strategy of using 80% of the omega-3 fatty acids in fish feedstock, leaving only 13% for human consumption. Microalgae are natural producers of omega-3 fatty acids, so they represent a logic source. *Nannochloropsis oceanica* is a natural producer of eicosapentaenoic acid (EPA), which is a precursor of docosahexaenoic acid (DHA), both omega-3 fatty acids. These microalgae produce high lipid quantity, and nuclear homologous recombination techniques have been described in order for genetic manipulation. Our main objective is to determine which genes are involved in EPA (and potentially DHA) production. Bioinformatics analysis of *N. oceanica* genome has allowed us to determine putative genes involved in these pathways, and preliminary experiments suggest that ABA could play an important role in the production of these fatty acids. Additionally, we are going to study them by making K.O. mutants and over-expressing lines of these putative genes.

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PS97

PREHARVEST EXOGENOUS METHYL JASMONATE APPLICATION ON NON-ENZYMATIC ANTIOXIDANTS OF *Vaccinium corymbosum* L. FRUITS UNDER FIELD CONDITIONS

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Highbush blueberry (*Vaccinium corymbosum* L.) represents an economically important crop, being widely cultivated in southern Chile. The fruits of this crop are a good antioxidant source. It is reported that exogenous application of methyl jasmonate (MeJA) could induce antioxidants. However, studies about the effect of MeJA applications on highbush blueberry are scarce. Thus, the aim of this study was to determine the effect of preharvest exogenous MeJA applications on non-enzymatic antioxidants of highbush blueberry cv. Legacy fruits under field conditions. Productive blueberry plants from Agricola Trucao farm (region de Los Lagos) were used. The experimental design was randomized complete block with five treatments and 15 plants per treatment. One group of plants was sprayed before harvesting with 0.01 and 0.05 mM MeJA and other group was sprayed two times: before harvesting and at harvesting time with the same concentrations of MeJA. Antioxidant activity, total amount of phenols, flavonoids and anthocyanins was determined. The results showed that antioxidant capacity increased at the higher dose of MeJA with one and two applications of treatment, while anthocyanins decreased at all treatments with exception to 0.01mM MeJA treatment. Flavonoids only increased at 0.01 mM MeJA with one application of treatment. Total phenols were only maintained with one application of 0.05 mM MeJA, decreasing significantly with other treatments. Total soluble solids and titratable acidity did not change at each treatment. Thus, we conclude that preharvest MeJA applications did not increase significantly the antioxidant compounds of blueberry fruits under field conditions, despite of the increase in total antioxidant capacity.

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PS98

IDENTIFICATION OF TRANSCRIPTIONAL COREPRESSORS OF THE PHENYLPROPANOID PATHWAY IN *Vitis vinifera*

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The MYB transcription factor family has been described as transcriptional modulators of the phenylpropanoid pathway in plants. The molecular mechanism by which MYB transcription factors regulate this pathway is not completely understood. One of these genes is *MYB4a* that has been previously described as a putative transcriptional repressor of this pathway in Arabidopsis. The *Vitis vinifera* MYB4a protein contain an EAR motif, which is highly conserved in negative regulators in a broad range of developmental and physiological processes across evolutionarily diverse plant species. It has been described that co-repressors interact physically with transcription factors through EAR motif recruiting chromatin-remodeling factors to their target genes to repress the expression. TOPLESS (TPL) and TPL-related proteins are plant homologues to the Groucho/Tup1-like corepressors identified in yeast and animals. Members of the TPL family emerged recently as key players in gene repression in plants. The goal of this work was to identify proteins that participate as corepressors of the phenylpropanoid pathway in *Vitis vinifera*. To pursue this aim, an *in silico* search was done in the grape genome to identify genes that encode TPL-like proteins. We identified 6 gene models (*VvTPL1-6*), which phylogeny was compared to the TPL proteins described previously in *Arabidopsis*; these putative grape proteins have the TPL characteristic domains suggesting that they are homologous. In addition, the expressions patterns of the *VvTPL*s family were analyzed by quantitative real time PCR in different organs, like flowers, seeds and fruits development. To assess the physical interaction of VvTPL1 with MYB4a, a yeast two-hybrid assay was performed. Using as bait the N-terminal of VvTPL1, we demonstrate the interaction with MYB4a. In conclusion, these results suggest that VvTPL1 participates with MYB4a in a protein complex involved in the repression of phenylpropanoid pathway in *V. vinifera*.

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PS99

IDENTIFICATION OF *LYCE* GENE MUTANTS TO POTENTIALLY INCREASE β-CAROTENE CONTENT IN DURUM WHEAT (*Triticum turgidum* L.ssp. *durum*) GRAINS THROUGH TILLING

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Increasing β-carotene (i.e., a vitamin A precursor) of durum wheat grains is important to potentially improve pasta quality. LYCE (Lycopene Epsilon cyclase) is a key enzyme that diverts the carotenoid biosynthetic pathway into two metabolic branches. The main objective of this work is to identify *LYCE* gene mutants to potentially increase β-carotene content in durum wheat grains using the TILLING method (Target Induced Lesions In Genomes). Due to the tetraploid nature of the durum wheat genome, we designed and validated genome-specific primers for the *LCYE A* and *LCYE B* genes. We also extracted CJE (Celery Juice Extract) that contains the Cel-1 enzyme, which is employed in TILLING to identify point mutations created with EMS (ethyl-methyl sulfonate) by cutting mismatched bases when heteroduplex are formed. To be more efficient, we created 6X DNA pools from the Kronos TILLING mutant population composed of 1,360 individuals obtained from the University of California-Davis. We visualized and identified the mutant pools using agarose and polyacrylamide gels. We are currently identifying individuals mutants, using six 2X pools for each 6X pooled mutant identified. LCYE TILLING mutants will show two double banding when visualized. When identified, these mutants will be sequenced and evaluated with bioinformatics tools such as SIFT and PSSM algorithms to find LCYE enzymes that may possess a knockout or a knockdown mutation. This has great value because it allows the creation of new alleles, which enriches breeding programs due to the generation of genotypes with higher grain quality (i.e., genotypes with increased levels of grain β-carotene). In addition, the TILLING technique also creates genetic variability that can be used in functional genomics research, and it may elucidate how specifically the carotenoid biosynthetic pathway works in cereals.

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PS100

In situ CHARACTERIZATION AND SEED PROPAGATION OF *Pasithea coerulea* (RUIZ ET PAVON) D. DON

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Nowadays there is great potential on the study of domestication and breeding of native species with high ornamental value. *Pasithea coerulea* is a species native to Chile distributed from Antofagasta to Valdivia, showing interesting features to study, considering for example its blue flowers. This study was focused on the characterization and propagation of *Pasithea coerulea.* The characterization considered the evaluation of 6 morphological descriptors (firmness and size of flower stem, flower size and color, leaf size, and number of secondary axes) in three populations growing in Central Chile: San José de Maipo, Pirque (Metropolitan Region) and Machalí (O'Higgins Region). The seed propagation study was carried out establishing 6 treatments: Control (T0); scarification (H_2SO_4) x no stratification (T1); scarification (water flow) x no stratification (T2); no scarification x stratification at 4 °C (T3); scarification (H_2SO_4) x stratification at 4 °C (T4); scarification (water flow) x stratification at 4 °C (T5). The seeds were subjected to scarification, disinfected with ethanol (97%) and NaOCl (3%) and then stratification treatments were applied. For treatments with stratification seeds were exposed to 4° C during 4 weeks. Subsequently they were sown (75 per treatment) in Petri dishes with filter paper in darkness at 24 ± 1° C. The results showed a longer flower stem, higher number of secondary axes and firmness in San José de Maipo population, whereas Pirque population showed larger flowers and leaves. The blue violet colour (RHS 94 A) has the highest frequency in both Machalí and San José de Maipo. Regarding the propagation, germination and plumule observation were significantly higher in T4 and T5 (93.33% 89.33% respectively) compared to the other treatments. Further studies will be focused on the relationship between the morphologic characters observed and the habitat of the different populations.

PS101

PHOTOCHEMICAL ACTIVITY OF *Deschampsia antarctica* FROM TWO ANTARCTIC POPULATIONS, POSSIBLE EFFECTS OF CLIMATE CHANGE

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Difference in temperature within the Antarctic latitudinal gradient, may determine that plants growing in more southern populations are exposed to temperatures lower than plants from boreal populations, which can trigger differences in the partitioning of energy. As the Antarctic plants grow usually under sub-optimal temperatures for photosynthesis, being this limited by the low temperatures in field, it is likely that increase in temperature product of climate change resulting in an increase in the photosynthetic activity. Given the greater warming trend in the south, this tendency should be higher plants coming from more southern conditions. On this basis, we analyzed the effect of increase temperature on *Deschampsia antarctica* coming from King George Island (62° 09' S, 58° 28' W) and Lagotellerie Island (67° 52'S, 68° 42' W), and cultured at 5°C (maximum temperature observed during summer in Antarctica) and 16°C (optimal photosynthetic temperature determined in plants coming from the field). Independent of the growth temperature and provenance, plants growth at 250 µmol photons m^{-2} s^{-1} did not show symptoms of photoinhibition, keeping values of Fv/Fm near 0.8. The increase in temperature caused an increase in the rate of electron transport (from about 80 to 130 µmol photons m^{-2} s^{-1}). This was always greater in plants coming from southernmost locations. Consequently, this increase in the photochemical route (qP) produced a decrease in the heat energy dissipation (NPq); this decrease was stronger in southern populations. Our results indicate that plants from different provenances respond differently to increase temperature, however, is necessary to include new variables to finally predict the real impact of climate change on the ecophysiology of Antarctic plants.

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PS102

CORRELATION BETWEEN THE AMOUNT OF ALKANES AND CRACKING IN DIFFERENT SWEET CHERRIES VARIETIES

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Fruit cracking, in sweet cherries, is a complex phenomenon associated to rainfall before harvest causing significant economic losses. Some physical factors involved in cracking have been studied, like water uptake by the fruit, osmotic factors, cuticle physical properties and anatomical aspects of fruit cells. Different studies show that an excessive water uptake through the fruit skin leads to fruit cracking. During the fruit development, waxes of the cuticle play an important role in water permeability. Nuclear magnetic resonance analysis (1H, and 13C), revealed that the fruits from the different sweet cherry varieties contain n-alkanes, mainly 29 carbons. GC/MS analysis of n-alkanes, revealed that fruit varieties with significantly major concentrations of nonacosane and total alkanes (Kordia, Regina and Lapins) were more tolerant to cracking than fruit varieties with lower levels of alkanes (Bing and Rainier). Some candidate transcription factors and genes such as ketoacyl-CoA synthase, involved in the extension of long-chain fatty acids, were selected. Transcript levels determined by qPCR showed an increase in gene expression in cracking resistant varieties (Regina and Kordia) at the ripening time. These results indicate a correlation between the quantity of n-alkanes with 29 carbons, gene expression and cracking tolerance in sweet cherry fruits. This difference could be a new important factor to explain the tolerance to cracking in fruits of different varieties.

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PS103

SILENCING OF THE *SlMYB60* GENE TO ENHANCE DROUGHT TOLERANCE IN TOMATO PLANTS

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Drought is the major abiotic stress factor limiting crop yield. One of the first plant responses to drought is stomatal closure to prevent water loss. Some transcription factors (TFs) have been shown to participate in this process. MYB60, a TF involved in light induced stomatal opening, has been characterized in Arabidopsis and grapevine. It is expressed under white and blue light and repressed by darkness, drought, salinity and abscisic acid. Furthermore, the Arabidopsis mutant *atmyb60-1* shows a reduction in light induced stomatal opening. In this work, we have isolated and sequenced the coding region of the MYB60 TF from *Solanum lycopersicum* (*SlMYB60*). The protein coded by this sequence presents characteristic domains and motifs of other plant MYB60 proteins. A putative promoter region upstream of the translation start site was also isolated, containing previously described DOF binding sites that could determine its guard cell-specific expression. This promoter was fused to a reporter gene to evaluate its activity in transformed Arabidopsis and tomato plants (Micro-Tom cultivar). The expression of *SlMYB60* in different tomato tissues was assessed by qRT-PCR. A silencing construct to downregulate *SlMYB60* expression was designed and used to transform tomato plants. The obtained tomato lines were analyzed by qRT-PCR to determine the expression of *SlMYB60*. We expect that the *SlMYB60* silenced lines show a decreased stomatal aperture compared to wild-type plants and thus have enhanced drought-tolerance.

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PS104

PROXIMAL ANALYSIS AND IDENTIFICATION OF SECONDARY METABOLITES FROM LEAVES OF THE ENDEMIC *Haplopappus remyanus*

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Haplopappus remyanus (Baylahuén) is an endemic shrub of central Chile found in the Andean foothills (above 1500 m. a .s. l.) from Coquimbo Region (28° S) to O'Higgins Region (35° S). Local people assignit medicinal properties and our aim was to investigate the nutritional state of this plant, including total polyphenol content by Molecular Absorption Spectrometry, tocopherol content by HPLC chromatography, fatty acid content by GC chromatography, identification of secondary metabolites by FL Chromatography and evaluation of antioxidant capacity in leaves. The proximal analysis included humidity, ashes (macro and micronutrients), crude fiber, crude protein contentand sugars. Saponificable and non saponificable lipids with 14.2% were the more abundant nutritive group in leaves of*H. remyanus*, identifying terpens, triterpens and esterols as the main secondary metabolites. Carbohidrates with 9.4% of crude fiber and soluble sugars with 2.4% were the second more abundant group in leaves, identifying flavonoids and cumarinesas the most relevant. In terms of ashes, the mineral content of8.9% was higher than normal values observed in other plants. Our results suggest that identification of several families of secondary metabolites in the leaves of *H. remyanus*might be a natural response to avoid oxidation by high sun irradiancesobserved at high altitudes and it might explain why people consumes these leaves in infusion as antioxidanttisane.

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PS105

INDUCTION OF WATER STRESS TOLERANCE IN CITRUS PLANTS THROUGH OVEREXPRESSION OF THE TRANSCRIPTION FACTORS CBF3 AND MYB61

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Citrus are evergreen fruit trees primarily known for its juice and pulp. Currently, most relevant worldwide citrus growing areas are located in Brazil, United States, India, Mexico and Spain. The main citrus grown worldwide are sweet orange (*Citrus sinensis* L.), lemon (*Citrus limon* L.), grapefruit (*Citrus grandis* L.), mandarin (*Citrus reticulata*) and persian lime (*Citrus latifolia*). Climate change, land use and population growth are limiting water resources in agriculture. By the aforementioned, this activity is facing one of the biggest challenges in its history: "*Produce more food with higher quality and lower water use*". The citrus fruits have high water demand (900-1200 mm/season) for optimal fruit production. The response of the plant in root level to water deficit and the regulation of gas exchange through the stomata can be targets for genetic manipulation to optimize the tolerance of citrus to limiting water conditions, by improving the efficiency in water use (WUE). The objective of this work is to generate citrus plants more tolerant to water stress. The strategy for achieving this goal is to overexpress the transcription factors CBF3 and MYB61, which are known to be involved in water stress tolerance in plants. CBF3 was expressed in rootstock *C. macrophylla* and *Carrizo citrange* and MYB61 in *C. sinensis* L. and *C. limon* L. Molecular and physiological characterization are due to be conducted on the transformed lines in order to asses water stress tolerance and WUE.

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PS106

DEVELOPMENT OF COLD HARDINESS IN GRAPEVINE BUDS IN THREE VALLEYS OF CHILE

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A dynamic thermal model of bud cold hardiness has been developed recently, the model assumes that bud-dormancy is divided in two phases, one of acclimation, in which the bud is more sensitive to low temperatures, and other of de-acclimation, in which the bud is more sensitive to high temperatures. The model use daily mean temperatures to calculate the change in low thermal exotherms (LTE), a measure of cold hardiness in grapevine buds. Thermal time threshold determines whether buds acclimates (gain hardiness) or de-acclimates (lost hardiness) and the turning point acclimation/deacclimation (EBD) occurs once a certain amount of chilling degree days (DDc) is reached. The model has been tested with different *Vitis* cultivars in the same region, but has not been tested with a same cultivar in regions with different temperature regimens. In this study, LTE of grapevine buds cv Thompson Seedless were determined in three valleys of Chile with different temperature regimens: Maipo (33º 27' S), Elqui (30º 2' S) and Copiapó (27º 22' S). Measurements were carried out every 2 weeks from April (full dormancy) to September (budbreak) and the data were fitted to the dynamic thermal model. In Maipo valley, using LTE data from two consecutive years, the model was effective in simulating seasonal trends of acclimation and de-acclimation; however, the predicted curve of LTE did not fit the experimental curve of Elqui and Copiapó valley when Maipo parameters were used. The model predicts that as chilling degree days are not reached in Elqui and Copiapó, LTE values do not increase and the bud not deacclimates, a fact that disagrees with experimental data. Therefore, since the experimental data showed that the turning point acclimation/deacclimation occurs near the same date in the tree regions, we change the model by incorporating a fixed time at which the turning point occur independent of the chilling accumulated. Under this new condition, the model is capable to reproduce the tendency of the LTE curves in the three regions

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PS107

DETERMINATION OF ANTIOXIDANT ACTIVITY *Nertera granadensis* (Mutisex L.f.) DRUCE

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Throughout the history of human civilization, natural products have served as a primary source of medicine, which is currently used by a large percentage of the world population. Antioxidant compounds are developed in plants in order to prevent cellular damage caused by free radicals. *Nertera granadesis* is a species belonging to the Rubiaceae family, distributed mainly around the Pacific Ocean. This work aims to evaluate the antioxidant activity of the species in study, by capturing the radical 2,2-diphenyl-1-picrylhydrazyl (DPPH) and 2,2'azinobis- (3-ethylbenzthiazoline) -6 sulfonic acid (ABTS), determine the concentration of total polyphenols and detect groups of secondary metabolites with phenolic structures involved in antioxidant activity. To determinate of antioxidant activity by radical DPPH methanolic extract concentrations were used from 0 to 5 mg/mL. For ABTS, concentrations from 0 to 1.4mg/mL were used. In both cases, the antioxidant capacity was evaluated by calculating the decrease percentage of the radical by absorbance, and the concentration of the extract was determined to produce 50% inhibition of free radical absorbance (IC50). To determine the total concentration of polyphenols present in the extract of *Nerteragranadensis* was used the Folin-Ciocalteu. The detection of groups of secondary metabolites was performed by chemical qualitative tests. DPPH antioxidant and ABTS assay, allowed observing a positive antioxidant activity, resulting in a maximum decrease of 79.11% and 87.99% respectively. Thereafter, the IC_{50} was calculated for both cases, obtaining a value of 2.6mg/mL (DPPH) and 0.7mg/mL (ABTS). The content of polyphenols gallic acid equivalents was 2.951µg/mL of extract. According to phytochemicals tests, it was possible to observe the presence of saponins.

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PS108

GENETIC RELATIONS AMONG FIFTY-ONE SWEET PEPPER AND HOT PEPPER ACCESSIONS (*Capsicum annuum* L.) BELONGING TO THE CHILEAN AGRICULTURAL RESEARCH INSTITUTE (INIA)

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The studies of genetic divergence and diversity are important tools in vegetable breeding programs. The aim of this work was to evaluate the genetic divergence in a subset of *Capsicum* accessions from the germplasm bank belonging to the Chilean Agricultural Research Institute (INIA) and its relationship to agronomic and fruit industrial traits. Fifty-one accessions (including sweet and hot peppers) were selected based on their agronomic and fruit industrial characterization. Eighty-seven putative microsatellite markers (SSR) were evaluated and twelve SSR markers were selected for further analysis. DNA samples were extracted in bulk and microsatellite regions amplified using a touchdown PCR protocol. Different alleles were scored and genetic distance estimation among genotypes was carried out based on the allelic similarities and dissimilarities. For cluster analysis, the Unweighted Pair Group Method with Arithmetic mean (UPGMA) and Neighbor Joining (NJ) methods were used. Results were verified with cophenetic correlation coefficient (CPCC). The fruit quality traits in the 51 accessions were analyzed by principal component analysis (PCA) and cluster analysis by Ward's method. The results showed a mean of 3.6 alleles per locus. The CPCC analysis differed between the two methods of clustering. The highest CPCC value, 0.802, was observed with NJ Cluster analysis. NJ analysis grouped the 51 Capsicum accessions into three groups: Group I with 16 accessions. Group II was the largest group, with a large percentage of hot peppers accessions. Group III with 13 accessions, includes four commercial genotypes. The traits that contributed most to the phenotypic diversity were pericarp thickness and fruit equatorial diameter into Component 1 and fruit polar diameter and sugar content into Component 2. The first two components explained an 81% of the total variation. *Phytophthora capsici* resistant accessions were clustered in two different groups.

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PS109

UUAT1: A NUCLEOTIDE SUGAR TRANSPORTER (NSTs) INVOLVED IN SEED COAT, TRICHOME AND ROOT CELL WALL COMPOSITION

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The pectin biosynthesis takes place in the lumen of the Golgi apparatus and requires the participation of many glycosyltransferases, which uses nucleotide sugars as substrates. Nucleotide sugars are synthesized in the cytosol and they are transported into the Golgi apparatus by nucleotide sugar transporters (NSTs). Therefore, NSTs are key elements in the biosynthesis of pectins. In Arabidopsis, NSTs belongs to a gene family constituted by more than 50 members. Here we present a Glucuronic acid transporter, UUAT1, involved in pectins biosynthesis in seed coat, trichomes and roots. Quantitative RT-PCR of *UUAT1* and histochemical analysis of *GUS* expression controlled by endogenous promoter show the accumulation of *UUAT1* trancripts in trichomes and roots; also in epidermal cells of seed coat this happened at stages when pectic mucilages are accumulated. Biochemical and immunological analysis of seed coat epidermal cells and roots in the *uuat1* mutants revealed changes in arabinose, rhamnose, and galactose content. Also enzymatic assays reveal a lower pectin methylesterase activity, which modify pectin methylation. These results suggest that alteration of one NST change the poll of UDP-Glucuronic acid incorporated in the Golgi, which affects both cell wall composition and enzymatic activities involved in the global pectin metabolism.

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PS110

EXOGENOUS APPLICATION OF GABA MODULATES ITS ENDOGENOUS LEVELS AND THE H_2O_2 CONTENTS ON *PRUNUS* ROOTSTOCKS UNDER ROOT HYPOXIA STRESS BY WATERLOGGING

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GABA shunt pathway occurs in a wide range of organisms, such as bacteria, yeasts, plants and animals. This pathway is responsible for the biosynthesis of the non-protein amino acid GABA from derivatives of tricarboxylic acid cycle. In plants, GABA level is normally low, but it quickly and extensively increases in response to stress (e.g., hypoxia). On two hypoxia contrasting rootstock genotypes, Mazzard F12/1 (sensitive) and Mariana M2624 (tolerant), a previous transcriptional study by RNA-seq detected an up-regulation of gene expression of a *glutamate decarboxylase* (*GAD*), which encodes the enzyme for the first step of the GABA shunt pathway. In order to study the GABA metabolism and its role in the plant response to hypoxia stress in such genotypes, we applied 500 mL of a solution of GABA 0.5 mM to the roots as a pre-treatment three hours before the submission of plants to waterlogging. Exogenous GABA activated a new endogenous biosynthesis of this amino acid. Additionally, a delay in the hypoxia-related alanine production was detected in GABA pre-treated plants. A reduction in H_2O_2 concentration was also observed in roots from both genotypes. Net photosynthesis values were lower in stressed plants than in control plants, but were higher in GABA supplemented plants compared to GABA-less ones. Transcript abundance of *GAD* was modified in an isoform dependent manner in GABA pre-treated plants. These results show physiological, biochemical and transcriptional effects of exogenous GABA application that would help to *Prunus* rootstocks to cope brief waterlogging events.

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PS111

In vitro CALLUS AND POLYPLOIDY INDUCTION IN *Actinidia deliciosa* WITH COLCHICINE

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Induction of polyploidy in plants has become an important tool for genetic improvement. Through this technique changes in plant morphology can be achieved and empower commercially interesting features. In this sense, seed and *in vitro* plant exposure to colchicine has been studied in *Actinidia deliciosa*. Seeds were sterilized, rinsed with sterile distilled water and sown in petri dishes with Murashige & Skoog media (MS). Dishes with seeds were kept for two weeks in a growth chamber with a 16/8 light/dark photoperiod at 21±1°C. For the study, MS callus forming media (CFM) was supplemented with 3.5 mg L^{-1} BAP and 0.5 mg L^{-1} IAA as a preliminary study. Cotyledons were removed from germinated plants leaving a portion of petiole. The cotyledons were immersed in colchicine solution at the following concentrations: T_0: 0% (control), T_1: 0.05% and T_2: 0.1% for 4 hours. Then, the cotyledons were rinsed with sterile distilled water and laid in petri dishes containing CFM. Meanwhile, petiole pieces were cut from the new leaves of *in vitro* plants after approximately one month of growth, following the same procedure and exposed to the same colchicine concentrations. White friable and translucent callus were observed in cotyledon treatments, however, in the petiole pieces the callus was darker and firmer. At the third week, shoots started to grow and were more abundant in cotyledons after a month in CFM. It was not possible to analyze the ploidy of the shoots; however, differences in size and thickness were observed, showing potentially duplicated genetic material.

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PS112

CHARACTERIZATION OF DIFFERENTIALLY EXPRESSED HEXOKINASE3 IN *PRUNUS* ROOTSTOCKS WITH CONTRASTING RESPONSE TO HYPOXIA

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In breeding of new *Prunus* sp rootstocks, tolerance to several abiotic stresses is desirable. Among these, the hypoxic stress, caused by flooding, poor soil drainage and/or deficiency irrigation practices, is one of the most important. Low availability of oxygen in roots reduces ATP production by oxidative phosphorylation in the mitochondria. Consequently, during hypoxic stress the energy generated is mainly obtained through glycolysis, which implies a differential expression of the principal genes involved in this pathway. Hexokinases (HXK) are enzymes that catalyze the phosphorylation of glucose to glucose 6-phosphate, the first essential step in glycolysis. In order to obtain a better understanding about the role of this enzyme in response to hypoxic stress, hexokinase gene family expressed in the root of two rootstock genotypes with contrasting response to hypoxic stress are being analyzed. By *in silico* analysis of previous RNA-seq studies, we had found the presence of six hexokinases genes expressed in the root of the two rootstock genotypes during hypoxia stress and qPCR experiments were conducted to confirm their differential pattern of expression. Results showed opposite regulation of the hexokinase 3 (ppa004715; HXK3) gene. The expression was up and down regulated in genotypes tolerant and sensitive to hypoxia, respectively. The promoter regions of the genes are being analyzed searching for differences that might explain their differential response to hypoxia conditions. In addition, SNPs of genes and predicted structural model of HXK3 of proteins are being analyzed to look for possible differences at protein activity/localization levels. Finally, we expect to confirm the subcellular localization of this enzyme through transient transformation that might explain their role in a differential response to hypoxia conditions.

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PS113

EFFECT OF INHIBITION/STIMULATION OF ETHYLENE RESPONSE ON GENES RELATED TO MALIC AND CITRIC ACID METABOLISM DURING RIPENING OF CHERIMOYA (*Annona cherimola* Mill.).

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Flavor is a major quality attribute in fruits, constituted by a mixture of volatile compounds, sugar and acid. Cherimoya (*Annona cherimola* Mill.) is a climacteric and subtropical fruit, which shows acidity increase during ripening in contrast to most fruits. The hypothesis of this study is that the ethylene regulates organic acids metabolism in cherimoya, causing a transcript increase of genes encoding phosphoenolpyruvate carboxylase and NAD-dependent malate dehydrogenase enzymes, and a transcript decrease of NADP-malic enzyme and aconitate hydratase, resulting in malic and citric acid accumulation. Cherimoyas cv. Concha Lisa were harvested and stored at 20°C under ethylene, 1-methylcyclopropene (1-MCP) and air conditions. To characterize the ripening process, the ethylene production, respiration rate, flesh firmness, total soluble solids and titratable acidity were determined, and malic and citric acid determination were performed by HPLC. Additionally, expression of genes encoding key enzymes involved in the synthesis and degradation of these metabolites was determined by real-time quantitative PCR, and activity assays were performed to measure the activity of the encoded enzymes. Results show that all the measured ripening parameters were delayed by 1-MCP. Also, analyses revealed a major ethylene-independent increase of malic acid throughout ripening associated to changes in transcript levels for the genes under study. Effects of ethylene on gene expression and enzymatic activity through the acidity increase during cherimoya ripening will be discussed.

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PS114

IDENTIFICATION OF UDP-GLCA TRANSPORTERS INVOLVED IN NON-CELLULOSIC POLYSACCHARIDES BIOSYNTHESIS

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The cell wall is a complex extracellular matrix mainly composed of polysaccharides. Non-cellulosic polysaccharides are synthesized in the Golgi apparatus by glycosyltransferases (GTs), which use nucleotide sugars as donors to glycosylate the nascent polysaccharide chain acceptors, which are going to be exported to the extracellular space. UDP-glucuronic acid (UDP-GlcA) is a key molecule involved in this processsince it serves as precursor for the synthesis of several polysaccharides of cell wall, contributing to 50% of the biomass present in the extracellular matrix. Nevertheless there isa topological problem, since UDP-GlcA is synthesized by UDP-glucose dehydrogenase (UGD) in the cytosol. This molecule needs to get into the Golgi apparatus lumen where the catalytic site of the GTsand epimerasesare located. In this process Nucleotide Sugars Transporters (NSTs) are essential. To date, no UDP-GlcA transporter has been identified so their role in non-cellulosic polysaccharides remains unclear. In this work we identified a family of UDP-GlcA transporters located in Golgi apparatus. To determine their contribution to non-polysaccharides synthesiswe worked with 3 members of this family (*UUAT3*, *UUAT4* and *UUAT5*), analysed their expression pattern and studied cell wall composition in plants with altered expression levelsof them. Quantitative-PCR data indicate that *UUAT3* and *UUAT4* are ubiquitously expressed. Transcriptional fusion of the promoter of *UUAT3* showed peak of expression in pectin rich tissues. Immunofluorescence analyses suggest *uuat3* and *uuat4* have diminished levels of pectic polysaccharides in roots. All togetherour results propose that UDP-GlcA transporters are important players in non-cellulosic polysaccharide biosynthesis.

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PS115

INHIBITION OF FREE RADICAL BECAUSE PHENOLS PRESENT IN *Luzuriaga radicans* (Ruiz & Pav.)

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Antioxidants are molecules able to prevent or slow the oxidation of other molecules, generally biological substrates such as lipids, proteins or nucleic acids. Today these antioxidants are requested because they help in preventing diseases associated with oxidative stress. *Luzuriaga radicans* is a woody climbing plant, an evergreen plant that sticks on the trunks through its fine roots, present in southern Chile and Argentina. The *in vitro* antioxidant activity of aqueous extracts of *L. radicans* has not been studied, therefore in this study was evaluated the antioxidant activity of aqueous extract obtained from *L. radicans* by determining the decrease in absorbance at a solution of the radical 1,1 biphenyl-2-picrilhidrazilo (DPPH). Furthermore, polyphenols in the aqueous extract were quantified and a phytochemical assay was performed to determine the presence of different secondary metabolites. The antioxidant activity was greater at a concentration of 15 mg / mL of extract, with an inhibition percent of 70.1% of DPPH absorbance and obtaining an IC_{50} of 5.713 mg / ml. The antioxidant activity on DPPH, expressed in relation to gallic acid equivalent was 3.90 mg to 1 mg of extract. The content of polyphenols gallic in acid equivalents was 19980 mg in 1 g of extract. Studies in *L. radicans* showed a good antioxidant activity is therefore important to further studies, which may have great potential for human health.

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PS116

MARKER ASSISTED SELECTION FOR MATURITY DATE IN *Prunus persica*

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Chile is the first peach exporter in the South Hemisphere and the fifth producer in the world. Chilean initiatives of peach breeding have been carried out, where the fruit quality and postharvest performance are the main goals for new peach varieties. Breeding is a time consuming and costly process. For this reason, the development of genomic tools to support the early selection of genotypes is quite relevant to improve the efficiency of breeding programs. Thus, the aim of this work was to develop molecular markers to early selection of individuals considering the maturity date and slow ripening fruit (normal fruit ripening/ very slow fruit ripening). We identified a candidate gene responsible of these traits using QTL strategy, which was sequenced from 'Venus' and the sequence was compared against 'Lovell' (peach reference genome). Structural variants were identified and were associated with phenotypic groups for each trait. We detected an insertion of 9 bp on the gene related to early season varieties. Primers were designed to amplify this region on 50 varieties to validate it as codominant molecular marker of length polymorphism (±9 bp) for maturity date. Furthermore, deletion of the entire gene produced the slow ripening phenotype. Two pairs of primers were designed to genotype the deletion in heterozygosis and were evaluated on 50 varieties to validate them. Finally, these markers are useful tools to early selection of individuals considering the maturity date and slow ripening traits.

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PS117

PREDICTED REGULATORY NETWORKS DRIVEN BY MADS-BOX TRANSCRIPTION FACTORS REVEAL ROLES IN DEVELOPMENT PROCESS IN *Fragaria vesca*

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MADS-BOX transcription factors (TFs) are a multigene family described as master switches in flower and fruit development in plants. Specifically, in tomatoes, strawberries, apples and grapes, SEPALLATA subfamily plays an important role in fruit ripening. MADS-BOX binds to specific and highly conserved DNA sequences named CArG-box (10 bp: CC(A/T)6GG). *Fragaria vesca* is the plant model of *Fragaria* genus, useful for genetic and functional studies, because is a diploid specie, has short life cycle, high fruit production rate and its genome has been recently fully sequenced and annotated. The goal of this study was to predict putative genes regulated by MADS-BOX TFs in the *F. vesca* genome. Using public experimental information of nine different MADS-BOX TFs binding sequences, we designed software based on probabilistic algorism that allowed us to look for CArG-box sequences in the promoter region (2KB upstream of start ATG) of each of the 24,000 genes annotated in this genome. The relevant result showed 5,828 genes putatively regulated by MADS-BOX TFs. Functional classification of these genes showed a subset related to development and fruit ripening. Interestingly, the first enzymes in the pathways of anthocyanins, phenyl propanoids and fatty acids biosynthesis could be regulated by MADS-BOX, as well as some amino acid degradation pathways. This reveals a putative master switch role of these TFs family in *F. vesca*. The data will be a useful tool to search for candidate genes and networks relevant in processes such as fruit development and ripening in the *Fragaria genus.*

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PS118

PROTEOMIC ANALYSIS IN TWO LATE VARIETIES OF *Prunus persica* FRUITS UNDER POSTHARVEST TREATMENTS AND THEIR EFFECTS ON CHILLING INJURY DEVELOPMENT

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Chile is the main exporter of peaches and nectarines (*Prunus persica*) from the Southern hemisphere. These fruits quickly ripe and deteriorate at ambient temperature and for this reason it is necessary to store them at low temperatures (0 °C), during the shipping time. However, late season varieties are susceptible to physiological disorders due to long-term cold storage and consequently develop chilling injury (CI). Typically, CI symptoms are mealiness, browning and flesh bleeding which diminish fruit quality. Looking for strategies to extend postharvest life and avoid CI, some treatments such as controlled atmosphere (CA) and conditioning has been applied. To understand the molecular mechanisms associated to these processes, we designed a 2-D proteomic approach to screen for proteins differentially accumulated in two late season varieties, 'Red Pearl' (nectarine) and DU88 (peach). The experimental design allowed us to compare soft and firm fruits, with or without cold storage and postharvest treatments (CA and conditioning). We detected 53 and 62 differentially accumulated spots in 'Red Pearl' and DU88, respectively. These spots were identified by mass spectrometry and classified using Gene Ontology annotation. The protein accumulation was found to be different between cold storage and postharvest treatments in processes involving cell wall metabolism, stress response and redox regulation. Some differences on spots accumulation between varieties were observed. In DU88, polygalacturonase and expansin were more abundant in soft conditioned fruit stored at 4 °C (juicy) than in fruit without conditioning (mealy). On the other hand, superoxide dismutase in 'Red Pearl' showed increased levels in soft cold stored fruits (juicy) comparing to soft cold stored fruit (mealy). These results indicate that both varieties exhibit different molecular processes regulated by CA and conditioning.

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PS119

ENZYME ANTIOXIDANT SYSTEM AND INCREASE THE CHILLING INJURY TOLERANCE OF POMEGRANATE FRUITS IS MODULATED BY BLOCKING OF ETHYLENE PERCEPTION

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Pomegranate (*Punica granatum var. Wonderful*) is very sensitive to chilling injury (CI) under low-temperature storage. CI induces small brown pits and necrotic areas on the skin that increase their intensity after transfer of the fruit from low temperature to 20ºC. Ethylene plays a key role in many developmental processes and additionally in the response of plants to different biotic and abiotic stresses. Towards the understanding of the involvement of ethylene in the responses to cold in the skin tissue, fruits were treated with 0, 0.5, 1 and 2 mL L^{-1} 1-methylcyclopropene (1-MCP) immediately after harvest for eight hours, and subsequently stored in air at 2°C for up to 50 days. The level of oxidative stress, through enzymatic antioxidant activities like superoxide dismutase (SOD), peroxidase (POX), catalase (CAT), and total antioxidant capacity (trolox equivalent antioxidant capacity TEAC) were determined. Damage on skin membranes was established by measuring of ion leakage. The changes in antioxidant potential of pomegranate fruits were related to the capacity of 1-MCP to increase their commercial shell life. Loss of firmness was significantly lower in 1-MCP-treated fruits. In addition, 1-MCP-treated fruits (1 mL L^{-1}) exhibited higher activities of superoxide dismutase, peroxidase and catalase. Treated fruits also exhibited higher trolox equivalent antioxidant capacity during storage. In accordance with these observations, lower ion leakage values were detected in 1-MCP-treated fruits. Preliminary, these results suggest that 1-MCP conferred a greater resistance to oxidative stress, reducing the incidence and severity of CI.

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PS120

TRANSCRIPT ANALYSIS OF *PHYTOENE SYNTHASE* (*PSY*) AND *CATALASE (CAT)* GENES DURING GRAIN DEVELOPMENT OF 12 DURUM WHEAT (*Triticum turgidum* L. SSP. *Durum*) GENOTYPES

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The yellow color of durum wheat grains is an important trait for the pasta industry and consumers due to the accumulation of yellow pigments (i.e. lutein) in the endosperm associated with the carotenoid biosynthetic pathway. This metabolic route includes enzymes and products that are useful to the plant and humans. The enzyme Phytoene synthase (PSY) is considered a key regulatory point in this pathway since it converts two geranylgeranyl diphosphates (GGPP) into phytoene, the first carotenoid compound. Conversely, Catalase (CAT) is an oxidative enzyme associated with the degradation of carotenoids and variations in the b* color of semolina. The main objective of this study is to determine the transcript accumulation of the *PSY1* homologous genes and *CAT* during grain filling using twelve durum wheat genotypes ranging between low and high grain yellowness. Samples were collected between the anthesis day (day 0), and sampled every 7 days, until dry grain (day 56). The preliminary data obtained shows that *PSY1-A, PSY1-B* and *CAT* transcripts are present from the anthesis day throughout the whole grain filling stage. The expression of *PSY1-B* is higher than *PSY1-A* in all the genotypes studied, suggesting that *PSY1-B* is a relevant gene during carotenoid accumulation. *CAT* expression did not vary strongly between the genotypes, but was more highly-expressed than the *PSY1* homologous genes. Additional tests are currently being conducted to confirm the results and to study the importance of the *PSY1* and *CAT* genes in the accumulation of carotenoids compounds and the determination of grain yellowness.

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PS121

IS THE HIGH EXPRESSION OF *VvFT* AND *VvAP1* AT THE APEX OF THE VINE PREVENTING SD-PHOTOPERIOD INDUCTION OF GROWTH ARREST AND DORMANCY?

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In grapevines (*Vitis vinifera*), both organs, the shoot-apex and the latent bud, contain a shoot apical meristem (SAM). Nevertheless, the growing behavior of the SAM differs depending on the organ. In the latent bud, in response to the shortening in day-length during late summer, the SAM stops growing and enters into a recess period or endodormancy (ED), while, in the shoot-apex, the SAM continues growing until the onset of the drop in the temperatures in autumn. Because a link between the genetic machinery that regulates flowering and seasonal growth cessation and dormancy has been previously suggested, we examined the expression of *FLOWERING LOCUS T* gene of *Vitis vinifera (VvFT)* and other genes involved in the floral signaling cascade in the latent bud and in the shoot-apex, during the transition from paradormancy (PD) to ED. Furthermore, the expression of genes involved in the regulation of *VvFT* and genes related with abscisic acid (ABA) biosynthesis and signaling were also analyzed. Our results showed that day-length shortening causes a reduction in *VvFT* expression in both, latent bud and shoot-apex. However, due to the higher expression level of *VvFT* found at the shoot-apex than at the latent bud, we suggest that high levels of expression of both *VvFT* and *VvAP1* at the apex prevents its fall, by the shortening in day-length, below a threshold level required to arrest growth and induce ED. Moreover, the low expression of *VvFLC*, a negative regulator of *VvFT,* and of ABA signaling and biosynthetic genes *VvABI4* and *VvNCED1* at the shoot-apex regarding to the high expression of these genes in the latent bud, could explain the expression profile of *VvFT* and *VvAP1* at the shoot-apex and at the latent bud. Finally, the mechanism whereby *VvFT* and *VvAP1* might define the behavior of the SAM in apex and buds is discussed.

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PS122

COMPARATIVE STUDY OF MOLECULAR BINDING SITES OF NITRATE AND AUXIN IN *Arabidopsis* NRT1.1 TRANSPORTER

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Nitrogen is an essential macronutrient and one of the main limiting factors for plant growth and agricultural productivity. Nitrate (NO_3^-) is the main source of nitrogen in agricultural soils. Plants uptake nitrate via specific transporters in root cells. To modulate uptake in the range of concentrations for nitrate found on soils, plants evolved low affinity transport systems (LATS) and high affinity transport system (HATS). The *Arabidopsis* NRT1.1 transporter is a unique transporter because it is a member of both HATS and LATS and it is able to transport the plant hormone auxin, a key regulator of plant growth and development. Using molecular modeling techniques we analyzed molecular binding sites for nitrate and auxin in the *Arabidopsis* NRT1.1 transporter. We wish to understand the structural basis for the dual function of NRT1.1 as a nitrate or auxin transporter. To achieve this goal, we performed molecular docking of auxin in the *Arabidopsis* NRT1.1 crystallographic structure and molecular dynamics simulations of NRT1.1-nitrate and NRT1.1-auxin complexes. By analysis of the molecular dynamics simulations of nitrate and auxin binding sites, we were able to identify residues that interact with the ligands over the simulation time (24 nanoseconds). Leu49 interacts with auxin by pi-alkyl interaction. An interaction with Leu49 has not been reported previously for the binding of nitrate. Secondly, the simulations show that Thr360 only interacts with nitrate by hydrogen bond and not with auxin molecule. These residues would be key players in the nitrate *versus* auxin transport capacity of NRT1.1.

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PS123

WHOLE GENOME SEQUENCING AND SNP GENOTYPING OF CONTRASTING SIBLINGS ASSOCIATED TO MEALY FRUIT IN SEGREGATING POPULATION OF *Prunus persica*

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During the past ten years, different studies focused on identifying gene expression profiles and molecular markers that may explain what caused the damage suffered by the peach during cold storage at low temperatures. Recent studies indicate that susceptibility of chilling injury would be associated at the genome level factors, which explain the changes observed between varieties. In this study, we sequenced the whole genome of contrasting siblings from a segregating population of self-cross 'Venus' nectarine variety. Eight segregants were sequenced using MySeq Illumina with paired-end libraries of long reads (250pb). BWA/SAMtools were used for alignment of filtered reads and GATK for SNP detection. Results showed SNP and indels present in mealy segregants, which are not present in juice segregants. Finally, 42.000 High quality SNPs and INDELs were detected. This study provides a better understanding of peach genomics and will allow the future development of a database with structural variants related to traits of economic importance in peach.

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PS124

Prosopis chilensis UNDER SALT STRESS: FROM SEED GERMINATION TO TRANSCRIPTOME SEQUENCING

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Plants living in arid environments have to cope with a plethora of stressors and the development of cellular, molecular, biochemical, physiological and genetic strategies are fundamental to survive in them. Algarrobo (*Prosopis chilensis*) is a native tree belonging to Fabaceae family, which is naturally adapted to arid stressors (salinity among them), and therefore it represents a good model for understanding woody plants adaptation to arid environments. Our aim was to identify the genotype most tolerant to salinity along the natural distribution of *P. chilensis* in Chile and then, to sequence its transcriptome for identifying putative genes involved in salt tolerance. First, we evaluated salt tolerance of several Algarrobo accessions at germination and their physiological responses. Then, using SSR microsatellite markers, we evaluated whether accessions were similar or distinct molecularly, and then, we selected the most salt-tolerant accession to sequence its transcriptome by RNA-Seq. By this approach we were able to identify more than 30.000 transcripts significantly modified by salt stress. Results obtained in each process will be discussed. This work is giving us important information about how *P. chilensis* can tolerate salt stress.

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PS125

NITROGEN FERTILIZATION EFFECT ON ANTIOXIDANT CAPACITY, PHENOLIC COMPOSITION AND PHENYLALANINE AMMONIA-LYASE ACTIVITY OF HIGHBUSH BLUEBERRY (*Vaccinium corymbosum* L.)

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There are controversial evidences with respect to N fertilization and its influence on phenolic compounds accumulation and antioxidant capacity in higher plants. In the present study, we evaluated in a soil kinetic assay the effects of N treatments on N accumulation, phenolic compounds concentration, antioxidant capacity and phenylalanine ammonia activity (PAL) in leaves of Legacy and Bluegold blueberries at controlled conditions. In N deprived conditions Legacy accumulated in average 15 g N kg^{-1}. However, both Legacy and Bluegold leaves increased their N concentration up to 20 g kg^{-1} at the highest N treatment. Although, CO_2 assimilation was not significantly altered in Legacy, Bluegold cultivated at 80 kg N ha^{-1} showed a reduction in this parameter at day 28 associated to high lipid peroxidation. It seems that plants accumulating up to 15 g N kg^{-1} increased PAL activity after day 7, and increase in antioxidant capacity, total phenols and anthocyanins will support this response. Conversely, antioxidant capacity and anthocyanins steadily decreased in Bluegold plants that accumulated above 15 g N kg^{-1}, which corresponded to high N addition. Anthocyanins profile showed a differential behavior between cultivars, being delphinidin, cyanidin, peonidin and malvidin higher in Legacy grown at 20 kg N ha^{-1}. Petunidin and cyanidin were diminished in Bluegold N-deprived plants. Considering our results, we conclude that leaves *of V. corymbosum* plants showing 15 g N kg^{-1} promotes physiological and antioxidant features, which could be reflected in further reproductive stage of blueberries.

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PS126

CHARACTERIZATION OF SUGAR AND ORGANIC ACIDS METABOLISM DURING CHERIMOYA DEVELOPMENT (*Annona cherimola* Mill.)

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Cherimoya (*Annona cherimola* Mill.) is a climacteric and subtropical fruit with a distinctive flavor that depends on the specific mixture of volatile compounds, and sugar and organic acid levels present in the fruit. Cherimoya is a unique fruit that presents an increase in titrable acidity (TA) during ripening, turning it into an interesting model of study for acidity in fruit flavor. In this work, we focused on sugars and organic acids metabolism during cherimoya development in two cultivars: 'Bronceada' and 'Concha Lisa'. Samples of flowers and developing fruits of both cultivars were collected between January and November 2013, obtaining samples at different fruit growth stages. By means of degenerate primers designed using the information available for other species and then specific primers and RACE-PCR, we are identifying and characterizing several key genes encoding putative proteins related to sugar, citric acid and malic acid metabolism. Also, we measured the accumulation of organic acids (malic, citric, ascorbic, tartaric and succinic) and sugars (fructose, glucose and sucrose) during cherimoya development and correlated their levels to the expression profiles of the identified genes in each developmental stage. Results show early accumulation of citric acid associated to transcript accumulation of citrate catabolism enzymes, whereas changes in malic acid throughout development correlated with levels of malate dehydrogenase and malic enzyme. Transcripts of sugar transporters were also associated to the accumulation of soluble sugars. Comparison of these data with enzymatic assays will provide insights into cherimoya development process and posterior ripening sugar and organic acids accumulation.

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PS-127

ANTIOXIDANT ACTIVITY AND PHYTOCHEMICAL OF THE METHANOLIC EXTRACT OF *Nassauvia dentata* Griseb. (ASTERACEAE)

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Nassauvia dentata native species belonging to the Asteraceae family, is found from the volcanic sands of the Mountain chain from Biobío to Magallanes, also is present in the mountains of southern Argentina, where environmental conditions are not favorable, which makes it ideal for studies of metabolites side and especially the study of antioxidant activity this species may possess. In this research, an evaluation on spectrophotometer was performed about the antioxidant effect of methanol extract, through trial with 2,2′-azinobis-(3-ethylbenzothiazoline-6-sulfonic acid) ($ABTS^{\bullet+}$) and a kinetic assay based on the IC_{50}. It was analytically quantified the total polyphenol content by Folin-Ciocalteu reagent. Besides, phytochemicals test were performed on recognition of secondary metabolites in the plant material. In the assay using ABTS, an inhibition of 94.9% with a concentration of 2 mg/mL was observed, and at higher concentrations of methanol extract no further inhibition was observed. The kinetic assay using ABTS reached a peaked inhibition percent of 96% in 30 min and the antioxidant effect remained stable over time (145 min). For the polyphenols, it got a equivalent of gallic acid of 28,56±1,3mg/g (GAEAC). In the plant material using phytochemicals qualitative tests, the presence of three sets of secondary metabolite was detected, showing the presence of derivatives of the steroid nucleus, coumarins and tannins. The results observed with the tested methods reveal the presence of polyphenols in methanolic extract *Nassauvia dentata* Griseb.

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PS-128

MOLECULAR CLONING AND HETEROLOGOUS EXPRESSION OF A *XTH* GENE DIFFERENTIALLY EXPRESSED DURING SOFTENING OF *Fragaria chiloensis*

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Xyloglucan endotransglycosidase/hydrolase (XTH) enzymes participate in hemicellulose dissembling required for cell wall remodeling, by means of its endotransglycosidase (XET; EC 2.4.1.207) and/or hydrolase (XEH; EC 3.2.1.151) activities. Previous studies have described the participation of XTHs during softening of *Fragaria chiloensis* fruit. XET and XEH activities, and the presence of XTH protein, have been detected in *F. chiloensis* fruit at the turning stage. Furthermore, two full-length cDNA sequences, *FcXTH1* and *FcXTH2*, have been isolated, showing the two isoforms a differential tissue specific expression profile. Interestingly, *FcXTH1* is highly expressed in fruit, mainly at the large green and turning stages, when major significant fruit firmness changes are taking place. In this study, we present the molecular cloning of *FcXTH1* and the heterologous expression of FcXTH1 protein. The gene was cloned in *Escherichia coli* and then subcloned and expressed in *Pichia pastoris*. The recombinant protein was secreted to the yeast culture and then purified through a His-tag affinity chromatography. The recombinant protein was detected by immuno-blotting, evidencing a size of ~44 kDa. *In silico* analysis predicted a lower molecular weight protein (~35 kDa). Additionally, the FcXTH1 amino acid sequence presents putative N-glycosylation sites, which suggests that these post-translational modifications might explain the differences in molecular weight between prediction and experimental results. The activity of the recombinant protein and the effect of N-glycosylation for activity are under study.

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PS-129

SYSTEMS ANALYSIS OF TRANSCRIPTOME DATA UNCOVERED A RELATIONSHIP BETWEEN NITRATE AND ROOT HAIR DEVELOPMENT IN *Arabidopsis thaliana*

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Nitrogen (N) is an essential macronutrient for plant growth and development. Plants adapt to changes in N availability partly by changes in global gene expression. Meta-analysis of publicly available root microarray data under contrasting nitrate conditions identified new genes and functions important for adaptive nitrate responses in *Arabidopsis thaliana* roots, among which is the development of root hairs. Root hairs are specialized epidermal cells involved in water and nutrient uptake. Our integrative bioinformatics analysis allowed us to postulate the hypothesis that root hair development is an important developmental process in response to nitrate in *Arabidopsis*. In order to test this hypothesis, we performed treatments with nitrate or potassium chloride in hydroponic media of wild-type plants that were previously grown for two weeks in a low nitrogen media. We observed a two-fold increase in root hair density in response to nitrate treatments. However, mutants related to nitrate transport and control of nitrate response have a small increase of root hair number. These results suggest that there is a strong link between nitrogen availability and the development of root hairs and identified regulatory factors that mediate this adaptive response in *Arabidopsis* roots.

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PS-130

COLD TOLERANCE EVALUATION AT MICROPOROGENESIS STAGE IN TEMPERATE RICE (*ORYZA SATIVA* L.)

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Low temperatures can cause an important decrease in yield of rice (*Oryza sativa* L.). Microsporogenesis is one of the most sensitive stages to cold stress in rice, affecting the development of pollen grains. Thus, the aim of the present study was to identify cold tolerant genotypes at the microsporogenesis stage in rice genotypes from Rice Breeding Program of the Instituto de Investigaciones Agropecuarias (INIA). Rice plants from 150 genotypes were grown in a 10 L plastic pot with rice soil (Vertisol), under mesh with 36 % of light reduction, until microsporogenesis stage. This stage was determined using auricular distance, previous verification based in microscopy analysis. At this stage, plants were treated with low temperature (5°C) for 24 h, under dark, and using Ambar-INIA and Susan as cold tolerant genotypes. After stress, plants were returned to field conditions for recovery, and ratio between panicle weight from control and treated plants was compared. In general, the 90 % of the genotypes were negatively affected for the low temperatures. Three genotypes presented a high ratio of total grain weight per panicle and 13 genotypes showed a very low ratio of grain weight. In conclusion, the cold tolerance of some rice genotypes can be key for the future generation of cold tolerant cultivar at reproductive stage.

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