



RAFV Conference 2023
XXXIV Argentinian Meeting of Plant Physiology
SEPT 24 - 27 > **ROSARIO** | Argentina



SOCIEDAD ARGENTINA
DE FISIOLÓGÍA VEGETAL



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Welcome

Welcome to the XXXIV Meeting of the Sociedad Argentina de Fisiología Vegetal (SAFV)!

Generating tools for sustainable production in the framework of global change

It is a pleasure to welcome all of you to RAFV2023. We have been given the privilege of organizing this meeting almost at the moment of celebrating the 65th anniversary of the creation of our Society and celebrating – at the same time – the forty years of democracy in Argentina. Our scientific society, throughout this period, has notably expanded its interests and multiplied the number of its members. Their work has reached a growing depth and the achievements of its members, while making us proud, allow us to glimpse a capacity not yet fully explored to face long-postponed debates. We dare to say that it is a scientific society that has long since reached its maturity and that is, therefore, in a position to contribute to the important challenges that, within our area of concern, the country and the future of its inhabitants demand us.

One of these challenges is to ensure more and better food for the inhabitants of our country and the world, taking into account the development of regional and local economies. Another challenge is the contribution to the development of new technologies to add value to our products as well as to the education of highly trained peers who would illuminate the public debate in different areas linked to agricultural production and plant biotechnology. The challenges posed are even greater in the context of the global change that our planet is experiencing as a result of anthropogenic activities. This meeting seeks to link the studies generated in basic science with those that involve the development of new technologies within the framework of the multiple stress conditions imposed by global change.

To do this, we have convened a wide group of outstanding scientists, with the purpose of sharing and exchanging their experiences with the almost 400 researchers registered for this meeting from our country, from other countries of Latin America, North America, as well as from other continents. At the same time, the meeting includes twelve short talk presentations and more than 250 presentations in poster form. Central to the purpose that motivates us, two round tables are proposed in which topics linked to agricultural production in the current context will be debated.

We cannot close this welcome without thanking all the state and private entities that, generously, have made a substantial contribution to make this meeting possible. To all of them: Thank you!

We hope that this meeting, held in the light of democracy and the recognition of the plurality of voices, constitutes an appropriate milestone for the celebration of our 65 years of existence!

Kind regards,

SAFV Board of Directors - RAFV 2023 Organizing Committee



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Acknowledgements

- Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET)
- Agencia Nacional de Promoción de la Ciencia, el Desarrollo Tecnológico y la Innovación (ANPCYT I+D+i)
- Provincia de Santa Fe
- Universidad Nacional de Rosario (UNR)
- Universidad Nacional de San Martín (UNSAM)
- Facultad de Ciencias Bioquímicas y Farmacéuticas
- American Society of Plant Biologists, Journal of Experimental Botany
- The Company of Biologists, EMBO
- The Annals of Botany Company
- Plant Physiology and Biochemistry
- The FEBS Journal, FEBS Letters
- YTEC
- Instrumentos del Sur
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Dr. Pablo Manavella	<i>IIL-CONICET, UNL</i>
Dr. Ezequiel Margarit	<i>CEFOBI-CONICET, UNR</i>
Dra. Gabriela Pagnussat	<i>IIB-CONICET, UNMDP</i>
Dr. Javier Palatnik	<i>IBR-CONICET, UNR</i>
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Dra. Carla Schommer	<i>IBR-CONICET, UNR</i>
Dra. Gabriela Soto	<i>INTA CASTELAR</i>
Dra. María Ines Zanor	<i>IBR-CONICET, UNR</i>



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September 24	September 25	September 26	September 27
From 13:30 hs. Acreditación	Room A: 08:30 - 10:00 Symposium: CRISPR and new technologies <i>Speakers: Dr Gabriela Soto, Dr Gabriela Massa, Dr Emilia Bottero</i>	Room A: 08:30 - 10:00 Symposium: Molecular farming <i>Speakers: Dr Silvana Petruccelli, Dr Marina Clemente, Dr Carlos E. Hernando</i>	Room A: 08:30 - 10:00 Symposium: Plant Molecular Biology <i>Speakers: Dr Nicolas Bologna, Dr Mariano Perales, Dr Ivana Viola</i>
	Room B: 08:30 - 10:00 Symposium: Crop Ecophysiology <i>Speakers: Dr Ignacio Hisse, Dr Peter Searles, Dr María Verónica Rodríguez</i>	Room B: 08:30 - 10:00 Symposium: Plant Mineral Nutrition <i>Speakers: Dr Carla Caputo, Dr Christian Danna, Dr Mariana Obertello</i>	Room B: 08:30 - 10:00 Symposium: Physiology of horticultural crops <i>Speakers: Dr Diego Lijavetsky, Dr Fernando Carrari, Dr Carlos Grellet</i>
	10:00 - 10:30: Coffee Break		
	Room A: 10:30 - 11:30 Keynote Lecture Dra. Danielle Way <i>"Winners and losers: Climate change effects on forests and crops"</i>	Room A: 10:30 - 11:30 Keynote Lecture Dr. Yunde Zhao <i>"New approaches to auxin biology: unexpected findings"</i>	Room A: 10:30 - 11:30 Keynote Lecture Dr. Marcelo Yanovsky <i>"Transcriptional and post-transcriptional regulatory networks that modulate the adaptation of plants to daily changes in light and temperature"</i>
	Room A: 11:30 - 12:00 Short talk <i>Speakers: Dr Mariana Carignani Sardo, Dr Rosario Pantaleno</i>	Room A: 11:30 - 12:00 Short talk <i>Speakers: Dr Yésica Chazarreta, Dr Ariel Gutierrez Oyarzum</i>	Room A: 11:30 - 12:00 Short talk <i>Speakers: Dr Pablo Calzadilla, Dr Paula Calace</i>
	Room B: 11:30 - 12:00 Short talk <i>Speakers: Dr Juan Cagnola, Lic Cesar Chavez</i>	Room B: 11:30 - 12:00 Short talk <i>Speakers: Dr Ana Cislaghi, Dr Pedro Bellis</i>	Room B: 11:30 - 12:00 Short talk <i>Speakers: Dr Ana Arruabarrena, Dr Ariel Orellana</i>
	12:00 - 13:30 Lunch time		
	Room A: 13:30 - 14:30 Keynote Lecture Dr. Gustavo Macintosh <i>"Vacuolar RNA salvage and cellular homeostasis in Arabidopsis"</i>	Room A: 13:30 - 15:00 Symposium: Plant Metabolism <i>Speakers: Dr Verónica Maurino, Dr Hannetz Roschztardt, Dr Leonardo Curatti</i> Room B: 13:30 - 15:00 Symposium: Forest Technology <i>Speakers: Dr María Elena Fernández, Dr Gustavo Oberschelp, Dr María Verónica Arana</i>	Room A: 13:30 - 14:30 Ann Bot Keynote Lecture Dra. Yoselin Benitez-Alfonso <i>"Plasmodesmata and callose interplay in the regulation of plant root development"</i>
	14:30 - 16:30 Coffee Break & Posters session I (posters 1 - 85)	15:00 - 17:00 Coffee Break & Posters session II (posters 85 - 170)	14:30 - 16:30 Coffee Break & Posters session III (posters 171 - 254)
	16:15 - 17:00 Opening Ceremony	Room A: 16:30 - 18:00 Round Table: Challenges of Agro-biotechnology in Argentina <i>Participants: Ing Agr Perla Godoy, Dr Claudio Dunan, Dr Sergio Romano, Ing Sebastián Reinoso</i>	Room A: 17:00 - 18:30 Round Table: Challenges of crop production and environmental sustainability <i>Participants: JO Jorgelina Hiba, Dr Virginia Luquez, Dr Leticia Mesa, Dr José Luis Vesprini, Dr Ruben Dario Quintana</i>
Room A: 17:00 - 18:00 EMBO Keynote Lecture: Dr. Crisanto Gutierrez <i>"Understanding root growth: more complex than anticipated"</i>	Room A: 18:00 - 19:00 SAFV Assembly	Room A: 18:30 - 19:30 ARG Plant Women	Room A: 18:00 - 18:30 Closing Ceremony
19:00 - 21:00 Welcome Cocktail			



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Scientific Program

September 24th

- 14.00 - 16.15** **Accreditation**
- 16:15 - 16:50** **Opening Ceremony**
- 16.50 - 17.00** **Appointment of Professor Edith Taleisnik as honorary partner**
- 17.00 - 18.00** **EMBO Keynote Lecture: Dr Crisanto Gutierrez**
"Understanding root growth: more complex than anticipated"
Coordinators: Dr Javier Palatnik & Dr Paula Casati
- 18.00 - 19.00** **Keynote Lecture: Dr Raquel Chan**
"Small and almost undetectable proteins play crucial roles in plant development and adaptation to environmental conditions"
Coordinators: Dr Nestor Carrillo & Dr Fabiana Drincovich
- 19.00 - 21.00** **Welcome Cocktail**

September 25th

- 08.30 - 10.00** **Symposia Room A: Symposium CRISPR and new technologies**
Coordinators: Dr Gabriela Soto & Dr Mariana del Vas
- 08.30 - 09.00 **Dr Gabriela Soto** *"Molecular Improvement of Alfalfa using CRISPR/Cas9"*
- 09.00 - 09.30 **Dr Gabriela Massa** *"Next generation potatoes obtained through gene editing"*
- 09.30 - 10.00 **Dr Emilia Bottero** *"Combining Synthetic Biology and Gene Editing for the Development of a New Generation of Non-GMO Crops"*
- Symposia Room B: Symposium Crop Ecophysiology**
Coordinator: Dr Cecilia Rousseaux
- 08.30 - 09.00 **Dr Ignacio Hisse** *"Genetic and physiological mechanisms responsible for maize kernel weight and source-sink relations under contrasting nitrogen supply levels"*
- 09.00 - 09.30 **Dr Peter Searles** *"Ecophysiological responses of olive trees to warming in different phenological stages of crop development"*
- 09.30 - 10.00 **Dr María Verónica Rodríguez** *"Problems caused by excessive or insufficient seed dormancy in crops. Search for solutions in sunflower and grain sorghum"*
- 10.00 - 10.30** **Coffee Break**
- 10.30 - 11.30** **Keynote Lecture: Dr Danielle Way**
"Winners and losers: Climate change effects on forests and crops"
Coordinator: Dr Cecilia Rousseaux
- 11.30 - 12.00** **Short Talks: Room A**
Coordinator: Dr Diego Sánchez
- 11.30 - 11.45 **Dr Mariana Carignani Sardoy** *"Importance of Calcium ATPases in root hair development in Arabidopsis thaliana"*
- 11.45 - 12.00 **Dr Rosario Pantaleno** *"The role of mitochondrial H₂S in stomatal immunity"*



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September 25th

Short Talks: Room B

Coordinator: Dr Paula Fernández

- 11.30 - 11.45** **Dr Juan Cagnola** "Did selection for tolerance to high plant density improve maize growth response in water stress conditions?"
- 11.45 - 12.00** **Lic Cesar Chavez** "Effects of flooding on the growth of different cultivars of cassava (*Manihot esculenta* Crantz) plants grown in greenhouse conditions"
- 12.00 - 13.30** **Lunch**
- 13.30 - 14.30** **Keynote Lecture: Dr Gustavo Macintosh**
"Vacuolar RNA salvage and cellular homeostasis in *Arabidopsis*"
Coordinators: Dr Carlos García Mata & Dr Susana Gallego
- 14.30 - 16.30** **Coffee Break and Posters session I: Posters: 1 - 85**
- 16.30 - 18.00** **Round Table: Challenges of Agro-biotechnology in Argentina**
Confirmed Participants: Ing Agr Perla Godoy, Dr Claudio Dunan, Ing Sebastián Reinoso, Dr Sergio Romano
Coordinators: Dr Fabiana Drincovich & Dr Raquel Chan
- 18.00 - 19.30** **SAFV Assembly (Asamblea de Socios)**

September 26th

08.30 - 10.00 Symposia Room A: Molecular farming

Coordinators: Dr María Victoria Busi & Marcela Dotto

- 08.30 - 09.00** **Dr Silvana Petruccelli** "Strategies to enhance foreign protein synthesis in the secretory pathway of plant cells"
- 09.00 - 09.30** **Dr Marina Clemente** "Molecular farming as a biotechnological tool in the production of vaccine antigens"
- 09.30 - 10.00** **Dr Carlos Esteban Hernando** "Making up for lost time: "Development of a New Breeding Techniques program and its application to the cultivation of Cannabis"

Symposia Room B: Mineral Plant Nutrition

Coordinators: Dr Andrea Galatro & Dr Jorge Moriconi

- 08.30 - 09.00** **Dr Carla Caputo** "Fluctuations in phloem transport of assimilates in response to mineral nutrition"
- 09.00 - 09.30** **Dr Christian Danna** "Plants' deceiving game to tame bacterial foes"
- 09.30 - 10.00** **Dr Mariana Obertello** "Improving nitrogen use in rice with gene networks"

10.00 - 10.30 Coffee Break

- 10.30 - 11.30** **Keynote Lecture: Dr Yunde Zhao**
"New approaches to auxin biology: unexpected findings"
Coordinators: Dr José Estevez & Dr Gabriela Pagnussat



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Scientific Program

September 26th

11.30 - 12.00

Short Talks Room A:

Coordinator: Dr Paula Fernández

11.30 - 11.45

Lic Yésica Chazarreta "Maize grain dry-down: improving predictive models"

11.45 - 12.00

Dr Ariel Gutierrez Oyarzún "Combined effects of cytokinins and brassinosteroids applied at flowering on grain yield and components of rapeseed"

Short Talks Room B:

Coordinator: Dr Carlos Bartoli

11.30 - 11.45

Dr Ana Cislaghi "The mitochondrial enzyme ProDH controls the cytosolic redox homeostasis in *Arabidopsis*"

11.45 - 12.00

Dr Pedro Bellis "NO Way Out: Nitric Oxide Blocks Autophagy"

12.00 - 13.30

Lunch

13.30 - 15.00

Symposia Room A: Symposium Plant Metabolism

Coordinators: Dr Carlos Figueroa & Elina Welchen

13.30 - 14.00

Dr Veronica Maurino "Optimization of NAD-ME for C4 physiology in eudicots: A three-way dance story"

14.00 - 14.30

Dr Hannetz Roschztardt "The diverse iron distribution in seeds"

14.30 - 15.00

Dr Leonardo Curatti "Genomic insights into the metabolism of endo-cyanobionts of diatoms"

Symposia Room B: Symposium Forest Technology

Coordinators: Dr Ezequiel Margarit

13.30 - 14.00

Dr María Elena Fernández "Forests facing drought and heat-waves: the need of a physiological-based forestry to increase plantations adaptability to climate change"

14.00 - 14.30

Dr Gustavo Pedro Javier Oberschelp "Is cold acclimation the key to frost tolerant *Eucalyptus* in a warming world?"

14.30 - 15.00

Dr María Verónica Arana "Unravelling the responses of non-model tree species to the environment: the case of *Nothofagus pumilio* a key species of the subantarctic forests"

15.00 - 17.00

Coffee Break & Poster session II: Posters 86 – 170

17.00 - 18.30

Round Table:

Challenges of crop production and environmental sustainability

Confirmed Participants: **JO Jorgelina Hiba, Dr Virginia Luquez, Dr Leticia Mesa, Dr José Vesprini, Dr Ruben Quintana**

Coordinators: Dr Mariana Saigo & Dr Juan José Guiamet

18.30 - 19.30

ARG Plant Women



September 27th

08.30 - 10.00 **Symposia Room A: Plant Molecular Biology**

Coordinators: Dr Ramiro Rodríguez & Dr Carla Schoemer

08.30 - 09.00 **Dr Nicolas Bologna** "RNA silencing pathways in plants"

09.00 - 09.30 **Dr Mariano Perales** "Circadian clock functions in woody perennials"

09.30 - 10.00 **Dr Ivana Viola** "Regulatory networks of TCP transcription factors during Arabidopsis seedling development "

Symposia Room B: Physiology of horticultural crops

Coordinators: Dr Valeria Lara & Dr Pedro M. Civello

08.30 - 09.00 **Dr Diego Lijavetzky** "Juvenile-to-adult phase transition in grapevine"

09.00 - 09.30 **Dr Fernando Carrari** "Regulation of vitamin E metabolism in tomato"

09.30 - 10.00 **Dr Carlos Grellet** "Ethylene receptors are required to activate the plant defense response induced by AsES"

10.00 - 10.30 **Coffee Break**

10.30 - 11.30 **Keynote Lecture: Dr Marcelo Yanovsky**

"Transcriptional and post-transcriptional regulatory networks that modulate the adaptation of plants to daily changes in light and temperature"

Coordinators: Dr Eugenia Zanetti & Dr Ana Laxalt

11.30 - 12.00 **Short Talks Room A:**

Coordinator: Dr Ramiro Lascano

11.30 - 11.45 **Dr Pablo Calzadilla** "Shedding light onto the role of the Plastid terminal oxidase (PTOX) as a safety valve for photoprotection in plants"

11.45 - 12.00 **Dr Paula Calace** "Unveiling the Role of NADP-ME and NAD-ME in C4 Photosynthesis of Setaria and Panicum"

Short Talks Room B:

Coordinator: Dr Pedro M Civello

11.30 - 11.45 **Dr Ana Arruabarrena** "Targeted disruption of tomato CYC-B gene improves postharvest color development and cold stress tolerance"

11.45 - 12.00 **Dr Ariel Orellana** "Blooming in the desert: Unraveling the secrets of Cistanthe longiscapa's adaptation"

12.00 - 13.30 **Lunch**

13.30 - 14.30 **Annals of Botany Keynote Lecture: Dr Yoselin Benitez-Alfonso**

"Plasmodesmata and callose interplay in the regulation of plant root development"

Coordinator: Dr Gabriela Auge

14.30 - 16.30 **Coffee Break and Posters session III: Posters: 171 - 254**

16.30 - 18.00 **Symposia Room A: Symposium Biotic and Abiotic Stress**

Coordinators: Dr María Inés Zanol & Dr Marina Pombo



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September 27th

- 16.30 - 17.00 **Dr Georgina Fabro** *"Enhancing insight into the function of plant filamentous-pathogens' Effectors: suppression of immunity via manipulation of developmental hormonal path"*
- 17.00 - 17.30 **Dr Erwan Michard** *"Function of Plant Glutamate Receptor-like channels (GLR) in adaptation to abiotic stress"*
- 17.30 - 18.00 **Dr Carlos Manacorda** *"Evaluation of the effect of TuMV infection on drought tolerance and water management at the whole plant level in Arabidopsis"*
- Symposia Room B: Symposium Vegetative and Reproductive Development**
Coordinators: Dr Silvina Pessino & Dr Alvaro Quijano
- 16.30 - 17.00 **Dr Fernanda Gonzalez** *"Photoperiod sensitivity and spike fruiting efficiency as alternatives to increase wheat yield potential"*
- 17.00 - 17.30 **Dr Silvina Pessino** *"From comparative transcriptomics in apomictic species to the induction of apospory-like phenotypes in Arabidopsis"*
- 17.30 - 18.00 **Dr Ramiro Rodríguez Virasoro** *"Mitotic and Endoreplication Cell Cycles in Plant Organ Growth"*
- 18.00 - 18.30 **Closing Ceremony**



Nº	Title	Presenting Author	Co-Authors
1	<i>Different strategies to optimize the inoculation of potato plants with Methylobacterium sp. 2A</i>	Martinez-Moyano, E.	Grossi, C.E.M.; Gitman, I.F.B.; Ulloa, R.
2	<i>Optimization of the TRAP technique in common bean to study translational dynamics during nitrogen-fixing symbiosis.</i>	Eylenstein, A.E.	Reynoso, M.A.; Zanetti, M.E.; Blanco, F.A.
3	<i>Study of the transcriptional regulation of genes involved in endocytic vesicular traffic by a WRKY transcription factor induced during response to sal</i>	Plata Arboleda, S.	Ruiz-Lara, S.
4	<i>Polymorphic inverted repeats near coding genes impact chromatin topology and phenotypic traits in Arabidopsis thaliana</i>	Arce, A.L.	Mencia, R.; Cambiagno, D.A.; Lang, P.L.; Liu, C.; Burbano, H.A.; Weigel, D.; Manavella, P.A.
5	<i>Generation of bioinformatics tools for the integrative analysis of environmental, genomic and transcriptomic data</i>	Da Ponte, M.	Gendelman, M.; Rabinovich, A.; Chernomoretz, A.; Hernando, C.E.
6	<i>ZmS5H: a multi-functional enzyme regulating plant development and senescence in maize</i>	Serra, P.	Petrich, J.; Righini Aramburu, S.; Falcone Ferreyra, M.L.; Casati, P.
7	<i>Temperature during seed maturation influences weedy rice seed dormancy and germination</i>	Auge, G.A.	Takama, R.; Imaizumi, T.
8	<i>First functional study of a subfamily III member of the Snakin/GASA family in Solanum tuberosum</i>	Vazquez-Rovere, C.	Nahirñak, V.; Almasia, N.I.
9	<i>Assessing the small RNAs profile between potato diploid hybrid and its resynthesized allopolyploid.</i>	Zavallo, D.	Leone, M.; Cara, N.; Cuello, R.; Marfil, C.M.; Masuelli, R.W.; Asurmendi, S.
10	<i>Germination proteins of soybean embryonic axes</i>	Montechiarini, N.	Yordán, E.; Perotti, V., Collado, A.; Martínez, M.; Gosparini, C.
11	<i>Getting out of the shade: characterization of the transcriptional network that modulates shade avoidance responses in soybean.</i>	Bianchimano, L.	Hernando, E.; Careno, D.; Marchionni, E.; Marzetti, M.; Dezar, C.; Vasquez, M.; Mora Garcia, S.; Yanovsky, M.; Casal, J.
12	<i>Auxin and coronatine signaling converge in guard cells</i>	Rios, C.A.	Pieckenstein, F.; Gudesblat, G.E.
13	<i>Identification and characterization of ATPase II-A type Ca²⁺ transporter systems (ECAs) involved in polar cell expansion of root hairs.</i>	Domínguez, G.D.	Estevez, J.M.
14	<i>COP1 as a key redox-controlled regulator of hypocotyl growth under shade in plants</i>	Iglesias, M.J.	Costigliolo Rojas, C.; Bianchimano, I.; Legris, M.; Schön, J.; Gergoff Grozeff, G.E.; Bartoli, C.G.; Blázquez, M.A.; Alabadi, D.; Zurbriggen, M.D.; Casal, J.J.
15	<i>RS31: a novel player involved in the regulation of light-induced seed germination and flowering in Arabidopsis thaliana</i>	Tognacca, R.S.	Rodríguez, F.S.; Cartagena, C.M.; Servi, L.; Kalyna, M.; Petrillo, E.
16	<i>Abscisic acid and ABI4 appears to be involved in Arabidopsis thaliana gamma carbonic anhydrases regulation during embryogenesis</i>	Valiñas, M.	Marchetti, F.; Pagnussat, G.; Zabaleta, E.
17	<i>DNA methylation regulates thermoresponsive growth in Arabidopsis by modulating CRY1 expression</i>	Capella, M.	Garro, M.
18	<i>A role for a CONSTANS gene homolog in Arabidopsis thaliana development</i>	Shalom, M.S.	Careno, D.A.; San Martín, A.; Mateos, J.L.; Yanovsky, M.J.

N°	Title	Presenting Author	Co-Authors
19	<i>Pleiotropic effects associated with the expression of a recombinant fibroblast growth factor in transplastomic plants</i>	Müller, C.	Abraham, M.; Guaglianone, M.; Bravo-Almonacid F.F.; Blanco, N.E.; Segretin, M.E.
20	<i>Interactions of Phytochromes B and C fine tune the response to ambient light signals</i>	Canelo, M.	Lorenzo, C.D.; Cerdán, P.D.
21	<i>Unraveling differential roles of ATG14 and VPS38 in Physcomitrium patens apical growth</i>	Saavedra, L.	Pettinari, G.; Liberatore, F.; Lascano, R.
22	<i>Deciphering dependent and independent roles for the families of circadian clock coactivators: what can we learn from high-order null mutants?</i>	de Leone, M.J.	Croas, C.L.; Yanovsky, M.J.
23	<i>Connection between AtSINA-L7 and auxin metabolism</i>	Tello León, C.G.	Busi, M.V.; Gómez-Casati, D.F.
24	<i>Cell architecture during plant growth and development</i>	Burachik, N.	Vacs, P.; Santin, F.; González-Schain, N.; Mazzella, A.
25	<i>The ecophysiology of seedling recruitment during floods: The case of Echinochloa colona, a harmful arable weed of extensive crops</i>	Mollard, F.	Echeverry Holguín, J.; Crepy, M.; Striker, G.G.
26	<i>Morphological diversity, selective signals and evidence of local adaptation in Argentinean maize landraces</i>	Freilij, D.	Defacio, R.A.; Heck, M.I.; Fariza, S.I.; De Lucia, A.D.; Ferreyra, M.; Paniego, N.B.; Domínguez, P.G.; Lia, V.V.
27	<i>Altitude-plant density interaction on Andean maize: contributions to decision making</i>	Salve, D.A.	Maydup, M.L.; Tambussi, E.; Salazar, G.; Antonietta, M.
28	<i>Dormancy release or viability loss? The fate of Lolium multiflorum Lam. seeds depends on temperature and seed water content.</i>	Royo Simonella, L.A.	Canchero, J. O.; Batlla, D.
29	<i>Critical periods for the expression of vegetative-reproductive plasticity in maize</i>	Espelet, F.	Rotili, D. H.; Maddonni, G. A.
30	<i>Yield and quality of buckwheat (Fagopyrum esculentum Moench) at different sowing dates and nitrogen fertility conditions.</i>	Antequera, S.A.	Guglielmini, A.C.; Alvarez Prado, S.; Rocca, C.M.; Miralles, D.J.
31	<i>Sensibility of seed yield and quality traits of rapeseed to increased temperature and reduced source-sink ratio in different phases of grain filling</i>	Verdejo, J.F.	Castro, C.; Bustos-Korts, D.; Calderini, D.
32	<i>Zinc, aminoacid and algae extract application seed treatments effect on growth and yield of Triticum aestivum with different predecessor herbicides.</i>	Arevalo, E.S.	Michel, A.; Ludi Barzante, L.; Foti, M.N.; Chajud, S.
33	<i>Validation of candidate genes associated to earliness per se, on chromosome 5D of bread wheat</i>	Pozzi, F.I.	Ghione, C.E.; Helguera, M.; Lombardo, L.A.; Felitti, S.A.
34	<i>Yield generation and radiation use in hybrids with and without a genetic alteration in height.</i>	Pluda, P.	Villavicencio, J.; Rotili, D.H.; Uribebarrea, M.; Röig, J.; Maddonni, G.; Cagnola, J.
35	<i>Genetic progress in malting barley in Argentina under contrasting environments</i>	Abeledo, L.G.	Ibañez, C.; Comacchio, J.; Rondanini, D.P.; Miralles, D.J.
36	<i>Flower bud abortion is associated with cavitation sensitivity in cotton (Gossypium hirsutum) cultivar.</i>	Colli, S.L.	Tarrago, J.R.; Mignolli, F.
37	<i>The water concentration of Acrocomia totai fruits as a predictor of the dynamics of fruit filling and oil accumulation</i>	Ploschuk, E.L.	Wassner, D.F.; Bertero, H.D.

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38	<i>Understanding the thermal regime and cultivar effects on quality parameters in olive fruits using a field network with contrasting Argentinian growing</i>	Torres, M.	Pierantozzi, P.; Contreras, C.; Tivani, M.; Mastio, V.; Gentili, L.; González Gilyam, A.; Searles, P.; Brizuela, M.; Fernández, F.; Toro, A.; Puertas, C.; Trentacoste, E.; Kiessling, J.; Maestri, D.
39	<i>Impact of color and anti-hail net installation system on microclimate and leaf water status in Vitis vinifera L. cv. Malbec in Mendoza, Argentina</i>	Nahuel, C.G.	Castro, P.; Giménez, V.; Osorio, R.; Lázaro, H.; Gómez, A.; Nahuel, E.D.; Vico, M.; Luna, A.; Carbajal Ramos, I.; Prieto, J.
40	<i>Differentiation of soybean quality parameters according to production environment: linkage to the origin</i>	Carpaneto, B.	Eiza, M.; Montoya, M.; González Belo, R.; Izquierdo, N.; Quiroz, F.
41	<i>Spatial and temporal variability of single and double soybean yields across Argentina</i>	Di Mauro, G.	Fernandez-Long, M.E.; Alvarez Prado, S.
42	<i>Effect of legume/cereal intercropping on the inhibition of N₂ fixation caused by exogenous N supply in faba beans and peas</i>	Salinas Roco, S.	Morales-González, A.; Carrasco, B.; Del Pozo, A.; Cabeza, R. A.
43	<i>OsOXR-Q12 protein is involved in cellular defense homeostasis and contributes to salt stress tolerance in Oryza sativa</i>	Becerra-Agudelo, E.	Welchen, E.
44	<i>The foliar application of Bacillus sp. CHEP5 protects peanut plants against phytopathogens by inducing systemic resistance</i>	Figueredo, M.S.	Tonelli, M.L.; Loser, U.; Fabra A.
45	<i>Screening of endophytic bacteria by protection against water deficit in peanut plants</i>	Espinosa Herlein, M.A.	Ruiz, O.A.; Guzzo, M.C.; Monteoliva, M.I.
46	<i>Frost tolerance in vegetative stages and allelic characterization in wheat</i>	Serrago, R.A.	Comacchio, J.E.; Vanzetti, L.S.; Miralles, D.J.
47	<i>Role of brassinosteroids in salt tolerance responses of halophytic woody plants: a study on Strombocarpa strombulifera (Lam.) A. Gray plants.</i>	Llanes, A.	Gatica, M.; López, E.; Masciarelli, O.; Iparraguirre, J.
48	<i>Participation of tomato ERF30 in plant immunity against Pseudomonas syringae pv. tomato (Pst)</i>	Sirvent, E.	Pombo, M.A.; Rosli, H.G.
49	<i>Brassica rapa L. and Rapistrum rugosum L.: species of remedial capacity in saline soils contaminated with effluents with high environmental impact</i>	Fiasconaro, M.L.	Abrile, M.; Osorio, J.; Orecchia, D.; da Silva Júnior, F.M.R.; Lovato, M.E.
50	<i>Auxin and ethylene are essential in the tomato response to mechanical treatment</i>	Castro Estrada, J.	Ramallo, A.; Salazar, S.; Cabello, J.V.; Filippone, M.P.; Chan, R.L.; Welchen, E.
51	<i>Physiological characterization of drought tolerance in peanut</i>	Monteoliva, M.I.	Guzzo, M.C.; Posada, G.A.; Suarez, P.; Luna, F.D.; Schenfeld, E.; Espinosa Herlein, M.A.; Bustamante, O.M.; Ruiz, O.A.
52	<i>Functional analysis of Ilex paraguariensis metallothionein genes in transformed Lotus tenuis plants subjected to abiotic stress: Preliminary results</i>	Alvarez, M.Y.	Espasandin, F.D.; Acevedo, R.M.; Sansberro, P.A.
53	<i>Integral analysis of morphophysiological variables associated with drought tolerance in Leptochloa crinita</i>	Dominguez, D.L.E.	Panasiti Ros, J.; Cavagnaro, J.B.; Cavagnaro, P.F.
54	<i>Production of Nanobodies for Potato Virus Y (PVY) detection</i>	Gudesblat, G.	Mora-Alvarado, E.; Bok, M.; Parreño, V.; Ibañez, L.I.

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55	<i>Frost tolerance and adventitious rooting in hybrid clones of Eucalyptus</i>	Ayala, P.G.	Vivas, V.L.; Sansberro, P.A.; Harrand, L.; Margarit, E.; Oberschelp, G.P.J.
56	<i>A vertically transmitted fungal symbiont prevents the drought-induced intergenerational inhibition of seed germination</i>	Zarraga Barco, F.	Ueno, A.C.; Casabella, M.P.; Casas, C.; Molina-Montenegro, M.; Ramos, P.; Schnyder, H.; Gundel, P.E.
57	<i>Streptomyces spp. alleviates drought stress in soybean plants, resulting in improved plant status and yield</i>	Maldonado, R.A.	Iacomozzi, O.; Villafañe, D.L.; Bianchi, J.S.; Rodríguez, E.; Chiesa M.A.
58	<i>Chlorophyll retention and low oxygen consumption rates in soybean seeds produced under heat-drought stress</i>	Martinez, M.A.	Montechiarini, N.H.; Gosparini, C.O.; Oppedijk, B.; van Duijn, B.
59	<i>Resistance response of soybean genotypes to Asian Soybean Rust under controlled temperature conditions</i>	Cambursano, M.V.	Cairo, C.A.; Bianchi, J.S.; Gomez, R.L.; Quijano, A.
60	<i>Nuclear-SnRK1 localization improve salt stress tolerance responses</i>	Lando, A.P.	Barbieri, G.; Nome, C.; Martínez-Noël, G.; Rodriguez, M.
61	<i>Role of proteins involved in miRNAs biogenesis in response to UV-B radiation in Arabidopsis thaliana plants</i>	Sheridan, M.L.	Casati, P.
62	<i>The RdDM pathway regulates root hair growth and development under moderate salt stress in Arabidopsis thaliana.</i>	Ferrer Vieyra, C.	Auge, G.
63	<i>Expression of the alfalfa gene MsMDHAR increases root biomass and promotes tolerance to hydric stress in transgenic Arabidopsis.</i>	Jaime, C.L.	Dezar, C.; Pagán Muñoz, I.; Dunger, G.
64	<i>PIF4 enhances the expression of SAUR genes to promote growth in response to nitrate</i>	Pereyra, M.E.	Costigliolo Rojas, C.; Jarrell, A.F.; Hovland, A.S.; Snipes, S.A.; Nagpal, P.; Alabadi, D.; Blázquez, M.A.; Gutiérrez, R.A.; Reed, J.W.; Gray, W.M.; Casal, J.J.
65	<i>Role of the jasmonic acid pathway in UV-B-mediated responses in Arabidopsis</i>	Medina-Fraga, A.L.	Crocco, C.D.; Ballaré, C.L.
66	<i>Exploring the role of the alternative-splicing regulator PRMT5 in temperature responses in plants.</i>	San Martín, A.	Yanovsky, M.J
67	<i>Role of PHYTOCHROME INTERACTING FACTOR 7 in the rapid response to elevated ambient temperature and shade in Arabidopsis</i>	Murcia, G.	Casal, J.
68	<i>Unraveling the impact of high temperature on autophagy-linked plant immunity</i>	Lescano López, I.	Mesquida Nardini, M.C.; Cecchini, N.M.; Lescano, R.H.
69	<i>Study of ZmNADP-ME3 transcriptional regulation</i>	Saigo, M.	Rolle, L.M.; Gismondi, M.
70	<i>Heat priming in seeds induces antioxidant defense in maize seedling</i>	Pena, L.B.	Eggel, M.L.; Pérez Chaca, M.V.
71	<i>Involvement of carbon and nitrogen metabolism in the recovery of plant health of Lotus spp.- Fusarium spp. interactions</i>	Nieva, A.S.	Erbán A.; Alsina, M.L.; Bernardi-Lima, N.; Ruiz O.A.; Kopka, J.
72	<i>Postharvest UV-B treatment in strawberry fruit (Fragaria x ananassa): effects on the signalling pathway and secondary metabolites biosynthesis.</i>	Barriga Lourenco, A.	Casajus, V.; Martínez, G.; Civello, M.
73	<i>The alteration of chlorophyll metabolism affects the germination of tomato seeds</i>	Santoro, L.J.	De Luca, M.B.; Echeverría, M.; Burgos, E.; Conte, M.; Olivari, F.; Beracochea, V.; Bermúdez, L.; Asís, R.; Carrari, F.

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74	<i>Evaluation of two contrasting sunflower inbred genotypes for leaf senescence trait under two different nitrogen supplies</i>	Corzo, M.	Trupkin, S.; Becheran, D.; Ploschuk, E.; Alvarez, D.; Heinz, N.; Fernandez, P.
75	<i>Hormonomics of Prunus persica (peach) leaves inoculated with Taphrina deformans</i>	Novello, M.A.	Petřík, I.; Karady, M.; Oklešková, J.; Novák, O.; Valentini, G.H.; Strand, M.; Lara, M.V.
76	<i>Free polyamines content and oxidative response during cold storage of sunburn apples</i>	Vita L. I.	Spera, N.; Colavita G.M.
77	<i>Biological nitrogen fixation in maize: a comparative exploratory analysis with soybean.</i>	Piccinetti, C.F.	--
78	<i>Compatibility of endophytic bacteria with Mesorhizobium ciceri R26 in chickpea (Cicer arietinum)</i>	Sardo, M.F.	Ruiz, O. A.; Monteoliva, M.; Valetti, L.
79	<i>Dynamics of tocopherol concentrations accumulation in soybean exposed to brief episodes of heat and drought stress during grain filling</i>	Veas, R.E.A.	Ergo, V.V.; Asís, R.; Lascano, R.; Carrera, C.S.
80	<i>Functional Implications of Tudor-SN (TSN) and PRMT5 in the regulation of arginine methylation in Arabidopsis</i>	Fontana, M.C.	Agrofoglio, Y.; Torres, S.; Née, G.; Iglesias, M.J.; Mateos, J.L.
81	<i>Macroautophagy and microautophagy in arabidopsis: effects on tonoplast content and vacuolar morphology</i>	Silva, B.	Bellis, P.; Lascano, R.; Robert, G.
82	<i>Autophagy modulates sugar cell efflux from leaves in Arabidopsis</i>	Martinez, D.	Gómez, I.; Hajirezaei, M.R.; Guimet, J.J.
83	<i>Influence of the epiphyte Bacillus velezensis HIII11 isolated from strawberry on the metabolism of Arabidopsis thaliana cell wall</i>	Hirsch, M.	Burges, P.L.; Wyss, B.; Villarreal, N.; Marina, M.
84	<i>Iron content in anthocyanin-deficient mutants of Arabidopsis thaliana</i>	Vizcaino, M.	Gomez-Casati, D.F.; Pagani, M.A.
85	<i>Effect of R-loop near MIRNA transcription start site region on co-transcriptional processing and miRNA movement</i>	Fernández, J.	Gonzalo, L.; Manavella, P.
86	<i>A new biolistic method in plants for barley transformation and regeneration</i>	Busi, M.V.	Gomez Ibarra, A.R.; Souza Canada, E.D.; Permingeat, H.
87	<i>Micro RNA biogenesis and movement in plant defense priming</i>	Cambiagno, D.A.	Quevedo, L.; Alanie, N.; Tenchi, A.; Lascano, H.R.
88	<i>Convergence between splicing and miRNAs machineries in plants</i>	Contino, G.	Agrofoglio, Y.; Frixione, L.; Fera, J.; Iglesias, M.J.; Mateos, J.
89	<i>BdPAP2, a SEPALLATA-Like gene, is involved in regulating flowering time and inflorescence architecture in Brachypodium distachyon</i>	Gaido, J.	Bassi, M.; Uberti Manassero, N.; Vegetti, A.; Dezar, C.
90	<i>Effects of conditioning and storage environment on dormancy release in malting barley grains</i>	Dominguez, C.P.	Benech-Arnold, R.L.; Rodriguez, M.V.
91	<i>Effect of water stress on the endogenous content of brassinosteroids in sunflower plants during late vegetative growth (V8)</i>	Ramirez, F.	Boero, A.; Oklestkova, J.; Strnad, M.; Vigliocco, A.; Andrade, A.; Alemanno, S.
92	<i>Interaction of ascorbic acid and gibberellins in the establishment of tomato fruits</i>	Alegre, M.L.	Baldet, P.; Rothan, C.; Bres, C.; Just, D.; Okabe, Y.; Ezura, H.; Gergoff Grozeff, G.E.; Bartoli, C.G.
93	<i>Cytochrome c levels establish a mitochondrial connection to SnRK1 pathway activity for the regulation of growth and metabolism</i>	Coronel, F.P.	Gras, D.E.; Canal, M.V.; Welchen, E.; Gonzalez, D.H.
94	<i>Identification of candidate genes controlling vernalization requirement and flowering onset in carrot</i>	Morales, A.	Wohlfeiler, J.; Cavagnaro, P.F.; Galmarini, C.R.

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95	<i>The miR390/TAS3/ARF pathway governs expression of an LBD member to regulate root nodule symbiosis and root architecture in Medicago truncatula</i>	Zanetti, M.E.	Kirolinko, C.; Hobecker, K.; Cueva, M.; Botto, F.; Christ, A.; Niebel, A.; Ariel, F.; Blanco, F.; Crespi, M.
96	<i>Epitranscriptomic marks in the root nodule symbiosis</i>	Cueva Morales, M.C.	Roda, C.; Blanco, F.; Zanetti, M.E.
97	<i>Evolutionary conserved submergence responsive transcription factors involved in the formation of lateral root organs in legumes</i>	Ibarra, E.	Zanetti, M.E.; Reynoso, M.
98	<i>Transcriptome analysis give insights into the role of miR394 in the regulation of flowering genes in Arabidopsis thaliana</i>	Belen, F.	Bernardi, Y.; Rosli, H.; Pombo, M.; Vegetti, A.; Dotto, M.
99	<i>The DC1 domain protein VACUOLELESS GAMETOPHYTES is necessary for Arabidopsis reproductive organ development and anther dehiscence</i>	Amigo, N.L.	Arias, L.A.; Marchetti, F.; D'ippolito, S.; Lombardo, C.; Casalongue, C.A.; Pagnussat, G.C.; Fiol, D.F.
100	<i>Identification of the regulatory network controlling root hair growth under inorganic phosphate deficiency and high salinity in Arabidopsis thaliana</i>	Estevez, J.M.	Ibeas, M.A.; Venegas, I.; Peralta, J.M.; Moyano, T.; Jhonson, N.; Riveros, A.; Grenett-Salinas, H.; Urzúa Lehedé, T.; Acha-Escobar, R.; Muñoz-Duman, T.; Vida, E.; Álvarez, J.M.; Meneses, C.
101	<i>NAC1 directs CEP1-CEP3 peptidase expression and modulates root hair growth in Arabidopsis</i>	Rodríguez García, D.R.	Marzol, E.; Rondón Guerrero, Y.d.C.; Martínez Pacheco, J.; Berdion Gabarain, V.; Lopez, L.E.; Díaz Dominguez, G.; Estevez, J.M.
102	<i>Integration of environmental signals via ROS-MAPKs that regulate polar growth of radical hairs in Thaliana Arabidopsis at low temperature</i>	Rondon, Y.	Martinez, J.; Núñez-Lillo, G.; Urzúa, T.; Meneses, C.; Estevez, J.M.
103	<i>CYP77A7 is essential for cell wall integrity during polar growth in Arabidopsis</i>	Cascallares, M.M.	Pagnussat, G.
104	<i>The transcription factor SCL28 controls the mitotic cell cycle, endoreplication and cell expansion and differentiation in Arabidopsis thaliana</i>	López Alsina, M.M.	Barrera, V.; Lopez, M.; Goldy, C.; Vena, R.; Rodriguez, R.E.
105	<i>Cytochrome c acts as a positive growth signal in early stages of plant development</i>	Roldan, F.	Barrera, V.; Mansilla, N.; Gras, D.E.; Canal, M.V.; Rodriguez, R.E.; Welchen, E.; Gonzalez, D.H.
106	<i>BBX21 integrates brassinosteroid biosynthesis and signalling in the inhibition of hypocotyl growth under shade</i>	Gómez-Ocampo, G.	Crocco, C.D.; Cascales, J.; Oklestkova, J.; Tarkowská, D.; Strnad, M.; Mora-Garcia, S.; Pruneda-Paz, J.L.; Blazquez, M.A.; Botto, J.F.
107	<i>Embryogenesis in plant: the mitochondrial pentatricopeptide repeat protein EMB2217 is essential to sustain embryo development in Arabidopsis thaliana</i>	Marchetti, F.	Balestieri, N.; Valiñas, M.; Pettenazza, J.; Berdun, F.; Mizrahi, R.; Ostersetzer-Biran, O.; Pagnussat, G.; Zabaleta, E.
108	<i>GIS3 controls flowering through the thermosensory pathway</i>	Ibarra, V.	Barber, M.R.; Jaskolowski, A.; Freytes, S.N.; Cerdan, P.D.
109	<i>Yield strategies under contrasting water conditions in winter cereals</i>	Barnada, F.J.	Miralles, D.J.; Diez, M.M.; Alvarez Prado, S.

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110	<i>Phenology and biomass production responses of malting barley to inoculation with Azospirillum argentinense</i>	Puente, M.L.	Martinez, C.; Ibarra, L.S.; Criado, M.V.
111	<i>Soluble carbohydrates dynamics in wheat and rapeseed crops under shading, high temperature and its combination in post-flowering</i>	Rivelli, G.M.	Calderini, D.F.; Abeledo, L.G.; Miralles D.J.; Rondanini, D.P.
112	<i>Bacillus amyloliquefaciens strain PTA-4838 associated with organomineral fertilizer improves CO2 assimilation rate and light saturation point of maize</i>	Silva, M.A.	Silva, K.P.O.M.; Santos, H.L.; Ferreira, L.S.; Cassemiro P.F.; Carnietto, M.R.A.; Modenese, J.F.
113	<i>Leaf area at anthesis as conditioning of wheat baking quality</i>	Mac Maney, M.	Benech-Arnold, L.; Fritz, N.E.; Miralles, D.M.; Abeledo, L.G.
114	<i>Aboveground biomass allocation in rapeseed in response to both the increase and reduction of the source-sink ratio during grain filling</i>	Rauque, C.	Verdejo, J.; García, S.; Gutiérrez, A.; Calderini, D.
115	<i>Effect of the delay in sowing date on the content and quality of arabinoxylans in corn (Zea mays, L.) and its relation with kernel hardness</i>	Laserna, M.P.	González Belo, R.; Cerrudo, A.; Izquierdo, N.
116	<i>The impact of canopy senescence on percentage grain nitrogen concentration and grain yield in maize</i>	Guiamet, J.J.	Montenegro, M.; Antonietta, M.; Girón, P.; Antonelli, C.; Bartolozzi, M.; Martínez, S.
117	<i>Understanding the dynamics of assimilate demand and growth during grain filling in potential yield of summer maize</i>	Ogando, F.	Vega, C.
118	<i>Warming effects on growth and photosynthetic gas-exchange during the autumn and winter in young olive trees (Olea europaea L.)</i>	Cortés Molina, V.M.	Miserere, A.; Argañaraz, R.A.; Castro, D.N.; Rousseaux, M.C.; Searles, P.S.
119	<i>Plant responses to far-red supplementation and photosynthetically active radiation in an olive cultivar common to super high-density orchards</i>	Ladux, F.J.	González, C.V.; Trentacoste, E.R.; Searles, P.S.; Rousseaux, M.C.
120	<i>Impact of heat waves during the spring on the ecophysiology of young olive trees (Olea europaea L.)</i>	Argañaraz, R.A.	Miserere, A.; Agüero Alcaras, L.M.; Rojas Barrionuevo, F.G.; Castro, D.N.; Herrera, C.J.; Cortes Molina, M.V.; Rousseaux, M.C.; Searles, P.S.
121	<i>Flowering responses of young olive trees (Olea europaea) to experimental warming during summer and autumn in Northwest Argentina</i>	Miserere, A.	Searles, P.S.; Federico, A.A.; Herrera, C.J.; Brizuela, M.M.; Rousseaux, M.C.
122	<i>First approaches in the development of phenological models and zonification for walnut (Juglans regia) production in Argentina</i>	Gallo, A.E.	Calderón, F.; Calvo, F.; Calahorra, A.; Robles, J.; Trentacoste, E.
123	<i>Soil moisture levels affect nodule development in field pea (Pisum sativum L.).</i>	Ré, D.A.	Michel, A.; Caviglia, O.P.
124	<i>Does an increase in available nitrogen during the seed-filling period improve soybean seed physiological quality under field water deficit?</i>	Ergo, V.V.	Gallo, C.D.V.; Salvagiotti, F.; Carrera, C.S.
125	<i>Soybean seed composition under different water conditions</i>	Lopez, E.	Angelozzi, V.; Antonelli, M.; Alvarez Prado, S.; Gerde, J
126	<i>The effect of dwarfing genes on the rhizosphere bacterial community colonization under limiting phosphorus conditions</i>	Figuroa, P.	Gualano, L.; Moriconi, J.; Sannazzaro, A.; Santa-María, G.E.
127	<i>Biphasic pattern of MsSnRK1-sucrose at early and late stages in salt stress.</i>	Barbieri, G.	Parola, R.; Rodriguez, M.S.
128	<i>Physiological and genetic characterization of wheat lines sharply differing in sodium accumulation</i>	Silva, M.M.	Moriconi, J.I.; Gualano, L.D.; Tranquilli, G.E.; Santa-María, G.E.

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129	<i>Phenotypic characterization of a sorghum association panel for salinity stress tolerance: Key input for GWAS analysis</i>	Luna, D.F.	Bustos, D.A.; Ortiz, D.; Vieira de Sousa, L.; da Silva, R.R.; Pittaro, M.G.
130	<i>Drought stress effects on transgenic tobacco plants expressing maize NADP-ME under KAT1 promoter: trade-off between seed size, quantity, and survival</i>	Guindon, M.F.	Saper, C.; Oitaven, P.A.; Olazarán, M.J.; Drincovich, M.F.; Müller, G.L.
131	<i>Analysis of secondary metabolites and their induction by salinity (NaCl) in hairy roots of Lycium humile</i>	Reginato, M.A.	Blank, T.; Palchetti, V.; Iparraguirre, J.; Papenbrock, J.
132	<i>Effect of water stress in Megathyrsus maximus during vegetative growth and early selection of promising genotypes</i>	Arias, C.V.	Carrizo, I. M.; Grunberg, K.; Hernández, U.M.; López Colomba, E.
133	<i>High temperature improves photosynthetic electron transport but reduces stomatal conductance in flooded tomato plants</i>	Sánchez, C.L.R.	Vidoz, M.L. ; Mignolli, F.
134	<i>Influence of GLRaV-3 infection on grapevine growth, phenology, and ripening: insights from Malbec and Torrontés Riojano varieties</i>	Barrios Bogado, P.E.	Hugalde, I.P. ; Delgui, L.R.; Catania, A.A.; Gómez Talquenca, S.G.
135	<i>Contrasting photosynthetic and biochemical adjustments in two aubergine (Solanum melongena L.) flooding-tolerant rootstocks subjected to waterlogging</i>	Adis, M.J.	Vidoz, M.L.; Mignolli, F.
136	<i>Silencing of a CCT domain containing protein in tomato plants leads to increased abiotic stress tolerance.</i>	Renzi, D.J.	Zayas, A.; Sossi, M.L.; Zanor, M.I.
137	<i>Native strain Enterobacter 64S1 enhances drought tolerance and melatonin levels of tomato plants</i>	Cohen, A.	Jofré, M.F.; Mammana, S.; Pérez-Rodríguez, M.M.; Gomez, F.J.V.; Silva, M.F.
138	<i>Chloroplasts localization of Citrus psorosis virus movement protein: implications on viral spread and host defense response evasion</i>	Marchesini, A.	Robles Luna, G.; Mazzolenis, R.; Peña, E.J.
139	<i>Identification of genes involved in salinity tolerance in a collection of alfalfa insertional mutants</i>	Jozefkowicz, C.	Fernández, K.; Gómez, C.; Ayub, N.; Soto, G.
140	<i>Nodule Number Control 1, a member of the AP2 family, functions as a negative regulator of bacterial infection and nodule organogenesis</i>	Yacullo, M.	Traubenik, S.; Reynoso, M.; Hummel, M.; Bailey-Serres, J.; Blanco, F.; Zanetti, M.E.
141	<i>Physiological classification of drought tolerance in soybean genotypes</i>	Bustamante, O.M.	Posada, G.A.; Suarez, P.; Espinosa Herlein, M.A.; Monteoliva, M.I.; Guzzo, M.C.
142	<i>Do soybean plants exhibit drought stress memory?</i>	Vannay, G.J.	Otegui, M.E.; Chan, R.L.; Capella, M.
143	<i>RPL10A promotes plant tolerance to drought and salt stresses</i>	Petrich, J.	Ramos, R.S.; Casati, P.; Spampinato, C.P.; Falcone Ferreyra, M.L.
144	<i>Role of hydrogen sulfide (H₂S) and participation of calcium (Ca²⁺) in stomatal immunity of Arabidopsis thaliana.</i>	Schiel, P.	Pantaleño, R.; Scuffi, D.; García Mata C.; Laxalt, A.
145	<i>Exploring the roles of DP_a and DP_b Proteins after UV-B exposure in Arabidopsis thaliana plants.</i>	Simonelli, L.B.	Sheridan, M.L.; Casati, P.
146	<i>OXR2 proteins improve UV-B tolerance in Arabidopsis</i>	Eusebi, D.	Sheridan, M.L.; Casati, P.; Welchen, E.
147	<i>Characterization of Arabidopsis thaliana heat shock protein Hsp81.2 in the plant apoplast</i>	Atela, A.	Uchiya, P.; Solmi, L.; Morales-Mendoza, L.F.; Ramos-Duarte, A.V.; Gárriz, A.; Rossi, F.; Sander, V.; Clemente, M.; Corigliano, M.G.

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148	<i>Flavonoids: a sustainable alternative for plant disease control and their interaction with plant growth-promoting microorganisms</i>	Vallejo, V.	Serra, P.; Villafañe, D.; Rodríguez, E.; Casati, P.
149	<i>Plastids targeted BNT1 immune receptor implicated in the organelle-associated defense responses in Arabidopsis.</i>	Peppino Margutti, M.Y	Herrera-Vasquez, A.; Cislaghi, A.P.; Palomeque, J.R.; Bellino, F.; Alvarez, M.E.; Blanco-Herrera, F.; Cecchini N.M.
150	<i>Canonical transcriptional gene silencing may contribute to long-term heat response and recovery</i>	Sanchez, D.H.	Torres, J.R.; Botto, J.F.
151	<i>Morphological plasticity of sunflower in response to light availability and carbohydrate accumulation with special attention paid to fructans.</i>	Dosio, G.A.A.	García, L.A.; Martínez-Noël, G.M.A.; Giorgi, M.E.; Tognetti, J.A.
152	<i>Characterisation of maize landraces from Argentina at the phenotypic and biochemical levels</i>	Domínguez, P.G.	Dudzien, T.L.; Defacio, R.; Paniego, N.; Lia, V.V.
153	<i>Dynamic expression of Kunitz protease inhibitors (KPI) in potato plants, sprouts and tubers exposed to light/dark conditions. Cloning of StKPI3.18520.</i>	Gitman, I.F.B.	Ulloa, R.M.
154	<i>Glucosinolate translocation from inflorescences to stems during postharvest senescence of broccoli</i>	Casajus, V.	Martínez, G.; Gómez Lobato, M.E.
155	<i>Understanding tolerance mechanisms of NO alleviating alkaline stress in tomato</i>	Steelheart, C.	Ganganelli, I.; Alegre, M.; Gergoff Grozeff, G.; Bartoli, C.G.
156	<i>Effect of abscisic acid foliar applications on phytochemical content and antioxidant capacity of purple and orange carrots</i>	Mauricci, M.T.	Malovini, E.; Valerga, L.; Cavagnaro, P.F.
157	<i>Role of GRP1a in tomato fruits: response to different postharvest conditions and possible targets for interaction and mRNA stabilization</i>	Denhoff, A.M.L.	Bustamante, C.; Drincovich, M.F.; Müller, G.
158	<i>Postharvest physiology and nutritional quality of strawberry under salicylic acid, melatonin, and cysteine treatments</i>	Ruiz, V.	Bonanza, M.; Camacho, C.; Gallay Ruba, C.; Chasco, S.; Martínez, G.; Bouzo, C.; Derita, M.; Bender, A.
159	<i>Effects of wind and deficit irrigation on secondary metabolite production in red grapevine varieties: insights from a field trial in windy conditions</i>	Alonso, R.	Muñoz, F.; Fontana, A.; Piccoli, P.; Bottini, R.; Berli, F.
160	<i>Isolation of tissue-specific nuclei to study transcriptional changes associated with strain preference in the nitrogen fixing symbiosis</i>	Cretton, M.	Barbán, M.; Zanetti, M. E.; Reynoso, M.; Blanco, F.
161	<i>Relationships between reactive oxygen species and growing variables of Pistum sativum L., under different soil moisture levels</i>	Michel, A.	Appelhans, S.C.; Sequin, C.J.; Bianchi, M.; Trossero, J.A.; Caviglia, O.P.
162	<i>Soybean seed coat: a key intermediary between maternal nutrient supply and embryonic metabolism</i>	Zucchetti, J.I.	Barat Carnino, M.; Lopez, E.; Gerde, J.A.; Borrás, L.; Saigo, M.; Gerrard Wheeler, M.C.
163	<i>Water dynamics in plant cells: unraveling the interplay between redox state and metabolism status</i>	Cabadas, M.	Lascano, R.H.; Robert, G.
164	<i>Changes in Nicotiana tabacum stem morphology due to expression of NADP-malic enzyme in drought tolerant transgenic lines</i>	Müller, G.L.	Guindon, M.F.; Oitaven, P.A.; Srebot, M.S.; Saper, C.; Olazarán Mainetti, J.; Drincovich, M.F.
165	<i>Impact of stomatal density on the hydraulic properties of Arabidopsis thaliana: Studies on transpiration rate and root hydraulic conductivity</i>	Cáceres, P.D.	Sutka, M.; Sampaolesi, M.R.; Fiorini, T.; Amodeo, G.; Baroli, I.
166	<i>Autophagy modulation in Legume-Rhizobia interactions: unraveling local and systemic responses in compatible and incompatible contexts</i>	Musso, M.	Bellis, P.; Lascano, R.; Robert, G.

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167	<i>Characterization of HH05, a transcription factor mediating nitrogen response in Arabidopsis and rice</i>	Romei, F.	Obertello, M.
168	<i>A study of the complex I mitochondrial carbonic anhydrase domain in A. thaliana</i>	Balestieri, N.	Marchetti, F.; Pagnussat, G.; Zabaleta, E.
169	<i>Unraveling the significance of arginine methylation in AGO1</i>	Martín-Merchán, A.	Lavatelli, A.; Rosano, G.; Bologna, N.
170	<i>Characterization of potential TE-derived inverted repeat regulatory elements impacting gene expression and genome topology</i>	Houriet, C.	Mencia, R.; Arce, A.
171	<i>Dissecting PLASMODESMATA-LOCATED PROTEIN 5 functional domains.</i>	Robles Luna, G.	Jiefu, L.; Wang, X.; Li, L.; Jung-Youn, L.
172	<i>Regulation of floral development in Arabidopsis thaliana by microRNAs.</i>	Lazzara, F.E.	Beltramino, M.; Ferela, A.; Palatnik, J.F.
173	<i>Application of plant growth regulators in sunflower seedlings under water stress conditions during early vegetative growth (V4)</i>	Boero, A.	Ramírez, F.; Vigliocco, A.; Andrade, A.; Alemanno, S.
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175	<i>First characterization of Torrontés Riojano in La Rioja, Argentina: impact of pruning intensity on vine vigor and grape production</i>	Miranda, R.	Silvente, S.; Assof, M.; Hugalde, I.
176	<i>Phenotypic characterization of a flower mutation in the grapevine cultivar Listán Prieto and its effects on productivity</i>	Oroño, T.	Muñoz, C.; López, M.; Gómez Talquenca, S.; Torres, R.; Lijavetzky, D.; Calderón, L.
177	<i>The role of BBX proteins in shade avoidance in Solanum lycopersicum (tomato).</i>	Botto, J.	Mejia, M.; Ponciano, G.; Gomez-Ocampo, G.; Rossi, M.M.
178	<i>Histone modifying enzymes alter rhizobia infection and bacterial survival in the root nodule symbiosis</i>	Ferrari, M.	Traubenik, S.; Banini, M.; Blanco, F.; Reynoso, M.; Zanetti, M.E.
179	<i>Does the altered expression of HD-Zip I transcription factors in roots affect soybean plants' fitness?</i>	Caraballo M.L.N.	Raineri, J ; Chan, R.L.
180	<i>Role of a submergence responsive Myeloblastosis transcription factor in the formation of lateral root organs in legumes</i>	Reynoso, M.A.	Bori, C.; Ibarra, E.
181	<i>Molecular mechanisms controlling early development in Arabidopsis.</i>	Vacs, P.	Rasia, R.; González Schain, N.
182	<i>Plant growth-regulating hormonal pathways are targeted by two effectors belonging to evolutionary unrelated filamentous pathogens.</i>	Bogino, M.F.	Lapegna Saenz, J.M.; Fabro, G.
183	<i>Role of auxin signaling in root hair growth at low-temperature in Arabidopsis thaliana</i>	Berdion Gabarain, V.	Ramirez Silva, C.; Estevez J.M.
184	<i>Unveiling hidden regulators: exploring non-coding transcripts arising from alternative splicing and their impact on protein function</i>	Rodríguez, F.S.	Tognacca, R.S.; Servi, L.; Legascue, M.F.; Ariel, F.; Petrillo, E.
185	<i>Unravelling maternal effects in Arabidopsis thaliana seeds: from controlled environments to the wild</i>	Authier, A.	Auge, G.A.
186	<i>HOP co-chaperones contribute to GA signaling by stabilizing F-box protein SNE in Arabidopsis thaliana</i>	Mangano, S.	Muñoz, A.; Castellano, M.M.
187	<i>Interplay between cytochrome c and hormones during early plant development</i>	Gras, D.E.	Coronel, F.P.; Canal, M.V.; Welchen, E.; González, D.H.
188	<i>Unraveling the role of TCP and GLK transcription factors in Arabidopsis seedling development</i>	Alem, A.L.	Gonzalez, D.H.; Viola, I.L.

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189	<i>Novel roles for Mediator complex in Arabidopsis thaliana flowering time</i>	Freytes, S.N.	Jaskolowski, A.; Viñas, E.; Iñigo, S.; Yanovsky, M.; Cerdan, P.
190	<i>A role for phytochromes in red light mediated alternative splicing in Arabidopsis thaliana</i>	Careno, D.A.	Assaf, C.H.; Eggermont, E.D.C.; Sanchez, S.E.; Yanovsky, M.J.
191	<i>Convergence between shade and submergence responses.</i>	Fernández, R.	Sellaro, R.
192	<i>Characterization of AtSINA-L7 function in auxin metabolism</i>	Tello León, C.	Busi, M.V.; Gomez Casati, D.F.
193	<i>SWEETs, MAX4, BRC1, and CLE44 genes are crucial players in the definition of Arabidopsis stem architecture impacting seed yield</i>	Raminger, B.L.	Chan, R.L.; Cabello, J.V.
194	<i>Role of RALF peptides in root hair development and response to low temperatures in Arabidopsis thaliana.</i>	Lopez, L.E.	Martinez-Pacheco, J.; Rodriguez Garcia, D.R.; Urzúa Lehedé, T.; Núñez-Lilo, G.; Meneses, C.; Estévez, J.M.
195	<i>Is soybean leaf senescence modulated by direct and indirect effects of post-flowering photoperiod?</i>	Kelly, S.J.	Cano, M.G.; Tambussi, E.A.; Guiamet, J.J.
196	<i>Photochemical efficiency of sugarcane (Saccharum spp.) in response to low radiation</i>	Cepeda, A.M	Quevedo, Y.M.; Mejía De Tafur, M.S.
197	<i>New approaches on source-sink relationships in maize: nitrogen accumulation during kernel development and effects on kernel weight</i>	Antonietta, M.	Saric, R.; Dominguez, H.; Fanello, D.D.; Maydup, L.M.; Guiamét, J.J.
198	<i>Phenotypic patterns of vegetative-reproductive plasticity in maize inbred lines and their derived hybrids</i>	Lutz, S.A.	Hisse, I.R.; Galizia, L.A.; López, C.G.; Maddonni, G.A.; D'Andrea, K.E.
199	<i>Yield and physical quality determinants of Flint maize in production lots.</i>	Seguí, M.	Gerde, J.A.; Espejo, J.; Gambín, B.; Borrás, L.
200	<i>Changes in the development and numerical components of reproductive primordia associated with genetic improvement in barley</i>	Comacchio, J.E.	Ibañez, C.; Abeledo, L.G.; Miralles, D.J.
201	<i>Water and nutritional budget of sunflower crop in a semiarid environment</i>	Dillchneider, A	Funaro, D.; Gigli, A.; Noellemeyer, E.
202	<i>Prediction of preharvest sprouting susceptibility in malting barley</i>	Ortiz, M.	Benech Arnold, R.L.
203	<i>Yield and grain number determination in maize iso-hybrids with and without genetic alteration of height</i>	Villavicencio, J.	Pluda, P.; Cagnola, J.; Uribebarrea, M.; Röig, J.; Maddonni, G.; Rotili, D.H.
204	<i>Sunflower: Early sowing dates and their impacts on the frost resilience in Córdoba Argentina</i>	Fabio, E.A.	Grieu, P.; Bigatton, E.D.; Salvay, M.L.; Biasutti, C.
205	<i>Chia (Salvia hispanica L.) yield is limited by sink strength during grain filling</i>	Acreche, M.M.	Burgos, S.; Diez, J.
206	<i>Comparative transcriptomic, proteomic and amino acid content analyses of quinoa (Chenopodium quinoa) seed accessions from Northwest Argentina</i>	Barberini, M.L.	Yun Sun, L.; Guerrero, L.D.; Obertello, M.; Mazzella, M.A.; Bertero, D.H.; Grotewold, E.; Muschietti, J.P.
207	<i>A coffee hope tale: Coffea arabica Castillo and Caturra varieties could survive in a dryer world with reliable physiological strategies.</i>	Hernandez, S.	Rada, F.; Lasso, E.
208	<i>Deciphering flavonoid production in Flaveria bidentis (L.) Kunze: Ecophysiological insights and implications for cultivation practices</i>	Davidenco, V.	Agnese A.M.; Giovanini, A.

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209	<i>Synchrony of the olive flowering in Catamarca-Argentina</i>	Aybar, V.E.	Ortiz, P.V.; Montalván, L.D.; Delgado, E.; Demín, P.E.; Prenol, L.V.
210	<i>Supplemental irrigation improves seed yield of a range of soybean cultivars in Entre Ríos</i>	Alaluf, C.	De Battista, J.J.; Puhl, L.E.; Rondanini, D.P.
211	<i>Growth, yield and water use efficiency of lanceolate and ovate soybean isolines grown under rainfed and irrigated field conditions</i>	Bianchi, J.S.	Palomino Martini, T.K.; Islas, M.; Gómez, R.L.; Quijano, A.
212	<i>Dissecting cadmium-induced metabolic changes in the root tip during early maize growth</i>	Gallego, S.M.	Matayoshi, C.L.; Jiménez Guaman, O.M.; Estesio, M.L.; Pavoni, M.; Arán M.; Pena, L.B.
213	<i>Graphene oxide or Bacillus subtilis with Bacillus licheniformis attenuates the drought stress of sugarcane through improving gas exchange</i>	Santos, H.L.	Silva, K.P.O.M.; Carnietto, M.R.A.; Silva, M.A.
214	<i>Trichoderma LR28 sp. as a potential biocontrol agent against peanut smut caused by Thecaphora frezzii</i>	Valetti, L.	Posada, G.A.; Bustamante, O.M.; Sardo, M.F.; Suarez, P.A.; Espinosa Herlein, M.A.; González, N.R.; Monteoliva, M.I.; Paredes, J.A.; Guzzo, M.C.
215	<i>Strategies for peanut smut control (Thecaphora frezii): resistant genotypes, a calcium amendment and bacterium Bacillus sp. CHEP5</i>	Marcellino, N.	Rovere, M.E.; Loser, U.A.; Peiretti, E.G.; Bongiovanni, M.D.; Ibañez M.A.; Tonelli, M.L.
216	<i>Physiological and biochemical responses to drought in Eucalyptus and their relationship to drought and freezing tolerance.</i>	Margarit, E.	Oberschelp, G.P.J.; Salto, C.S.; Harrand, L.; Margarit, E.
217	<i>Evaluation of chlorophyll "a" fluorescence parameters in tomato (Solanum lycopersicum) under nitrogen and calcium deficiency.</i>	Ludi Barzante, L.	Foti, M.N.; Michel, A.
218	<i>Contributions of symbiosis with native rhizobacteria to salt stress tolerance in Neltuma flexuosa</i>	Mesquida Nardini, M.C.	Melchiorre, M.; Lescano López, I.; Palomeque, J.
219	<i>The miR394 pathway in tomato fruits and its role in the response to Botrytis cinerea</i>	González-Muñoz, J.C.	Favaro M.A.; Civello, P.M.; Dotto, M.C.
220	<i>Effector repertoire of a dominant Phytophthora infestans isolate in Argentina and its relevance for late blight resistance deployment in potato.</i>	Juarez, M.E.	Lucca, M.F.; Azcue, J.; Bravo Almonacid, F.F.; Cano Mogrovejo, L.M.; Segretin, M.E.
221	<i>Antioxidant response mechanism in leaves of tomato plants subjected during flooding and post-flooding stress</i>	Chavez, C.A.	Mignolli, F.; Medina, R.D.; Vidoz M.L.
222	<i>Proteomic aspects of Ascochyta rabiei-Cicer arietinum interaction related to defense mechanisms.</i>	Guzzo, C.	Crociara, C.S.; Vaghi, G.; Valetti, L.; Diaz, S.; Iglesias, J.; Pastor, S.E.
223	<i>What domestication took away: phytochrome B-mediated responses to environmental change.</i>	Manzur, M.E.	Vujanic, T.; Pinciaroli, C.; Talarico, L.; Fernández, P.C.
224	<i>Exogenous ascorbic acid enhances the aluminum resistance of sensitive plants of Vaccinium corymbosum</i>	Cárcamo-Fincheira, P.	Nunes-Nesi, A.; Soto-Cerda, B.; Inostroza-Blancheteau, C.; Reyes-Díaz, M.
225	<i>Physiological responses of two species of the genus Colobanthus to water stress.</i>	Villena Fernández, K.	Gajardo, H.; Bravo, L.A.
226	<i>Molecular mapping of the Rdm3 locus controlling local isolates of Diaporthe aspalathi. Analysis of its presence in Argentinian soybean varieties</i>	Chiesa M.A.	Maldonado, R.A.; Moser, V.; Bianchi, J.S.

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227	<i>Effects of phosphorus (P) deficiency on growth and N₂ fixation in legumes</i>	Morales González, A.B.	Salinas-Roco, S.; Pera, J.; Carrasco, B.; Del Pozo, A.; Cabeza, R.A.
228	<i>Natural coating for inoculant delivery in bean seeds</i>	Melchiorre, M.	Sarmiento, A.; Lattanzi, S.; Grasso, F.; Montoya, P.
229	<i>Participation of lipooxygenases in ferroptotic cell death in Arabidopsis thaliana.</i>	Bauer, M.V.	Distéfano, A.; Pagnussat, G.; Zabaleta, E.
230	<i>Transcriptomic changes triggered by ferroptosis inhibitors drive heat stress tolerance in Arabidopsis thaliana.</i>	López, G.A.	Distéfano, A.; Bauer, M.V.; Pagnussat, G.C.
231	<i>Constitutive expression of a soybean HD-Zip I transcription factor enhances drought tolerance in Arabidopsis</i>	Alfonso Belloni, Y.	Gaido, J.; Jaime, C.; Vegetti, A.; Dunger, G.; Dezar, C.
232	<i>Temperature and shade: How plants perceive and transduce different signals with common sensors?</i>	De Luca, M.B.	Murcia, G.; Bianchimano, L.; Iglesias, M.J.; Casal, J.J.
233	<i>Exploring the Role of Autophagy in Defense Priming and Systemic Resistance in Arabidopsis</i>	Robert, G.	Lacase, L.; Cambiagno, D.; Cecchini, N.; Lascano, R.
234	<i>TCP transcription factors fine-tune chlorophyll biosynthesis to prevent photo-oxidative damage during de-etiolation in Arabidopsis thaliana</i>	Jure, R.M.	Alem, A.L.; Viola, I.L.; González, D.H.
235	<i>Arabidopsis interaction with beneficial pseudomonas strains that confer tolerance to drought stress and promote root development</i>	Llamedo, I.	Chaín, J.M.; Gudesblat, G.; Amodeo, G.; Baroli, I.
236	<i>Deciphering HLR1 function in photoprotection</i>	Balparda, M.	Böhm, J.M.; Zaplatnikov, Y.; Maurino, V.G.
237	<i>Wheat lines, suffering structural rearrangements between wheat-1BS and rye-1RS chromosomes, display differential patterns of magnesium accumulation</i>	Gualano, L.D.	Moriconi, J.I.; Tranquilli, G.E.; Santa-María G.E.
238	<i>Characterization of genes relevant to the biological functionality and transcriptional regulation of the ZmNADP-ME3 malic enzyme</i>	Sosa, M.M.	Nasello, F.; Sosa, M.; Gismondi, M.; Saigo, M.
239	<i>Involvement of abscisic acid in modulating ascorbic acid synthesis and accumulation: responses under basal and high incident irradiance conditions.</i>	Senn, M.E.	Mazorra Morales, L.M.; Gergoff Grozeff, G.E.; Galatro, A.; Da Cruz Saraiva, K.D.; Pereira dos Santos, C.; Costa, J.H.; Gonçalves de Oliveira, J.; Bartoli, C.G.
240	<i>Floodwater depth effects on nitrogen and phosphorus partition in young willow plants during the post-stress period.</i>	Luquez, V.M.C.	Mozo, I.; Monteoliva, S.
241	<i>Characterization of 4-coumarate-CoA ligase family in potato (Solanum tuberosum L.)</i>	Valiñas, M.	Lanteri, L.; ten Have, A.; Andreu, A.
242	<i>Anatomy and metabolite content of high relative humidity-induced adventitious roots in tomato (Solanum lycopersicum L.)</i>	Revollar Ochatoma, P.A.	Mignolli, F.; Vidoz, M.L.
243	<i>Carotenoid rich tomato fruits due to overexpression of an endoplasmic reticulum specific sHSP isoform.</i>	Zayas, A.	Renzi, D.J.; Sossi, M.L.; Zanor, M.I.
244	<i>Exploring early signaling events under phosphorus restriction in soybean plants</i>	Luquet, M.	Antonelli, C.J.; Gergoff Grozeff, G.E.; Buet, A.; Galatro, A.
245	<i>Soybean growth promoting autochthonous Trichoderma spp. for biocontrol</i>	Santone, A.	Campos Bermudez; V.A.; Smpampinato, C.P.
246	<i>Assessing the role of branched-chain amino acids metabolism in soybean responses to drought stress</i>	Barbot, C.	Vidal, S.; Castro, A.; Ibañez, F.
247	<i>Overexpression of ADC2 in Arabidopsis improves nitrogen use efficiency under nitrogen limitation</i>	Benavides, M.P.	Recalde, L.; Cabrera, A.V.; Rossi, F.R.; Groppa, M.D.



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249	<i>Unveiling the BAG Protein Family in Physcomitrium patens: identification and functional characterization</i>	Castro, A.	Saavedra, L.; Silva, S.; Vivas, A.; Vidal, S.
250	<i>Autophagy as an energy regulator? Its impact on the growth and development of P. patens</i>	Liberatore, F.	Pettinari, F.; Schenfeld, E.; Lascano, R.; Saavedra, L.
251	<i>Nitric oxide regulation of temperature-dependent growth in Arabidopsis seedlings</i>	Tebez, N.M.	Iglesias, M.J.; Correa-Aragunde, N.; Casalongué, C.A.; Terrile, M.C.
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253	<i>Evaluation of the effect of livestock density on the vegetation of wetlands of the Middle Paraná River</i>	Treisse, I.	Sabattini, J.; Lorente, C.; Berón, C.; Mesa, L.
254	<i>Azospirillum argentinense biofilm: implication of polyamines</i>	Díaz Herrera, S.	Zawoznik, M.S.; Benavides M.P.; Groppa M.D.



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RAFV Awards



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RAFV Awards

The **RAFV2023 awards** seek to encourage the development of young researchers from all areas of the country.

The prizes awarded, the juries involved and the winners are detailed below.

- **FEBS Letters Poster Prize:** for the best paper presented by a young researcher in basic research related to Molecular Biology and Plant Biochemistry with a strong mechanistic component.

Jury: Drs. Ana Laxalt, Paula Casati, Ramiro Lascano.

Winner: Ezequiel Ibarra for the paper titled "*Evolutionary conserved submergence responsive transcription factors involved in the formation of lateral root organs in legumes*"

- **FEBS Journal Poster Prize:** for the best work presented by a young researcher related to plant signaling.

Jury: Drs. Carlos García Mata, Elina Welchen, Silvina Mangano.

Winner: Nehuen Balestieri for the paper titled "*A study of the complex I mitochondrial carbonic anhydrase domain in A. thaliana*".

- **YTEC Award: Technology:** for the best paper presented by a young researcher in areas related to ecophysiology and crops and plant processes improvement.

Jury: Drs. Cecilia Rousseaux, Marina Clemente, Paula Fernández.

Winner: Mauro Silva for the paper titled "*Physiological and genetic characterization of wheat lines sharply differing in sodium accumulation*".

- **Per J Award I:** for the best paper presented by a young researcher in the areas of Biotic and Abiotic Stress.

Jury: Drs. Carlos Bartoli, Eduardo Zabaletta, Sebastián Asurmendi.

Winner: Evelyn Becerra-Agudelo for the paper titled "*OsOXR-Q12 protein is involved in cellular defense homeostasis and contributes to salt stress tolerance in Oryza sativa*".

- **Per J Award II:** for the best paper presented by a young researcher in the area "Other Technologies: Forest, horticultural and native species; post-harvest technologies".

Jury: Drs. Marcos Civello, Fernando Carrari, María Victoria Busi.

Winner: Diego Javier Renzi for the paper titled "*Silencing of a CCT domain containing protein in tomato plants leads to increased abiotic stress tolerance*".

Congratulations to all of them!!



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**Abstracts:
Keynte Lectures**

Understanding root growth: more complex than anticipated

Gutierrez, C. (1); Desvoves, B. (1)

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The transition to multicellularity required the evolution of novel structures and mechanisms to coordinate cell division, acquisition of cell fates and the establishment of complex regulatory networks. Organogenesis relies on the production of new cells together with the formation of organ domains and cell types directed by patterning genes. A fundamental question in cellular and developmental biology is to understand the coordination between cell patterning cues and cell division. The mechanisms linking the local activity of stem cell regulators with the cell cycle machinery and the control of division of stem cells and their derivatives remain largely unknown. We focus our studies on the *Arabidopsis thaliana* root as a model to understand how cell proliferation, transcriptional regulation, genome replication and epigenetic information are coordinated during root development. I will describe recent results in this line and discuss the complexity in understanding root growth where we are identifying the multiple layers of control.

Keywords: Cell cycle, stem cell, transcription factor, root development, root apical meristem, Arabidopsis, plant.

Small and almost undetectable proteins play crucial roles in plant development and adaptation to environmental conditions

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Transcription factors (TFs) are proteins that can induce or repress entire signal transduction pathways. These proteins are abundant in the plant kingdom, modulating developmental events in response to environmental conditions. They are classified in families mainly according to the DNA binding domain and also to the presence of other motifs. Among these families, homeodomain (HD) – leucine zipper (LZ) TFs are small proteins unique to plants.

We investigated TFs from the HD-Zip I family in several species like *Arabidopsis*, tobacco, sunflower, and rice. These TFs participate in different developmental events in normal growth conditions, such as primary and lateral root development, pollen hydration, gravitropic response, and the response to abiotic stress factors like water deficit and excess, extreme temperatures, etc. Some of these proteins became biotechnological tools. The divergent sunflower HaHB4 conferred drought and salinity tolerance to *Arabidopsis*, wheat, and soybeans, whereas HaHB11 improved yield, flooding, and defoliation tolerance to the model plant, rice, soybean, and maize. We conducted culture chamber, greenhouse, and field trials in different environments, and notably, the results indicated that crops partially conserved the beneficial traits observed in the model. After long regulatory processes in several countries, HaHB4 soybean and wheat became rare successful cases commercially released in 2022.

A careful analysis of these and other transformed plants exhibiting enhanced yield as a shared trait led us to develop a mechanical treatment, allowing to enlarge the stems conducting to improve the production and health of tomatoes, pepper, chia, strawberry, and other species. The development of this manual technique, useful in family agriculture and small farmers, exemplifies how the connection between fundamental research and its application is a two-way road. Although the frequent failures, basic research is essential to reach innovative applications.



Winners and losers: Climate change effects on forests and crops

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Rising atmospheric CO₂ concentrations could reach >1000 ppm by 2100, increasing global temperatures 3-4 °C. Both elevated CO₂ and warming affect photosynthesis, plant growth, survival, and crop yield and quality. Climate change-induced shifts in photosynthesis and plant growth also affect the global carbon cycle, mitigating or accelerating further climate change. Understanding how plants acclimate to future climate conditions is therefore critical for accurately predicting the trajectory of future climate change, as well as for estimating plant productivity in a warmer, high CO₂ world. I'll discuss how elevated temperatures, high CO₂ concentrations and vapor pressure deficit impact forest and crop performance using results from my lab and meta-analyses.

Keywords: global warming, photosynthesis, plant biomass.

Vacuolar RNA salvage and cellular homeostasis in *Arabidopsis*

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Ribosomal RNA accounts for most of the RNA present in any living cell. However, despite its abundance, rRNA turnover has received less attention than that of other RNA species. Work in our group has characterized the vacuolar RNA salvage pathway in *Arabidopsis*, and shown that this pathway is the main route for rRNA turnover in plants and other eukaryotes. In addition to identifying the main enzymes and transporters that participate in the pathway, we showed that RNA salvage is essential to maintain nucleotide homeostasis. Defects in this pathway cause inhibition of the protein kinase target of rapamycin (TOR), a central growth regulator that modulates nutrient status and energy signaling to promote cell proliferation and growth, resulting in a compensatory shift in carbon flux through the pentose phosphate pathway and an increase in de novo synthesis of nucleotides. Our current research is focused on understanding the cellular mechanisms that sense and regulate nucleotide homeostasis, and the vacuolar import systems that allow for vacuolar uptake of RNA. We are also interested in the conservation of this salvage pathway throughout the Eukaryota, and the application of knowledge obtained using a plant model system to human health.



New approaches to auxin biology: unexpected findings

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Plants have evolved sophisticated mechanisms to control auxin homeostasis and signaling, making it challenging to study the molecular mechanisms by which auxin regulates plant development. My group has developed several technologies that enable precise modifications of genes in plants. The technological advances provide unprecedented tools to study auxin biology. In this presentation, I will first describe the technologies we developed including in situ tagging genes with GFP. Our technologies avoid the pitfalls of transgenic approaches such as co-suppression and ectopic overexpression. Our gene editing technologies played a key role in elucidating the main auxin inactivation pathway. The technologies have led to surprising insights into several well characterized auxin genes. Finally, I will present the potential applications of our auxin research in crop improvement.

Transcriptional and post-transcriptional regulatory networks that modulate the adaptation of plants to daily changes in light and temperature

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Plants undergo changes in gene expression in response to daily and seasonal fluctuations in light and temperature. These changes are in part modulated by the circadian clock, a biological timekeeping system that consists of a network of interacting clock genes. To better understand the circadian network, we have used forward and reverse genetic approaches to identify new modulators of clock function. Among several new clock regulators, we identified a family of co-transcriptional activators named LNKs that connect light signals to the control of the core oscillator by interacting with the RVE family of single MYB transcription factors. In addition, we and others have found that the LNKs also modulate the interplay between the circadian clock and temperature responses. Besides transcriptional regulators, we also identified several core splicing factors that modulate the circadian network, including Protein Arginine Methyltransferase 5 and GEMIN2. More recently, we showed that PICLN, an adaptor protein that is part of the methylosome complex, displays altered photomorphogenic and photoperiodic responses. These changes are associated with changes in pre-mRNA splicing, partially overlap with those of prmt5 mutants and also modulate light and temperature responses. Taken together, our results are contributing to identify novel factors operating at the transcriptional and post-transcriptional level to allow plant adaptation to daily and seasonal fluctuations in environmental conditions.



Plasmodesmata and callose interplay in the regulation of plant root development

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Intercellular communication via plasmodesmata (PD, channels connecting the cytoplasm of neighbouring cells) regulates the spreading of molecular signals including RNAs, proteins, sugars and hormones. In 2018, we reported the role of PD mediated transport in the formation of legume-rhizobia nitrogen-fixing symbiosis impacting root development in poorly fertilized soils (Gaudioso-Pedraza et al., 2018). We identified callose-degrading enzymes induced during nodule development to facilitate rhizobia infection and root colonization. Callose is a beta-1,3 glucan cell wall component that deposits at PD sites restricting its cytoplasmic aperture and symplasmic transport. Additional evidence supporting a role for callose and PD in the regulation of nodulation in nitrogen repleted conditions, in drought/salinity stress and in root interactions with other symbiotic microbes are presented. I also introduce our efforts to understand the structural properties of callose at and outside PD/ pit fields and discuss the implications of our findings in light of the context presented by different cell walls.

Keywords: plasmodesmata, intercellular communication, plant stress responses, models.



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**Abstracts:
Symposia**



Molecular improvement of alfalfa using CRISPR/Cas9

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Alfalfa is the main forage crop in Argentina and, in terms of planted area, it is the second most important crop in our country. It is a perennial leguminous species, which makes it a crucial crop in agricultural rotations due to its ability to fix nitrogen and its outstanding nutritional quality as forage. Its broad genetic variability gives it the capacity to adapt to diverse regions.

For several decades, INTA has carried out a successful genetic improvement program for alfalfa. Our research team has played an active role in this program, studying genes of agricultural interest and using biotechnological tools to introduce variability in those traits where its natural genetic diversity is insufficient.

In this presentation, we will share the advances achieved in recent years in the molecular improvement of alfalfa through the revolutionary gene editing technology CRISPR/Cas9. We will discuss new genes under study, focusing on flowering control and forage quality.

Keywords: crispr/cas9; alfalfa; improvement; quality; genetics.

Next generation potatoes obtained through gene editing

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The potato is the third most consumed food crop in the world, following rice and wheat. In Argentina, modern cultivated potato production is mainly concentrated in Buenos Aires and Córdoba. Among the most used varieties are cv. Spunta for fresh consumption and cv. Atlantic for the potato chip industry. The main industrial characteristics to improve in cultivated potatoes are enzymatic browning and cold-induced sweetening (CIS), both of which lead to reduced quality in fresh produce and/or processed products. Regarding production-related traits, the objective is to obtain potatoes that utilize available water more efficiently. Due to the agamic and polyploid nature of potatoes, traditional breeding methods can take 15 years. Therefore, the use of new biotechnological techniques allows for shorter development times for new varieties. In our group, we utilize the CRISPR/Cas9 gene editing technique to obtain improved varieties with one or more of the aforementioned characteristics. The first development in our group was the bruise-resistant potato derived from cv. Desiree, by knock out (KO) the polyphenol oxidase gene (StPPO2), responsible for enzymatic browning. We performed the KO of the vacuolar invertase gene (StInvVac) from cv. Atlantic to obtain the potato resistant to CIS. To obtain potatoes that use the available water more efficiently, we performed KO of the CBP80 gene, a transcription factor involved in the ABA signaling pathway, in cv. Spunta. We are progressing in obtaining cv. Spunta potatoes with both StPPO2 and StInvVac genes edited simultaneously. The lines with CIS resistance and with improved available water use efficiency will be submitted to CONABIA for evaluation. In the current year, the bruise-resistant line will be registered as a new variety with INASE. Our results demonstrate that gene editing applications can generate superior quality products that provide benefits for both the production and industrial sectors, as well as consumers.



Combining synthetic biology and gene editing for the development of a new generation of Non-GMO crops

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BioHeuris develops herbicide-tolerant crops with the aim of efficiently managing weeds and reducing their environmental impact. The product development is based on the synergy between two technological platforms. The first one, known as HEURIK™, merges targeted protein evolution strategies with synthetic biology to identify mutations that confer herbicide resistance in crops. HEURIK™ relies on the use of microbial chassis and high-throughput tools, enabling the achievement of results within a matter of weeks that traditional mutagenesis techniques would require vast hectares and years of field testing.

The second technological platform, named SWAP™, combines in vitro culture protocols with CRISPR/Cas-based gene editing techniques to precisely introduce the mutations identified through HEURIK™ into elite lines. It is important to mention that the company's vision focuses on developing technologies that exhibit tolerance to herbicide active ingredients classified with low Environmental Impact Quotient (EIQ) values, ensuring minimal risk to the health of producers, consumers, and the environment.

The key advantages of using these technologies to enhance crops against biotic and/or abiotic stresses, as well as for weed control, encompass reduced development timelines and costs compared to traditional mutagenesis methods.

Furthermore, the genetic alterations induced by these gene editing tools are genetically indistinguishable from those arising from conventional mutagenesis, thus being classified as non-GMO in most countries in America and Asia.

Keywords: gene editing, CRISPR/Cas, herbicide, crops.

Genetic and physiological mechanisms responsible for maize kernel weight and source-sink relations under contrasting nitrogen supply levels

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Agricultural production is requesting the use of increasingly efficient inputs, especially those with high environmental pollution-risk associated, as in the case of nitrogen fertilization. Consequently, analyses performed under N stress conditions are highly desirable; however, studies based on grain yield genetic control in suboptimal environments are scarce, particularly those associated with the physiological components responsible for the individual kernel weight determination (KW). The main objective was to evaluate the genetic and physiological mechanisms underlying maize grain yield determination under contrasting soil nitrogen availability. A set of traits formed by KW and grain-filling traits, kernel number, plant growth during the critical and grain-filling periods, and source-sink relationships in both periods were analyzed on six inbred lines from different origins and their 30 single-cross derived hybrids, using a full diallel mating design. Under contrasting nitrogen supply, differences in KW were mainly attributable to changes in the source-sink ratio during grain filling ($r^2 \geq 0.50$, $P < 0.001$) because of an enhanced post-flowering growth at a high N level. This was evident for hybrids but not for inbreds, probably due to the negative inbreeding depression effects on traits controlling seed expansion. At low nitrogen (i) broad-sense heritability estimates were increased (43% on average) for grain-filling traits but were reduced (5% on average) for most plant growth traits and source-sink relationships, and (ii) the proportion of additive genetic effects (i.e., heritable) was increased for most traits. Those traits representative of kernel water dynamics had higher heritability and additive effects than KW, particularly under low nitrogen. Enhanced additive effects and heritability at the low nitrogen level support the idea of increased selection efficiency under low-input conditions, particularly for grain-filling traits.

Keywords: Zea mays L, grain weight, nitrogen offer, genetic analyses, secondary traits.

Ecophysiological responses of olive trees to warming in different phenological stages of crop development

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Global warming is an important aspect of climate change. Yet, little research on how the vegetative growth and reproductive development of fruit trees will respond to increasing air temperature has been conducted. For this reason, a long-term research program was initiated in 2014 in northwest Argentina to study the effects of warming on young olive trees (*Olea europaea* L.). A series of warming experiments (+4 °C) have been conducted using open top chambers to assess responses during oil accumulation (summer and fall), early vegetative growth and reproductive development (late winter and spring), and chilling accumulation (fall and winter) for flowering. The results indicate fruit size as well as oil accumulation and its quality are reduced by warming, and that available carbon is preferentially allocated to leaf area. When warming in the late winter and spring, flowering is much earlier and there are adverse effects on fruit set that appear to be cultivar dependent. In contrast, shoot elongation is less affected by warming. The most important responses to warming appear to be related to chilling accumulation in the fall and winter, which is necessary for spring flowering. Flowering intensity is severely reduced by warming and the flowering period is much longer. It appears that fruit and oil yields in olive trees will be greatly reduced in northwest Argentina considering the currently available cultivars. Both adaptation strategies for current cultivars and a search for new cultivars could reduce the impact of warming in the coming decades.

Keywords: flowering, fruit set, fruit size, oil accumulation, open top chambers.



Problems caused by excessive or insufficient seed dormancy in crops. Search for solutions in sunflower and grain sorghum

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Seed dormancy allows adjusting germination to those environments that maximize the chances of survival of species in the wild. However, in crops, the beginning of the cycle is defined by the sowing date, and the presence of dormancy threatens crop emergence and yield achievement. Domestication and genetic improvement selected against this trait and reduced dormancy levels in many crops, bringing another problem associated with early loss of dormancy: pre-harvest sprouting, frequent in cereals. On the other hand, cultivated sunflowers still maintain high levels of dormancy, causing problems during the production of commercial hybrid seed. In this symposium, different approaches and advances in the study of dormancy in grain sorghum and sunflower are presented, with the combined purpose of understanding the underlying mechanisms and proposing agronomic solutions.

Keywords: Seed dormancy; germination quality; dry afterripening; pre-harvest sprouting; QTL mapping; post-harvest storage; grain sorghum; sunflower.

Strategies to enhance foreign protein synthesis in the secretory pathway of plant cells.

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Most proteins of commercial interest require modifications typical of secretory pathway to be produced in an active form. Different engineering strategies have been used in yeast and mammalian cells to enhance the synthesis, folding, and transport capacity in the secretory pathway, however, in plant cells, such approaches have not yet been tested. Developing seeds have a huge capacity for protein synthesis, so we hypothesized that a key regulator of seed development could increase the ability of leaves to produce proteins in the secretory pathway. By transient expression in *Nicotiana benthamiana* leaves, we show that the *Arabidopsis* Leafy Cotyledon 2 (AtLEC2) transcription factor augment accumulation of endoplasmic reticulum-targeted beta-glucuronidase, but not of its cytosolic variant. In addition, AtLEC2 increases yields of reporter proteins sorted to different compartments of the secretory pathway. To understand AtLEC2-induced changes, differentially expressed genes (DEGs) between leaves infiltrated with agrobacteria carrying AtLEC2 versus control empty agrobacteria were analyzed by RNAseq. AtLEC2 modified the expression of 835 transcripts ($q < 0.01$), 574 up-regulated and 261 down-regulated. Gene Ontology analysis of the DEGs indicates that these genes participate in ribosome and chloroplast biogenesis, photosynthesis, translation, auxin metabolism, membrane synthesis, etc. Similar to yeast and mammalian transcription factors involved in the differentiation of professional secretory cells, AtLEC2-modified genes involved in translation and energy production. By CLSM, we show that AtLEC2 induces secretion of vacuole-sorted proteins and increases the stability of apoplast-targeted proteins. This the first report that shows the impact of a key regulator of seed development in secretory pathway protein synthesis. Our results contribute to the knowledge of plant secretory cell differentiation processes and to the development of novel genetic engineering strategies.

Keywords: molecular farming, plant secretory pathway, Arabidopsis Leafy Cotyledon 2, protein synthesis, transcriptome analysis.

Molecular farming as a biotechnological tool in the production of vaccine antigens

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The search for more cost-effective and safer antigen production systems led to the exploration of plants as biofactories (PBPs, plant-based platforms) for recombinant molecule synthesis. After 30 years of development, PBPs have been consolidated in various well-characterized niches, with standardized processes and good production practices. In particular, the vaccine development for livestock production using PBP constitutes a strategic solution for the agro-industrial sector of developing countries. Our working group has evaluated different plant-based heterologous expression strategies to optimize their use in the production of vaccine antigens. The results obtained so far encourage us to propose the fusion of these antigens (non-vegetable proteins) to the 90-kDa heat shock proteins (Hsp90) from plants, in this case in their dual role as carrier and adjuvant, as a novel strategy to increase the expression level of recombinant proteins. Through this approach, we have obtained recombinant protein production yields that are competitive with those obtained by other conventional expression systems. Likewise, we standardized the purification conditions by affinity chromatography on Ni²⁺ resin. Our investigations suggest that this platform is a suitable and powerful biotechnological system for the expression of immunogenic antigens.



Strategies to enhance foreign protein synthesis in the secretory pathway of plant cells.

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Most proteins of commercial interest require modifications typical of secretory pathway to be produced in an active form. Different engineering strategies have been used in yeast and mammalian cells to enhance the synthesis, folding, and transport capacity in the secretory pathway, however, in plant cells, such approaches have not yet been tested. Developing seeds have a huge capacity for protein synthesis, so we hypothesized that a key regulator of seed development could increase the ability of leaves to produce proteins in the secretory pathway. By transient expression in *Nicotiana benthamiana* leaves, we show that the *Arabidopsis* Leafy Cotyledon 2 (AtLEC2) transcription factor augment accumulation of endoplasmic reticulum-targeted beta-glucuronidase, but not of its cytosolic variant. In addition, AtLEC2 increases yields of reporter proteins sorted to different compartments of the secretory pathway. To understand AtLEC2-induced changes, differentially expressed genes (DEGs) between leaves infiltrated with agrobacteria carrying AtLEC2 versus control empty agrobacteria were analyzed by RNAseq. AtLEC2 modified the expression of 835 transcripts ($q < 0.01$), 574 up-regulated and 261 down-regulated. Gene Ontology analysis of the DEGs indicates that these genes participate in ribosome and chloroplast biogenesis, photosynthesis, translation, auxin metabolism, membrane synthesis, etc. Similar to yeast and mammalian transcription factors involved in the differentiation of professional secretory cells, AtLEC2-modified genes involved in translation and energy production. By CLSM, we show that AtLEC2 induces secretion of vacuole-sorted proteins and increases the stability of apoplast-targeted proteins. This the first report that shows the impact of a key regulator of seed development in secretory pathway protein synthesis. Our results contribute to the knowledge of plant secretory cell differentiation processes and to the development of novel genetic engineering strategies.

Keywords: molecular farming, plant secretory pathway, Arabidopsis Leafy Cotyledon 2, protein synthesis, transcriptome analysis.

Fluctuations in phloem transport of assimilates in response to mineral nutrition

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In cereals, remobilization of assimilates (mainly sucrose and amino acids) from vegetative tissues is an important source of carbon (C) and nitrogen (N) for the developing grains. In the Argentinian Pampas (main barley growing area) N, phosphorus (P) and sulphur (S) are the nutrients that most commonly limit crop production. Several experiments were carried with or without N, P or S fertilization in barley plants in field or under controlled conditions (both in greenhouse and growth chamber) in order to analyze several key components involved in C and N assimilation and remobilization and their relation with grain protein content and composition. Phloem amino acids fluctuated in response to nutrient availability, increasing at the beginning of grain filling under N or P deficiency, decreasing all along the process under S deficiency, remaining constant in well provided plants and decaying at the end of the grain filling period in non-fertilized ones. The contribution of amino acids from the phloem was found to be of great importance for the protein content of the grain, while the contribution of sugars showed a potential role in regulating the expression of the B-hordein genes (most abundant grain proteins). In recent years, we have focused on the effects of S availability and we observed that S deficiency leads to a delay in the phyllochron, leaf expansion and senescence, as well as an inhibition of C and N assimilation and recycling by down-regulation of the diffusional, photochemical and metabolic processes involved in photosynthesis, together with a down regulation of glutamine synthetase and several sugar and amino acid transporter genes. Altogether, the results indicate that C and N remobilization to sink tissues are highly influenced by nutrient availability, with a particularly significant role of S for the nutrient delivery to sink tissues.

Keywords: plant nutrition, plant physiology, cereal production.

Plants' deceiving game to tame bacterial foes

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Plant immunity relies on Pattern Recognition Receptors (PRRs) to perceive Microbe-Associate Molecular Patterns (MAMPs) from invading bacteria to induce defense responses that prevent attempted infections. Since the expression of virulence genes is key for bacterial pathogens to colonize plants, alterations in the expression of virulence, induced by MAMPs perception, are key for the host to remain healthy. The activation of plant immunity with MAMPs prior to the infection suppresses the onset of bacterial virulence by promoting the accumulation of Gln and Ser in the leaf apoplast. This seems paradoxical considering that, among other free amino acids, pathogenic bacteria use Gln and Ser as only sources of carbon and nitrogen to support bacterial growth. Indeed, when colonizing naive (non-immunized) plants, bacterial pathogens suppress plant immunity to prevent the early accumulation of apoplastic amino acids. Later on in the infection, and after suppressing plant immunity, pathogenic bacteria produce and secrete small molecules that impact plant amino acid metabolism and transport. This manipulation of the host physiology leads to the accumulation of apoplastic amino acids, Glu and Asp among other amino acids that support fast bacterial growth and virulence expression. In brief, plants have evolved defense mechanisms to deceive incoming microbes with easy-to-use metabolites (i.e. Gln and Ser) at a time when the priority of the incoming bacterium should be the expression of virulence genes to suppress plant immunity.

Keywords: plant immunity amino acid transport bacterial pathogens.



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Symposia

Mineral Plant Nutrition

Improving nitrogen use in rice with gene networks

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Plants exhibit remarkable plasticity, enabling them to adapt their morphology in response to environmental stimuli, crucial for survival and growth. Among the important nutrients for plant growth, nitrogen (N) stands out as a limiting factor. The indispensable role of N fertilizers in ensuring world food security together with the significant threats they pose to the ecosystem, makes the usage of N fertilizer a major challenge for sustainable agriculture. Genetic improvement of crops with high N-use efficiency (NUE) emerges as a promising solution to mitigate these challenges.

It is well-established that different plant species signal the presence of N transcriptionally. Although the genes constituting these signal transduction pathways are under intensive scrutiny, the quantitative relay of environmental signals has received less attention.

To bridge this gap, we conducted a systematic comparison of transcriptomic responses between two model species, rice and *Arabidopsis*. Our findings reveal a core network response, indicating a conserved mechanism of nitrogen response between these two plant species. Within this network, we identified a GARP G2-like as one of the rice core responsive transcription factors involved in mediating the amplitude of N-dose responses at both transcript and phenotypic levels. In addition, the analysis of the promoter region indicates that this transcription factor is involved in ABA and stress responses as well.

Therefore, our cross-species analysis proves to be a fruitful approach for identifying key loci of interest and sheds light on the shared aspects of transcriptional responses to N and other abiotic stress across plant species. These findings contribute to our understanding of the molecular basis underlying plant adaptation to varying N conditions, with potential implications for enhancing N use efficiency in crop plants.

Keywords: Nitrogen, transcription factor, rice.

Optimization of NAD-ME for C4 physiology in eudicots: A three-way dance story

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In plant mitochondria, NAD-malic enzyme (NAD-ME) has a housekeeping function in mitochondrial malate metabolism. In different plant lineages, NAD-ME was independently co-opted in C4 photosynthesis. In the C4 Cleome species, *Gynandropsis gynandra* and *Cleome angustifolia*, all NAD-ME genes (*NAD-ME α* , *NAD-ME β 1*, and *NAD-ME β 2*) were affected by C4 evolution and are expressed at higher levels than their orthologs in the C3 sister species *Tarenaya hassleriana*. In *T. hassleriana*, the NAD-ME housekeeping function is performed by two heteromers, NAD-ME α / β 1 and NAD-ME α / β 2, with similar biochemical properties. In both C4 species, this role is restricted to NAD-ME α / β 2. In the C4 species, NAD-ME α / β 1 is exclusively present in the leaves, where it accounts for most of the enzymatic activity. *G. gynandra* NAD-ME α / β 1 exhibits high catalytic efficiency and is differentially activated by the C4 intermediate aspartate, confirming its role as the C4-decarboxylase. We show that during evolution, NAD-ME β 1 repeatedly lost its catalytic activity; its contribution to the enzymatic activity of the heteromer results from a stabilizing effect on the associated α -subunit and the acquisition of regulatory properties. We conclude that in mitochondria of C4 species, the functions of NAD-ME as C4 photosynthetic decarboxylase and as a housekeeping enzyme coexist and are performed by isoforms that combine the same α -subunit with differentially adapted β -subunits.

Keywords: C4 photosynthesis, mitochondrial malate metabolism, C4 evolution.

The diverse iron distribution in seeds

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Most of our knowledge on seed iron accumulation is mainly based on studies performed in the model plant *Arabidopsis thaliana* for which it has been described that iron accumulates in the vacuoles of the endodermis cell layer during seed maturation. However, little is known about iron allocation and distribution in seeds of other plants. Interestingly, we have found that different strategies exist in other plant species. Our results indicate that dicot seed embryos have a different iron distribution pattern compared to *Arabidopsis*. Using mutants and transgenic plants approaches we modified iron distribution in *Arabidopsis* embryos, however, these changes had not impact in the total iron content in seeds, suggesting that embryonic iron distribution do not control total seed iron content.

In order to study the effect of agriculture in monocot seeds, we performed a histological and quantitative study of iron in archaeological maize seeds from prehispanic times recovered from Tarapacá, Atacama Desert. Our findings revealed changes in iron distribution at the sub-cellular level in embryos from ancient versus new varieties of maize, and a progressive decrease in iron content from the oldest maize to modern specimens was observed. We interpret the results as an effect of prehispanic agriculture over the micronutrient composition of maize.

Keywords: seed, iron, histology.



Genomic insights into the metabolism of endo-cyanobionts of diatoms

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Diatoms of the genus *Epithemia* contain cytosolic spheroid bodies which turned out to be entities phylogenetically related to N₂-fixing cyanobacteria. These symbiotic diatoms are widespread in the environment, especially in oceans, and appear to be key players of the Earth's geochemical cycles of C and N, and the overall food chain. Unfortunately, cultivation under laboratory conditions proved to be very challenging, and thus progress towards understanding the details of this symbiosis was very slow. During the last years we committed to contribute to this issue and isolated from the environment a few *Epithemia* species and developed methods for cultivation and maintenance under laboratory conditions at the expense of C and N from the air. We started to analyze regulatory aspects of the expression of genes for N₂-fixation and obtained the genome sequence of the spheroid body (cyanobacterial-like endosymbiont) of *E. adnata* and a draft genome of the host diatom. The *E. adnata* symbiont showed a large reduction of genome size, in comparison to the free-living closet relative *Chroocospaera subtropica*, and the absence of genes for photosynthesis. Overall, the genomic reconstruction of metabolism suggests several adjustments to the endophytic lifestyle which are going to be commented during this talk and discussed in view of current projects towards genetic engineering of N₂-fixation into plant cells, and the phylogenetic origin of organelles.

Forests facing drought and heat-waves: the need of a physiological-based forestry to increase plantations adaptability to climate change

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Increased tree mortality is a phenomenon widely reported over the last decades in different species and forests around the world. About 70% of the global drought-induced tree die-offs have been related to the combined effects of drought and heat waves (i.e. "hotter-drought" events) mainly associated with global warming. The hydraulic disfunction of the trees has been proposed as the main physiological driver of tree death. In forest plantations intensively managed to feed different industries this kind of event is rarely reported. However, they are not immune to extreme climate events, as was shown in a recent mortality event occurred in Corrientes province, Argentina, due to the combination of prolonged extreme drought and heat waves. In this sense, even when mortality events might not be observed, decreased productivity due to abiotic stress (alone or in combination with biotic agents), may represent a serious threat for their sustainability. New paradigms are needed to face climate change impacts posed on planted forests since most of the strategies applied until now has been oriented to increase productivity (and sometimes, also for wood quality). However, due to functional relationships and constraints, these objectives are sometimes compromised with abiotic stress resistance. In this talk, three major strategies are discussed and exemplified with study cases of *Pinus spp* and *Eucalyptus spp*, aiming to show possibilities and current limitations to develop a climate-smart forestry: a) species and genotype selection as well as genetic improvement oriented to abiotic stress resistance (and the potential trade-offs with growth and wood quality traits); b) planting site selection at landscape level to decrease mortality risks; and c) silvicultural management to reduce climate sensitivity and increase resistance and/or resilience to extreme climatic events.

Keywords: drought resistance, planted forests, tree mortality, climate-smart forestry.

Is cold acclimation the key to frost tolerant *Eucalyptus* in a warming world?

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Trees have evolved a plethora of mechanisms to cope with multiple stresses to ensure survival and reproductive success. While annual plants can regulate their life cycle to fit optimal conditions, perennial plants have to regulate pathways to survive winters and regulate growth to sustain life cycle. This process has been fine-tuned over millions of years and is now under severe pressure from climate change. Trees have thrived over similar challenges many times before, but this time they are threatened by the speed and intensity of change. Moreover, crop plants and trees are closely linked to the economy and development of particular ecoregions, making crop and population migration a last resort. As the climate warms, extreme events could become more frequent, exacerbating the effects of climate change. Recent years have seen an increase in the occurrence and duration of cold spells and disruptive snowfalls around the world. Climate change is causing both an earlier start to the growing season and warmer frosts, but the former effect dominates the latter. Frost-tolerant *Eucalyptus* species are capable of withstanding cold stress by a process termed cold acclimation. It relies on sensing cold non freezing temperatures and converting them into an internal signal to trigger a defense mechanism through a transcriptional cascade to synthesize various protective biomolecules. Under climate change, this strategy is threatened. Therefore, to safeguard planted forest productivity, frost tolerance strategies need revamping. Fortunately, some *Eucalyptus* species under study can thrive in this scenario. Research on frost tolerance mechanisms and genes must continue to deliver them into new tolerant genotypes.

Unravelling the responses of non-model tree species to the environment: the case of *Nothofagus pumilio* a key species of the subantarctic forests

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Forests cover about 41 million km² of the surface of the planet, and by sequestering large amounts of carbon they comprise a key element in countering the effects of increased CO₂ production, such as global climate change. Despite this, predicted changes in climate are expected to have major impacts in trees. Revealing the physiological and molecular bases of their responses to the environment is therefore crucial for the development of conservation strategies and for breeding stress-resistant genotypes. *Nothofagus pumilio* is one of the tree species with the larger distribution area in Patagonia. This species ranges in elevation from 0 to 2000 meters above sea level in high latitudinal zones (55°S). However, north of 41°S, it occurs only in the sub-alpine zone –the coldest environments-, suggesting that it lacks adaptation to heat. In this talk I will show the way in which we use genomic tools in combination with laboratory and field experiments to explore the molecular bases of abiotic stress response in *N. pumilio*. We mainly focused on stress by high temperatures given that this factor resulted a major driver of seedling mortality in the forest. We generated a draft genome that nowadays condenses the analysis of differential expression experiments, genotype-phenotype associations and functional studies. We identified a wide spectrum of heat-responsive transcripts, including 59 transcription factors, alongside spliceosome machinery and hormone pathways. Both in field and laboratory experiments photosynthesis is apparently affected by stress. Preliminary association studies in seedling growing in natural environments identified nucleotide polymorphisms related to the phenotypic variation in photosynthetic traits, with the corresponding genomic regions encompassing genes related to development and stress response. Overall our work provides the first clues in the stress response of *N. pumilio*, and provides information of potential use in biotechnological programs.

Keywords: Abiotic stress, ecophysiology, genomics, trees, seedling.



RNA silencing pathways in plants

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RNA silencing controls gene expression via 19-36 nucleotide small RNAs (sRNA) to regulate development, control stress responses, and preserve genomic integrity, among other essential processes. To fulfil their biological function, sRNAs are loaded into ARGONAUTE (AGO) proteins. The number of AGO genes varies among different organisms. The *Arabidopsis thaliana* genome encodes ten At-AGO, which can be grouped in three major phylogenetic clades. Whereas At-AGO1, -5, and -10 clade binds ~21nt molecules acting in cytoplasmic post-transcriptional silencing, the clade formed by At-AGO4, -6, -8, and -9 associates with 24nt sRNA mediating nuclear transcriptional silencing. A third clade composed of At-AGO2, -3, and -7 performs different functions including antiviral defense, tasiRNA biogenesis, and DNA repair. Since the discovery of the first eukaryotic AGO in *Arabidopsis*, our understanding of these proteins has grown exponentially throughout all the eukaryotes. However, many aspects of AGO proteins' modes of action and how they are influenced by their subcellular localization are still to be elucidated. Here, we provide an updated view of the subcellular localization and shuttling mechanism of AGO proteins in plants.

Circadian clock functions in woody perennials

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The correct cycling between active growth and dormancy is critical for the survival of trees growing in temperate and boreal regions. Trees use photoperiod and temperature as precise indicators of seasonal changes, allowing them to properly synchronize the environment with plant phenology. The timings of cyclical or seasonal biological events rely on the circadian clock. Functional genomics in the poplar tree model dissects the biological rhythms' fundamental role in tree phenology. In poplar, the daylength signal converges to control the expression of FLOWERING LOCUS T 2 (FT2). FT2 daily expression level is essential to promote shoot apex development which sets poplar annual growing period. We have developed a minimal data-driven model based on experimental data that mimics FT2 expression changes in response to day length. This computer model predicts that a regulation driven by the circadian clock core genes can explain FT2 expression and the short-day downregulation. Analysis of CRISPR/Cas9 loss of function lines supports the model. Winter temperatures disrupt the biological rhythms in trees. Circadian clock genes show a transcriptional activation during the winter, which significance is under investigation. Our functional study of circadian clock-regulated genes highlighted their importance in dormancy break regulation, mainly through chilling-dependent regulation of RNA metabolism. Apart from seasonality, our functional study of poplar circadian clock LATE ELONGATED HYPOCOTHYL (*lhy1/2*) double mutant lines linked circadian clock with leaf developmental patterning. Our poplar functional genomics unravels the conserved and novel roles of the circadian clock in woody perennials.



Regulatory networks of TCP transcription factors during Arabidopsis seedling development

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After germination, exposure to light promotes the opening and expansion of the cotyledons and the development of the photosynthetic apparatus in a process called de-etiolation. This process is crucial for seedling establishment and photoautotrophic growth. However, transition to light is a challenge for dark-germinated seedlings, since light can be harmful to the plant during the de-etiolation process. When the plant grows in dark conditions, illumination can produce photooxidative damage, which affects the accumulation of chlorophyll, photosynthesis and, eventually, the growth or survival of the plant. To avoid this, a number of key regulatory factors are required for the control of chlorophyll biosynthesis during this transition.

TEOSINTE BRANCHED 1, CYCLOIDEA, and PROLIFERATING CELL FACTORS (TCP) transcription factors constitute a plant-specific protein family that participates in the regulation of numerous processes of growth and development during the life cycle of plants, acting through the recruitment of other factors and the modulation of different hormonal pathways. In our laboratory, we found that different TCP proteins participate in processes associated with de-etiolation, like cotyledon opening and expansion, as well as the induction of genes encoding components of the photosynthetic apparatus, physically interacting with the transcription factor GLK1 and integrating into the transcriptional network associated with this transcription factor. TCP proteins also affect the accumulation of chlorophyll precursors in etiolated seedlings supporting a role of these proteins in the protection from photooxidative damage after light exposure. The molecular mechanisms related to the action of TCP transcription factors in these processes will be discussed.

Keywords: molecular biology, Arabidopsis thaliana, transcription factors, TCP, GLK, photomorphogenesis.

Juvenile-to-adult phase transition in grapevine

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The sequential activity of miR156 and miR172 on their targeted genes (i.e., SQUAMOSA PROMOTER BINDING PROTEIN-LIKE -SPL-), controls the juvenile to adult phase transition in several plants. A decrease in miR156 abundance and an increase in miR172 abundance are associated with the phase transition. Very little is known about phase transition in horticultural tree crops, which have a substantially long vegetative phase. In grapevine, phase transitions are dissociated, presenting a transition from juvenile to adult state in the first year and a subsequent induction of flowering in later years. Being a highly heterozygous species, generating a genetically homogeneous material for replicated transcriptomic analyses from seeds is not a trivial task. Here, we present a detailed global expression analysis of the main genes involved in the juvenile to adult phase transition during the development of the grapevine plant from seeds. RNA-seq analysis showed a clear repression of miR156 in the adult phase, marked in the grapevine by the appearance of tendrils. Consistent with what was observed in other annual plants, we observed the consequent activation of several SPL genes, known to be targets of miR156, and providing evidence for the conservation of the regulatory module miR156-SPLs in grapevine. No variation was detected in the expression of miR172, determining the floral induction, which is expected given that the grapevine does not flower during the first year. However, we were able to observe the over-expression of several genes involved in the floral meristem identity transition. This would be consistent with the common origin of tendrils and inflorescences, considered homologous organs. Our results indicate the conservation of the juvenile to adult phase transition mechanisms in grapevine and a differentiation with annual species given the absence of floral induction during the first year of development of the plant from seeds.

Keywords: miR156, miR172, miR156 targeted SPLs, phase transition, juvenility and adult, microRNA.

Regulation of vitamine E metabolism in tomato

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The genetic bases of the yield-associated traits and nutritional values of crop plants have been studied in several species but are largely restricted to classical molecular genetic analyses and less effort have been devoted to uncover epigenetic mechanism(s) underlying these traits. Our research group study the regulation of biochemical pathways that ultimately impact these kinds of traits in tomato plants. Three main issues will be discussed in this presentation: 1) analyses of the epigenetic nature of the regulation of metabolite content variations in tomato focusing on the vitamin E pathway; 2) results from metabolic engineering strategies of chlorophyll recycling pathways and 3) an overview on fundamental knowledge about the molecular mechanisms determining hybrid vigor (heterosis) in plants.

Keywords: tomato, epigenetics, chlorophyll metabolism, hybrid vigor.



Ethylene receptors are required to activate the plant defense response induced by AsES

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AsES (*Acremonium strictum Elicitor Subtilisin*) is a fungal protease that induces a defense response in *Arabidopsis thaliana* and in many commercial crops by activating the ethylene signaling pathway in plants. In the present work we study the action of AsES on ripening and disease resistance in climacteric (avocado) and non-climacteric (strawberry) fruits, and its association to the ethylene synthesis and the ethylene receptors. Results showed that AsES accelerates ripening and enhances parameters of fruit quality, induces an increase in ethylene production and confers higher resistance to the grey mold disease in both types of fruits. Experiments carried out with strawberry plants and fruits treated with AsES and the ethylene perception inhibitor 1-methylcyclopropene revealed a differential and unexpected regulation of the ethylene biosynthesis while increasing the susceptibility to the grey mold disease.



Enhancing insight into the function of plant filamentous-pathogens' Effectors: suppression of immunity via manipulation of developmental hormonal path

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Filamentous pathogens, such as oomycetes and fungi, produce a wide array of molecules during their interactions with plant hosts. Among these, effector proteins play a crucial role as specialized weapons that these pathogens deliver into plant tissues. By generating and delivering multiple effectors at different stages of infection, pathogens manipulate various cellular and metabolic processes to create a favorable environment for survival and reproduction. They also undermine host immunity to access nutrients and building blocks. Our research focuses on effector biology, aiming to identify the plant targets of these effectors, uncover their molecular activities, explore their recognition by resistance proteins, and assess the potential to generate resistance by eliminating susceptibility factors. We specifically delve into understanding the virulence mechanisms of effectors involved in the balance between defense signaling and growth signaling. Comprehending the molecular basis of these tradeoffs is crucial for developing resistant plants without compromising growth, ultimately maximizing crop yields.

Keywords: filamentous pathogen, oomycete, effector, immunity, growth-hormones.

Function of Plant Glutamate Receptor-like channels (GLR) in adaptation to abiotic stress

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Sensing of abiotic stress involves the sensing of various biophysical parameters, including pH, redox potential, mechanical and chemical cues. Downstream stress sensing, the transduction of the stress signal is ensured by more or less specific transduction pathways where second messengers, phosphorylation cascades, voltage changes play major roles. Plant ionotropic glutamate receptors (GLRs) are strategically located within the network: on one hand GLRs participate in signal propagation by permeating the second messenger Ca^{2+} and transporting other ion species that control membrane voltage. On the other hand, GLR activity is sensitive to several key signal messengers including amino-acids ACC, D-serine, Glutamate, second messengers H^+ , Ca^{2+} , electric and redox potential. I will present electrophysiological data acquired in heterologous system expressing plant GLRs and characterizing their regulation. So far, the mechanism of action of GLR in the context of cell signaling has been elusive. I will discuss the consequences of the data presented on role of GLRs in signal propagation and transduction in the context of abiotic stress response.

Keywords: Calcium, channel, abiotic stress, physcomitrella patens, moss.



Evaluation of the effect of TuMV infection on drought tolerance and water management at the whole plant level in *Arabidopsis*

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The assessment of the interaction effect between different types of stresses simultaneously affecting plants has received great interest in recent years, since it is considered that it represents in a more realistic way the conditions that crops must face in the field. In the present work, the effect that TuMV infection has on the water balance in *Arabidopsis* was evaluated both at the rosette level (stomatal conductance, instantaneous dehydration rate, relative water consumption, RWC, osmolarity) and at the root level (root hydraulic conductivity, osmolarity). These physiological measurements were accompanied by anatomical measurements to estimate the relative growth under infection in different organs. In addition, survival measurements were carried out to estimate putative changes in drought tolerance produced by the viral infection. TuMV was found to cause profound changes in water management at both the foliar and root levels. In addition, drought competition experiments showed that TuMV lowers drought tolerance in *Arabidopsis*, evidencing a negative synergistic effect for the plant under the interaction of both stressors when they act simultaneously.

Keywords: Turnip Mosaic Virus, drought, *Arabidopsis*, root hydraulic conductivity, osmolarity, water management, combined stresses.



Photoperiod sensitivity and spike fruiting efficiency as alternatives to increase wheat yield potential

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Breeding cultivars with higher yield potential (the yield of an adapted cultivar without water or nutritional restrictions and free of biotic stresses) is an alternative to improve wheat production in a sustainable way. Photoperiod sensitivity during stem elongation has been proposed a long time ago as a potential trait to increase duration of that phase, which would result in higher spike growth and grains, the main determinants of yield potential. Photoperiod sensitivity could also help to adapt new cultivars to warming temperatures associated to climate change. How the known genes associated to photoperiod sensitivity control development of the different phases of the wheat cycle is necessary for assessing their usefulness in breeding. More recently, the spike fruiting efficiency (grains per gram of spike dry weight at anthesis) has been proposed as a trait to increase grain number and yield potential. The physiological, and particularly, the genetic bases determining the trait need to be understood to use it as selection criteria in breeding programs. The state of art of both traits will be discussed during the oral presentation at the Vegetative and Reproductive Development Symposia of the RAFV 2023.

Keywords: wheat yield, photoperiod sensitivity, fruiting efficiency.

From comparative transcriptomics in apomictic species to the induction of apospory-like phenotypes in *Arabidopsis*

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The combined use of sexuality and apomixis in plant breeding programs have a positive impact on the time and cost required to produce improved cultivars. This methodology has potential for crop diversification and decreasing of seed costs. Currently, this strategy is being used only in natural apomictic species like those included in the *Paspalum*, *Brachiaria* and *Panicum* genera, but molecular research in the field is evolving quickly, making its transference to the breeding of sexual major crops a conceivable possibility. In last two decades, we used RNAseq to extensively characterize gene differential expression in ovules of sexual and aposporous apomictic *Paspalum notatum* plants and identified numerous guilty-by-association genes, some of which map in the genomic region responsible for apomixis in the species. Reverse genetics analyses using *GFP*-fusion expression lines, DIC and confocal cytoembryology, crosses with cell-identity fluorescent marker lines, *in situ* chromosome counting and flow cytometry in both wild type and mutant/transformant contexts are revealing that the orthologs of some of these candidates can induce apospory-like phenotypes (i.e., the formation of multiple non-reduced functional megaspores and supernumerary mature gametophytes with altered polarity and unusual cell identity) in the sexual model species *Arabidopsis thaliana*. This work establishes a proof of concept that candidate genes identified in the *Paspalum* system can be used to develop molecular tools, in order to induce reproductive mode changes within breeding programs.

Keywords: apomixis, apospory, plant development, plant reproduction.



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Symposia

Vegetative and Reproductive Development

Mitotic and Endoreplication Cell Cycles in Plant Organ Growth

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Within plant meristems, the mitotic cell cycle (MCC) produces new cells that subsequently engage in cell expansion and differentiation programs. The latter is frequently associated with endoreplication (ER), an alternative cell cycle that replicates the DNA without nuclear division, causing an increase in somatic ploidy. MCC regulators have oscillating activities regulated by transcriptional and posttranscriptional mechanisms. For example, the E2F and MYB3R transcription factors (TF) control gene expression during the G1/S and G2/M transitions. Genomic studies indicated that only a subset of the genes with expression enriched at the G1/S or G2/M transitions are directly regulated by the E2F or MYB3R TFs, suggesting that other regulators remain to be identified.

To identify these genes we first analyzed the transcriptome of cells in G2/M and found hundreds of genes whose expression is reduced or enriched in G2/M cells. This dataset enabled us to identify new potential regulators, including TFs, proteins involved in redox and calcium metabolism, motor proteins, etc.

Here, we focus on SCARECROW-LIKE 28 (SCL28), a GRAS transcription factor, whose mRNA accumulates to the highest levels in G2/M and is regulated by MYB3R transcription factors. Functional analysis indicates that SCL28 promotes progression through G2/M and modulates the selection of cell division planes.

Surprisingly, gene expression studies indicated that SCL28 regulates SIAMESE-RELATED genes, encoding CDK inhibitors with a role in promoting mitotic cell cycle exit and endoreplication. Consistent with this, mutants in SCL28 displayed reduced endoreplication. We also found evidence indicating that SCL28 regulates genes related to the biogenesis, assembly and remodeling of the cytoskeleton and cell wall.

Altogether, our results suggest that SCL28 controls plant organ growth by modulating not only cell proliferation, but also endoreplication, cell expansion and differentiation.

Keywords: mitotic cell cycle, development, endoreplication, cell expansión.



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Abstracts: Short Talks

Importance of Calcium ATPases in root hair development in *Arabidopsis thaliana*

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Root hairs are specialized root epidermal cells important for water and nutrient uptake as well as necessary for attaching plants to the soil. These cells present polarized growth, meaning they go through an elongation process in only one direction. This type of growth is characterized by an oscillatory behavior based on cytosolic Ca²⁺ and extracellular ROS gradients as well as a decrease in cytosolic pH towards the tip of the root hair. In this project we aim to study the cytosolic Ca²⁺ oscillations associated with polarized growth. Our research focuses on Ca²⁺ ATPases, and their importance in keeping the Ca²⁺ homeostasis in root hairs. To do this, we made an analysis of RNA seq microarrays of *Arabidopsis thaliana* to determine the expression pattern of these proteins in root and root hairs. Based on these results, we chose four different Ca²⁺ ATPases and performed an analysis of root hair length in insertional mutants for these four ATPases (SALK and SAIL lines). So far, we have identified a very strong phenotype in one of these mutants. In addition, we treated these lines with Eosin Y (a known inhibitor of Ca²⁺ ATPases) and analyzed the resulting root hair length. Our following steps center around the study of this protein's structure and function as well as an in vivo analysis of cytosolic Ca²⁺ dynamics in the root hair tips by using the Ca²⁺ biosensor YC3.6.

Keywords: Arabidopsis thaliana, root hairs, molecular biology, calcium oscillations.

The role of mitochondrial H₂S in stomatal immunity

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Land plants have little holes in their epidermis, known as stomata, responsible for the gas exchange between plants and their environment. Stomata are formed by pairs of specialized cells, the guard cells, delimitating a central pore. Guard cells sense different stimuli and integrate them into a complex signalling network that regulates the pore size. When compared with their neighboring cells, guard cells have unique characteristics, like a higher mitochondrial density and respiration rate. Nevertheless, the role of mitochondrial activity on stomatal closure is not fully understood.

Some pathogens use natural apertures like stomatal pores to invade plants. Hence, plants evolved to recognize conserved motifs in pathogens, the pathogen-associated molecular patterns (PAMPs). The perception of PAMPs triggers multiple defense responses, including ROS production, gene reprogramming and stomatal closure, as a first mechanical barrier to reduce infection.

The gasotransmitter hydrogen sulfide (H₂S), is a very reactive molecule that regulates different physiological processes, including stomatal closure. Despite that *Arabidopsis* has enzymatic H₂S sources in different subcellular compartments, most works on the biological effect of H₂S in plants have focused on the main cytosolic source DES1.

In this work, we studied the role of the mitochondrial H₂S source β-CYANOALANINE SYNTHASE (CAS-C1) on stomatal immunity. Previous results obtained in our lab show that flg22-triggered stomatal closure, apoplastic and cytosolic ROS increase, were impaired in cas-c1. In this work, we present evidence indicating that cas-c1 shows a differential expression of flg22-induced genes. Moreover, using radiometric sensors we show that flg22 increases the mitochondrial activity in guard cells, response that is disrupted in cas-c1. Taken together, results suggest that CAS-C1 is needed for flg22-induced stomatal immunity, response that involves mitochondrial activity.

Keywords: stomata, hydrogen sulfide, mitochondria, pathogens.

Did selection for tolerance to high plant density improve maize growth response in water stress conditions?

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Modern maize cultivars for higher grain yield have changed plant architecture, allowing deeper light penetration. We investigated if breeding-induced architectural changes indirectly affected hydraulic traits via changes in transpiration. Using the PhenoArch phenotyping platform, we grew 10 maize hybrids released in France between 1951 and 2012. They were tested under two plant densities (7 and 14 plants per square meter) and well-watered conditions. We hypothesized that recent hybrids with higher plant density tolerance have improved water use efficiency due to moderate transpiration across canopy layers. Daily RGB images were used to estimate plant growth, leaf area, and height. Water uptake was estimated by weighing pots four times daily, with weight differences as evapotranspiration. Leaf area, transpiration, and time between weighings were used to estimate transpiration rates. Final plant height ranged from 762.8 to 1348.8 mm pl⁻¹, biomass from 161.5 to 328.7 g pl⁻¹, and leaf area from 2128.6 to 4224.4 cm² pl⁻¹. This variability was mostly associated with the Genotype variability, which explained 44, 23 and 25 % of the variability in plant height, biomass and leaf area, respectively. Genotypic response to plant density was not significant for plant height neither for old nor for modern genotypes. However, for biomass and leaf area, old genotypes showed negative or no response to density reductions, while modern genotypes increased both. Preliminary analysis suggests modern hybrids altered plant architecture. At the canopy level, genotypic responses to changes in plant density were weaker in modern hybrids. At high densities, evapotranspired water increase compared to low densities but less in modern than older hybrids. Findings support modern hybrids' modified architecture through leaf area and biomass changes. Provisional conclusion: modern maize hybrids, at higher densities, consume water-cycle more profitably.

Keywords: Breeding, water use, architecture.



Effects of flooding on the growth of different cultivars of cassava (*Manihot esculenta* Crantz) plants grown in greenhouse conditions

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Cassava is an economically and nutritionally important crop for many developing countries. However, it is susceptible to abiotic stresses, including flooding. Due to an increase in the intensity and frequency of torrential rains, flooding events have become more critical. Despite this, there has been little research on the effect of flooding on cassava. This study aimed to evaluate the impact of flooding on the growth of two cassava cultivars in a greenhouse in Corrientes, Argentina, during two campaigns in 2021 and 2022. The cultivars used were CA145 and CM3306-4, maintained in the BGCTES germplasm bank (IBONE-CONICET-UNNE/FCA-UNNE). Plants were regenerated *in vitro* and then grown in a controlled growth chamber for four weeks before being moved to a greenhouse for 14 weeks. During this time, plants were partially flooded with water at 3 cm above the substrate level for 18 days, while control plants were irrigated at field capacity. The parameters evaluated were: stomatal conductance and chlorophyll fluorescence, dry weight of the aerial and root parts (including fibrous and tuberous roots), percentage of dry matter and loss of dry matter caused by flooding. Results were analysed with ANOVA and Duncan's multiple comparison test ($p \leq 0.05$). The study found no effect of the campaign or differences between the cultivars. However, significant differences were observed between treatments (control vs. flooded plants). After 18 days of flooding, there was a significant decrease in stomatal conductance and chlorophyll fluorescence, and a significant reduction in shoot and root dry matter of about 60 and 80%. While the loss of aerial dry weight was due to growth arrest and leaf shedding, root biomass reduction was caused by tuberous roots emptying the storage parenchyma.

Keywords: Cassava, dry matter, flooding, growth, tuberous roots.



Maize grain dry-down: improving predictive models

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Predicting the optimal harvest date after crop physiological maturity is highly relevant for maize (*Zea mays* L.). While harvesting before achieving commercial kernel moisture implies additional costs of grain drying, a delayed harvest of maize crops is linked to grain yield and quality losses. Grain dry-down after physiological maturity follows a curvilinear response over time until equilibrium moisture is achieved and is affected by a post-maturity kernel dry-down coefficient (k), which indicates the resistance to water diffusion and refers to the proportion of moisture that can be exchanged in each time step. Previous dry-down models for estimating changes in kernel moisture considered the post-maturity kernel dry-down coefficient as a constant value. Current changes in farming management practices, particularly the delay in the sowing date expose kernels to diverse environmental conditions during the dry-down, affecting the capability of available models to capture the kernel moisture loss. The main objective of this work was to identify weather variables affecting the post-maturity grain dry-down coefficient to develop models to predict kernel moisture loss and time to harvest under a wide range of sowing date environments. Kernel moisture datasets from field experiments in Pergamino (Argentina) and Kansas (US) were used for training and testing post-maturity grain dry-down models. Two k coefficients were defined based on the solar radiation and the vapor pressure deficit explored during the pre- and post-maturity periods (k_{pre} and k_{post}). Models including k_{pre} and k_{post} were tested under a wide range of sowing date environments, presenting high accuracy in predicting kernel moisture ($R^2 \sim 0.80$; RRMSE ~ 0.15) and harvest readiness ($R^2 = 0.99$; RRMSE ~ 0.05). This study provides the foundation for incorporating maize grain dry-down models in interactive digital platforms to estimate harvest time to assist farmers and agronomists with this critical decision.



Combined effects of cytokinins and brassinosteroids applied at flowering on grain yield and components of rapeseed

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It has been shown that the combined use of cytokinins (CK) and brassinosteroids (BR) applied during flowering increases grain number in *Arabidopsis thaliana* L. due to a synergistic effect between both phytohormones. These results could be emulated in a specie of the same Brassicaceae family. The objective of this study was to evaluate this effect on grain yield, its components and quality traits (oil and protein concentration) of rapeseed (*Brassica napus* L).

The spring hybrid Click CL (NPZ-Lembke) was sown on September 3 (2022) under field conditions in Valdivia, Chile (39°47'S, 73°14'W). The experiment consisted of a control, and three hormonal treatments; CK only, BR only and the combined application of CK and BR. Phytohormones were applied 10 days after start of flowering. The hormonal treatments were carried out using the commercial products Cytoplant-400 (400 ppm CK) and Brassinost-1 (20 ppm BR) at doses of 1 L/ha and 2 L/ha, respectively. Statistical differences were tested by ANOVA.

Grain weight was increased under the BR treatment by 11.7%, followed by 9.8% when CK was applied and by 6.7% in the combined treatment ($P=0.009$). These increments have not statistical impact on grain yield increase ($P>0.050$) causing a tendency to increase (16% for BR and 4% for the combined treatment), which was not significant due to a no existent trade-off between grain weight and grain number. Grain oil and protein concentration were not affected ($P>0.050$) by the hormonal treatments.

These results do not agree with previous reports in *A. thaliana*. Thus, the likely trade-off between grain weight and number found in rapeseed seems to be the cause of these contrasting results. The grain number and weight responses would be dependent on the type of brassica specie to which the treatment is applied. Additionally, grain weight in the combined treatment of CK and BR was lower compared to the other treatments, which suggests some negative interaction between both hormones in rapeseed.

1 Zu, S.-H., Jiang, Y.-T., Chang, J.-H., Zhang, Y.-J., Xue, H.-W., & Lin, W.-H. (2022). Interaction of brassinosteroid and cytokinin promotes ovule initiation and increases seed number per silique in *Arabidopsis* [<https://doi.org/10.1111/jipb.13197>]. *Journal of Integrative Plant Biology*, 64(3), 702-716. <https://doi.org/https://doi.org/10.1111/jipb.13197>

The mitochondrial enzyme ProDH controls the cytosolic redox homeostasis in Arabidopsis

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Proline (Pro) metabolism is proposed to transfer reducing power from different subcellular compartments by consuming NADPH in the cytosol and generating FADH/NADH in the mitochondria. However, it is unknown how this would impact on other redox buffers, such as glutathione and ascorbate, and redox sensitive proteins, such as RBOHD. We investigated these issues by inducing oxidative stress in WT and *prodh* plants with H₂O₂, flg22 or pathogens, and monitoring dynamic changes in GSH/GSSG and NADP⁺/NADPH ratios using the genetically encoded biosensors Grx1-roGFP2 (for EGSH) or NERNST (for NADP/H) both targeted to cytosol. In WT, H₂O₂ and flg22 caused a rapid and transient oxidation of the cytosolic glutathione pool, as expected. However, the *prodh* mutants showed enhanced or reduced GRX1-roGFP2 oxidation after H₂O₂ or flg22 treatment, respectively. Curiously, Pst DC3000 activated a biphasic oxidation of GRX1-roGFP2, and the second oxidation phase was higher in *prodh*. Interestingly, the NERNST biosensor displayed a rapid oxidation in response to flg22, mirroring the behavior of GRX1-roGFP2. However, after the first oxidative wave, the NADP⁺/NADPH ratio gradually increased again. The lack of ProDH activity reduced NERNST oxidation after treatment with flg22 and pathogen. These findings indicate that ProDH plays a crucial role in regulating the cytosolic redox homeostasis by balancing NADPH and glutathione oxidation during biotic stress.

Keywords: ProDH, redox, oxidative stress, phytopathology.

NO Way Out: Nitric Oxide Blocks Autophagy

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Autophagy is a conserved key process related to the development, stress responses, and remobilization in plants and eukaryotes in general. It is well established that nutrient deficiency conditions induce autophagy. Although certain molecular components that regulate the activation of this process have been elucidated, the signal transduction pathways governing the molecular machinery remain underexplored. In this study, we investigated the effects of nitric oxide (NO) as a possible regulator of autophagy. NO is a free radical produced as a byproduct of the enzyme Nitrate Reductase (NR) during the reduction process of nitrates. It functions as a second messenger, playing a crucial role in various developmental and stress response processes. Our results showed a correlation between nitrate availability, NR activity, NO levels, and the regulation of the autophagic process. To further investigate the impact of NO on autophagy modulation, we employed pharmacological approaches, including treatments with the NO donor SNP and the NO scavenger cPTIO. Our findings demonstrated that NO effectively inhibits autophagy activation in response to both nutrient deprivation and pharmacological inhibition of the target of rapamycin (mTOR). Conversely, scavenging NO leads to a slight increase in autophagy under nitrate-sufficient conditions. To address the mechanistic of NO in the regulation of autophagy, we explored putative S-nitrosylation sites in key components of the autophagy machinery through in silico analysis. Currently, we are evaluating the effects of NO on the activity of the redox-sensitive ATG4 protein, which has been shown to be inhibited by S-nitrosylation in mammals. By integrating the physiological aspect of nitrate reduction and NO production with molecular mechanisms, our study provides a comprehensive understanding of how the autophagic process is modulated by nitrogen availability.

Keywords: autophagy, nitrate, nitric oxide.

Shedding light onto the role of the Plastid terminal oxidase (PTOX) as a safety valve for photoprotection in plants

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The Plastid Terminal Oxidase (PTOX) is a chloroplast localized plastoquinone oxygen oxidoreductase which has been suggested to have the potential to act as a photoprotective safety valve for photosynthesis. However, PTOX overexpression in plants has been unsuccessful at inducing photoprotection, and significant PTOX activity has only been observed in a small number of stress-tolerant species. Thus, until now, the role of PTOX in photoprotection has been questioned, and the factors that control its activity remain elusive.

Here, we show that significant PTOX activity is induced in response to high light in the model extremophile plant *Eutrema salsugineum*. This activation correlates with structural reorganization of the thylakoid membrane. Over-expression of PTOX in mutants of *Arabidopsis thaliana* perturbed in thylakoid stacking also results in such activity, in contrast to wild type plants with normal granal structure. We conclude that structural re-arrangements of the thylakoid membranes, bringing Photosystem II and PTOX into proximity, are both required and sufficient for PTOX activation. Further, we show that overexpression of PTOX in *Arabidopsis* stacking mutants protects against photoinhibition of Photosystem II and reduces reactive oxygen production under stress conditions.

Our findings thus demonstrate a role for PTOX in photoprotection and set the basis for new strategies to redesign photosynthesis using PTOX, aiming to the generation of higher stress tolerance plants.

Keywords: plastid terminal oxidase, photosynthesis, electron transport, photoprotection, stress, acclimation.

Unveiling the Role of NADP-ME and NAD-ME in C4 Photosynthesis of *Setaria* and *Panicum*

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Understanding the functioning of C4 photosynthesis is of vital importance due to the impact of climate change and the need to improve the efficiency of carbon fixation in plants. In the context of this work, closely related species, *Setaria viridis* and *Panicum virgatum*, which belong to different subtypes of C4 photosynthesis, named NADP-ME and NAD-ME, were investigated.

In order to better understand the role of NADP-ME and NAD-ME isoforms in C4 photosynthesis, an integrative analysis was performed combining kinetic and regulatory studies with proteomics in both subtypes. A comparison of the proteomes of mesophyll and bundle sheath cells in both *Setaria* and *Panicum* was carried out, and these data were related to transcriptomic information from these species and other widely studied nearby species, such as maize. In both *S. viridis* and *P. virgatum*, evidence was found for the combined involvement of both decarboxylase enzymes in the process of C4 photosynthesis. This finding is of great relevance for understanding and optimising metabolism, and raises the need to further investigate the conditions under which these pathways coexist in both plants.

In summary, this work highlights the importance of studying C4 photosynthesis in the context of climate change, focusing on the relationship between *S. viridis* and *P. virgatum* species, which, although closely related, belong to different subtypes of C4 photosynthesis (NADP-ME and NAD-ME). The findings obtained provide valuable information on C4 metabolism and open new research perspectives in this field.



Targeted disruption of tomato CYC-B gene improves postharvest color development and cold stress tolerance

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Red color development is a very important fruit quality trait in tomato breeding, especially during postharvest storage. When exposed to low temperatures, tomato fruits are sensitive to cold and develop chilling injury (CI). Lycopene is the main pigment present in tomatoes and is responsible for its red color. In other cold-sensitive fruit, it has been described that lycopene contributes to alleviating CI disorder during postharvest cold storage. Therefore, increasing lycopene content in tomato fruit could enhance its cold stress tolerance in addition to improving fruit quality.

In tomato, *og* and *ogc* mutants have high lycopene content in fruit because these alleles encode for non-functional CYC-B enzymes and are unable to transform lycopene into β -carotene. These natural mutations have not been found in indeterminate growth tomato germplasm because they are linked to the *sp* mutant allele that is responsible for determinate growth habit. In greenhouse production of fresh market tomatoes, indeterminate growth is preferred in many countries, including Uruguay. In this work, we used CRISPR-Cas9 to generate CYC-B non-functional fruit-specific enzymes in tomato lines exhibiting indeterminate growth habit. We compared the postharvest color development of ripening fruit from edited and non-edited plant lines and evaluated CI symptoms during cold storage in autumn 2022 and 2023. Fruits from edited plants showed earlier and more uniform red color development during ripening at 25°C as well as a lower chilling injury incidence during cold storage. This work suggests that an earlier and higher accumulation of antioxidants such as lycopene contributes to reducing tomato CI during postharvest cold storage.

Keywords: CRISPR-Cas9, *Solanum lycopersicum*, chilling injury, fruit quality.

Blooming in the Desert: Unraveling the Secrets of *Cistanthe longiscapa*'s Adaptation.

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Understanding how plants adapt to environmental conditions and exhibit phenotypic variability is essential for unraveling their adaptive strategies. The arid Atacama Desert harbors the unique plant species *Cistanthe longiscapa*, a blooming desert constitutive Crassulacean acid metabolism (CAM) species. This study investigated three sites with diverse soil types and precipitation levels, analyzing nocturnal leaf acid accumulation, $\delta^{13}\text{C}$ isotopic ratio, photosynthetic pigments, Carbon to Nitrogen ratio, leaf mass per area (LMA), and succulence (SWC) in leaves from each site. Significant differences in these traits were observed, correlating with the varying precipitation recorded for each location. A Principal Component Analysis (PCA) revealed strong associations between specific variables and the geographical segregation of sampling sites.

In addition to ecophysiological investigations, we study the leaf transcriptome of *Cistanthe longiscapa* through de novo assembly and differential gene expression analysis. RNA-seq reads from 18 libraries were generated from different sites and times of the day. A comprehensive pipeline yielded 88,770 non-redundant transcripts and 37,253 predicted proteins. Gene expression patterns were identified based on location and time of collection through PCA. Differential gene expression analysis highlighted significant changes in transcripts such as the LHY transcription factor, NADP-dependent malic enzyme, and P5CS. Functional enrichment analysis revealed metabolic divergence among sites, with specific processes enriched in different locations.

Overall, this comprehensive investigation sheds light on the ecophysiological and transcriptomic responses of *Cistanthe longiscapa* to diverse environmental conditions, providing valuable insights into the plant's adaptation mechanisms in the challenging Atacama Desert.

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Keywords: CAM, Phenotypic variability, Blooming Atacama Desert, Cistanthe longiscapa, Extremophyle, Transcriptomic analysis, Ecophysiology.



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**Abstracts:
Posters**

P. 01

Different strategies to optimize the inoculation of potato plants with *Methylobacterium sp. 2A*

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A plant growth-promoting rhizobacteria (PGPR) belonging to the genus *Methylobacterium* was isolated from roots of potato plants. This PGPR, named *Methylobacterium sp. 2A*, enhanced the growth of Arabidopsis and potato *in vitro* plants exposed to salt conditions, antagonized plant pathogens and reduced disease symptoms in potato plants infected with *Phytophthora infestans* (Grossi et al 2020). We aim to understand if the inoculation of *Methylobacterium sp. 2A* enhances plant defense in potato plants through an induced systemic resistance (ISR) or by direct antagonism with the pathogen. To this end, we employed three inoculation strategies using a suspension of *Methylobacterium sp. 2A* cells (0.05 OD₆₀₀ units in 0.85% NaCl) or only 0.85% NaCl (control): i) roots of plants grown in solid MS for 3 weeks were inoculated with 100 µl of the suspension. Inoculated plants and controls were multiplied three consecutive times using internodes from the upper portion of the plants and the presence of *Methylobacterium* was checked; ii) plants grown in solid MS for 3 weeks were transferred to liquid MS for 24 h and then roots were inoculated with 0.8 ml of the suspension and harvested at 3, 10-, and 13-days post inoculation (dpi). The presence of *Methylobacterium* in the liquid media was checked; iii) plants grown in solid MS for 3 weeks were transferred to liquid MS for 24 h and then inoculated with 0.8 ml of the suspension. At 8 dpi, plants were transferred to pots and placed in the greenhouse. Two weeks later, *Methylobacterium* was recovered from a leaf extract of inoculated plants and plant growth was evaluated in each condition. Plants had a better fitness in hydroponics and the growth promotion was evident in inoculated plants. *P. infestans* infection assays will be conducted on plants inoculated using the three different strategies to evaluate ISR.

Keywords: plant growth-promoting rhizobacteria, *Methylobacterium sp. 2A*, *Phytophthora infestans*, *Solanum tuberosum*.

P. 02

Optimization of the TRAP technique in common bean to study translational dynamics during nitrogen-fixing symbiosis.

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Throughout their evolution, legume plants have maintained the ability to engage in a mutualistic interaction with soil bacteria known as rhizobia, leading to the development of nitrogen-fixing nodules in plant roots. The establishment of this symbiosis is regulated at different levels of gene expression. To gain insight into the translational regulation of mRNAs at early stages of nitrogen-fixing symbiosis in common bean (*Phaseolus vulgaris*), we adapted the TRAP technique (Translating Ribosome Affinity Purification) to this legume. TRAP allows the isolation of RNAs associated to the translational machinery, referred to as the translome, by immunoprecipitation using an epitope-tagged version of the RPL18 ribosomal subunit. The isolated RNAs can be sequenced to assess translational changes at a genome-wide scale. Furthermore, we aim to characterize the population of RNAs in active translation from the two main root tissues involved in nodulation by expressing the RPL18 fused to the FLAG epitope under the control of the Expansin7 or the Scarecrow promoter for purification of the epidermal or cortical translomes, respectively. Based on the expression pattern, we selected the Phvul.007G197900 gene encoding the *P. vulgaris* RPL18 subunit and expressed it fused to a His-FLAG tag (HF-PvRPL18) in composite plants using the *Agrobacterium rhizogenes* transformation method. The expression of the HF-PvRPL18 transcript was confirmed by reverse transcription followed by PCR. Ribosomal RNA and mRNAs were detected in TRAP samples from plants expressing the HF-PvRPL18 protein, but not in samples from plants transformed with the empty vector. Based on these results, we concluded that the expression of HF-PvRPL18 in *P. vulgaris* allows us to affinity purify ribosome-RNA complexes, providing a useful tool to study translational dynamics during root nodule symbiosis in this legume.

Keywords: legume, nitrogen-fixation, ribosome immunopurification, common bean.

P. 03**Study of the transcriptional regulation of genes involved in endocytic vesicular traffic by a wrky transcription factor induced during response to sal**

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Soil salinity restricts water and nutrients uptake and causes ionic toxicity to the plants. Sodium compartmentalization in the vacuole is an essential response during salt stress, and this is partially mediated by endocytic vesicular trafficking (EVT). Different proteins are currently known to be involved in directing EVT to the vacuole during the salt stress response, whose genes are induced by salt. To date, the posttranslational regulation of these proteins has been extensively investigated, but no transcriptional regulation. This research set out to identify transcription factors (TF) that regulate genes involved in EVT that contribute to sodium compartmentalization in the vacuole during salt stress. Previously, a WRKY TF was selected by several bioinformatics analyses as Evaluation of spatiotemporal gene expression under salinity conditions and the comparison of homolog expression between salt stress sensitive and salt stress tolerant species. The promoter sequences of 5 genes related to EVT were analyzed in search of cis-elements to binding of TF WRKY. Next, 18-day-old *Arabidopsis thaliana* plants of wild-type genotype were submitted to a salt stress treatment and the expression of EVT-related genes was evaluated by qPCR. *Agrobacterium tumefaciens* strains were utilized to assess protein-DNA binding by transient cotransformation of *Nicotiana benthamiana* leaves. One strain with the WRKY CDS under the control of the 35S promoter, while other strain included one of the EVT gene promoters binded to the GUS reporter. Histochemical tests and qPCR was used to examine GUS activity and transcription. The rate of internalization of the indicator FM4-64 was measured to examine the rate of EVT in roots of wild-type and mutant for WRKY seedlings. The results showed that this WRKY TF positively regulated the transcription of 3 of the genes evaluated. Furthermore, plants mutant for this TF showed a significantly lower EVT level under saline conditions than wild-type plants.

Keywords: WRKY, Salt stress, endocytic vesicular trafficking.

P. 04**Polymorphic inverted repeats near coding genes impact chromatin topology and phenotypic traits in *Arabidopsis thaliana***

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Transposons are mobile elements that are commonly silenced to protect eukaryotic genome integrity. In plants, transposable element (TE)-derived inverted repeats (IRs) are commonly found near genes, where they affect host gene expression. However, the molecular mechanisms of such regulation are unclear in most cases. We recently studied these IRs in *Arabidopsis thaliana*

(doi:10.1016/j.celrep.2023.112029) and showed that their expression is associated with the production of 24-nt small RNAs which trigger DNA methylation of the IRs through the RNA-dependent DNA methylation (RdDM) pathway. This process can be initiated by the RNA Polymerase II and be independent from RNA-dependent RNA polymerases, since IR transcripts fold into hairpin loops. Using mutants in the RdDM pathway, we showed that these IRs are responsible for drastic changes in local 3D chromatin organization. Notably, many of the IRs differ between *Arabidopsis thaliana* natural accessions, causing variation in short-range chromatin interactions and gene expression. CRISPR-Cas9-mediated disruption of two IRs leads to a switch in genome topology and gene expression with phenotypic consequences. Our data show that the insertion of an IR near a gene provides an anchor point for chromatin interactions that profoundly impact the activity of neighboring loci. This turns IRs into powerful evolutionary agents that can contribute to rapid adaptation.

Keywords: MITE, transposon, inverted repeat, small RNA, chromatin loop, DNA methylation, chromatin organization, RdDM, natural variation, CRISPR/CAS9.

P. 05**Generation of bioinformatics tools for the integrative analysis of environmental, genomic and transcriptomic data**

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As the generation of information accelerates, there is a growing gap between the speed of data production and the evolving capacity of the tools to analyze it. Many of the approaches currently used do not tend to focus on integrating the different layers of information that surround a particular biological system, but rather, border on superficiality by isolating and studying these layers separately. In this work, we sought to develop innovative bioinformatics tools that couple genetic and transcriptomic variability with environmental information. These tools were implemented using *Python* and *R* as programming languages, and they were tuned with data from different ecotypes of *Arabidopsis thaliana* from the 1001 genomes collection, which come from different geographic regions and are exposed to various environmental contexts. In the refinement process, promising results were obtained that served as validation of these tools. It was found that, as expected, there was a correlation between known flowering factors and the latitude where each ecotype grows. In addition, unsupervised clustering of the transcriptomic profiles was performed by means of graph-based algorithms. This mentioned analysis contributed to the validation of the tools since it showed that a large part of the genes whose expression was specific to particular groups were related to circadian rhythms and photosynthesis, identifying these genes as variability factors between ecotypes. Finally, we have extrapolated this analytical approach by applying the developed tools to sets of genes of agronomic interest, such as genes involved in crop metabolism and yield. Although many aspects remain to be improved, the results presented here confirm the potential of the tools generated thanks to the application of a novel holistic approach.

Keywords: bioinformatics, data science, transcriptomics.

P. 06**ZmS5H: a multi-functional enzyme regulating plant development and senescence in maize**

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Salicylic acid (SA) is a phytohormone that plays a crucial role regulating various aspects of plant life, including disease resistance, leaf senescence, flowering time, and thermogenesis. SA undergoes chemical modifications such as methylation, hydroxylation, or conjugation with sugars or amino acids. SA hydroxylation is catalyzed by enzymes known as SALICYLIC ACID HYDROXYLASES (SHs) and plays an essential role in plant development and response to pathogens. In our lab, we successfully identified the first SA hydroxylase in maize plants, known as salicylic acid 5-hydroxylase (ZmS5H), a 2-oxoglutarate dependent dioxygenase (2-ODD) that catalyzes the conversion of SA into 2,5-dihydroxybenzoic acid (2,5-DHBA) by hydroxylating the C5 position of its phenyl ring. Since some 2-ODD enzymes involved in plant phenolic metabolism can accept various phenolic compounds as substrates, we tested two flavanones (naringenin and eriodictyol) and one dihydroflavonol (dihydroquercetin, DHQ) as putative substrates of ZmS5H. We observed that ZmS5H also exhibits flavonol synthase activity, as it can convert dihydroquercetin (DHQ) into the flavonol quercetin (QUE). To validate the dual functionality of ZmS5H, we quantified SA, 2,5-DHBA, and QUE levels by LC-MS in young maize leaves of wild type (W22) and mutant *s5h* plants, quantifying reduced levels of both 2,5-DHBA and QUE in the absence of S5H. However, in adult maize leaves, the *s5h* mutant lines showed an accumulation of QUE. Furthermore, a phenotypic characterization of maize plants indicated that *s5h* mutant lines exhibited increased senescence and affected plant growth. These findings strongly suggest that ZmS5H adapts its functionality based on the specific needs of each stage of plant development, playing a pivotal role in both plant growth and senescence.

Keywords: maize, flavonoids, salicylic acid, 2-ODDs, growth, senescence, plant physiology

P. 07**Temperature during seed maturation influences weedy rice seed dormancy and germination**

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The maternal environment during seed development and maturation significantly influences many properties of progeny seeds. In Japanese weedy rice, warmer temperatures following flowering impede progeny seeds to release dormancy, likely increasing their persistence in the soil seed bank. However, the timing of establishment of such effects remains unresolved. In our study, we examined how warm temperatures during early and late seed maturation stages affect progeny germination, while also exploring transcriptomic changes in seeds before dispersal from mother plants and their association with progeny responses. Our findings show that late post-flowering warming (3-6 weeks) reduced progeny germination compared to control plants without temperature treatment, similarly to higher temperatures during the entire reproductive period. Conversely, progeny seeds from plants exposed to early warming (0-3 weeks after flowering) exhibited high germination similar to those of control plants. Field validation involved two cohorts of plants transplanted 1.5 months apart: mid-May transplants experienced higher late seed maturation temperatures and produced more dormant seeds than late-June transplants. At 6 weeks after flowering, warm temperatures throughout the reproductive period resulted in changed expression of a substantial number of genes (1059 up- and 864 down-regulated). In turn, early (up: 54, down: 50) or late (up: 58, down: 50) warming exposures had a significant effect on a smaller set of genes compared to control plants. Gene-ontology analysis revealed 'metabolic pathway' category enrichment across all gene groups, indicating that warm temperatures profoundly influence seed metabolism and subsequently impact progeny seed germination. These findings provide valuable insights into the responses and mechanisms associated with maternal effects, which can potentially modify weed emergence in the field, particularly in the context of climate change.

P. 08**First functional study of a subfamily III member of the Snakin/GASA family in *Solanum tuberosum***

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Snakin/GASA peptides are cysteine-rich AMPs whose functions are not fully understood. Their participation in various aspects of development and biotic or abiotic stress tolerance has been described.

In potato we have identified 18 genes of the Snakin/GASA family, being *Snakin-1*, *Snakin-2* and *Snakin-3* members of subfamilies I, II and III, respectively. So far, SN1 and SN2 have been functionally characterized by demonstrating their antimicrobial activity against fungi and bacteria.

In order to study the role of a member of the 3rd subfamily in plant development and responses to various stresses, we obtained transgenic potato lines with altered levels of *Snakin-3*, we conducted *in-silico* and *in-vivo* studies of its promoter and we determined its subcellular localization. The results obtained so far suggest a functional differentiation of *Snakin-3* since it has a differential expression regulation with respect to *Snakin-1* and *Snakin-2* and presents a different subcellular location, being found in the endoplasmic reticulum. Likewise, in this work we will present the advances made in the molecular and morphological characterization of transgenic lines and in challenge tests against bacterial pathogens.

Keywords: SNAKIN/GASA, potato, snakin-3, antimicrobial, cystein-rich.

P. 09

Assessing the small RNAs profile between potato diploid hybrid and its resynthesized allopolyploid.

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Allopolyploidy, characterized by interspecific hybridization combined with whole genome duplication, is a dynamic process that plays a crucial role in plant evolution, resulting in the emergence of new phenotypes. Polyploids often present phenotypic novelties that improve their adaptability, allowing them to compete with their parental species and occasionally to colonize new habitats. Whole genome duplication represents a “shock” to the genome and can trigger genetic and epigenetic changes that will lead to new expression patterns. In this work, we explore the effect of polyploidization on a diploid interspecific hybrid arising from the cross between the cultivated potato *S. tuberosum* and the wild potato *S. kurtzianum*. We focused on the sRNA profile of the parental diploid hybrid and its resulting allopolyploid to decipher the role of sRNAs in the context of epigenetic mechanisms, particularly in RNA-directed DNA Methylation (RdDM). We conducted a sRNA-seq experiment and implemented bioinformatic analysis on 21-22-nt and 24-nt length separately considering their distinct biogenesis and mechanism of action. The composition and distribution of different characteristics throughout the potato genome, especially those with differentially accumulated (DA) sRNAs, were evaluated and discussed. Furthermore, a subset of genes with DA sRNAs associated was selected to perform mRNA expression to address if the sRNA profile could have an impact on the transcriptome and in consequence on the phenotype. Interestingly, we observed that 24-nt DA sRNAs exclusively mapped to exons were linked to differentially mRNAs expression levels between genotypes. However, this behavior did not apply when 24-nt DA sRNAs were mapped to intronic regions. These findings highlight the intricate interplay between polyploidization, sRNAs population and gene expression in an interspecific potato hybrid.

Keywords: Allopolyploid, potato, sRNAs, epigenetic.

P. 10

Germination proteins of soybean embryonic axes

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Seed germination is completed by the expansion process defining the embryonic axis (Ax) growth before cell division starts. Thus, the cell walls in the elongation zone (EZ) of Ax have to be weakened while the water entries and Ax consequently grow. Expansin proteins primarily promote cell wall remodelling, with the other cell wall proteins secondarily completing the expansion process. This work aimed to identify cell wall remodelling proteins during soybean (*Glycine max* L. Merr) Ax germination. One hundred soybean Ax, cv. Williams 82, were incubated for 9 h in distilled water at 27 ± 1 °C. The respective EZ (1 g of tissue) were powdered in liquid N₂ and homogenized in 50mM Sodium acetate; 2 mM EDTA; pH 4.5. The wall fragments were collected by centrifugation at 4 °C and 10000 rpm and extracted in 2 mL 20 mM HEPES; pH 6.8; 1 M sodium chloride; 2 mM EDTA; 3 mM sodium metabisulfite by shaking at 4 °C for 4 h. Cell wall fragments were removed by centrifugation at 4 °C and 10000 rpm and the solubilized fraction was precipitated with 0.78 g ammonium sulfate (0.390 g/mL), incubated on ice for 1h and centrifugated at 4 °C. The precipitate was resuspended in 50 mM sodium acetate. Protein identification was performed by Mass Spectrometry using Uniprot and Phytozome. A total of 2984 unique soybean proteins with, at least, two peptides of high confidence were identified. Thirty-five were cell wall remodelling proteins: 7 Expansins, 2 Xyloglucan endotransglucosylase/hydrolases, 22 Endoglucanases, and 4 Pectinesterases. The classification by gene ontology (AgriGO) showed enrichment in biosynthesis, regulation, response to stimulus, reproduction, developmental, anatomical structure development, catabolism and energy processes. These results evidenced a great cellular activity associated with the expansion process and the early events defining soybean embryonic axes germination.

Keywords: early proteomic profile, expansin, germination, glycine max.

P. 11

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

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The demand for food and vegetable oils and the use of crops for industrial purposes is increasing significantly. In modern agriculture, the increase in production is linked with the increase of planted area, which presents ecological drawbacks, and to the intensification of grain production per unit area. One of the ways to increase productivity per unit area is to increase sowing density. However, plants grown at high crop densities receive reduced light irradiance because of mutual shading. To avoid shade, some plants readjust phenotypic traits such as growth rates of the stems, internodes, and petioles. Collectively, these responses are known as the shade avoidance syndrome. Generating shade-tolerant plants is the target for breeders to achieve high-yielding crops in a dense plantation. To reveal the molecular mechanisms behind shade avoidance in soybean (*Glycine max*), plants were grown in contrasting densities in the field and under simulated shade in controlled conditions. We performed a high throughput transcriptome analysis of petioles and leaves that allowed us to develop a tissue-specific shade avoidance gene expression network. Our work is the first to describe the molecular orchestration behind soybean shade avoidance responses, as a starting point to introduce novel approaches for crop improvement.

Keywords: Shade avoidance, crop improvement, soybean, transcriptional regulation.

P. 12

Auxin and coronatine signaling converge in guard cells

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Certain hormones and bacterial compounds are known to inhibit ABA-induced stomatal closure, including auxins and coronatine, a bacterial toxin which is a structural analog of the jasmonate-isooleucine conjugate. Both are known to affect the activity of inward rectifying potassium channels as well as ROS synthesis in guard cells. In this work we sought to understand the mechanism through which auxins and coronatine inhibit ABA-induced stomatal closure. Through the analysis of various *Arabidopsis* mutants affected in the signaling or transport of auxins and coronatine, we found that mutants insensitive to inhibition by coronatine of ABA-induced stomatal closure *coi1-16*, *lecrkVI-2.1*, *mpk3*, *mpk6*, *npr1* and *rbohD* were also insensitive to the auxin IAA. On the other hand, *tir1-1* and *aux1* mutants, affected respectively in the perception and transport of auxins, display markedly reduced stomata reopening after three hours of incubation with the coronatine-producing bacterium *Pseudomonas syringae* pv. tomato DC3000 (which initially induces stomatal closure through PAMPs). In addition, natural variability was found for stomatal sensitivity to both coronatine and auxins. As far as it is known, the perception of both types of compounds occurs independently, so it is complex to explain the simultaneous insensitivity of auxin and coronatine in the aforementioned mutants.

On the other hand, we have found that mutants affected in the silencing mechanism *ago4*, *dcl2/3/4* and *rdd* also presented stomatal insensitivity to auxins, which may suggest that the regulation of sensitivity to this hormone could be partly mediated by transcriptional mechanisms.

Keywords: stomata, auxin, coronatine, silencing, PAMPs.

P. 13

Identification and characterization of ATPase II-A type Ca²⁺ transporter systems (ECAs) involved in polar cell expansion of root hairs.

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PIIA type Ca²⁺ ATPases (ACEs) make up a family of four proteins (ACE1, ACE2, ACE3 and ACE 4) found in the membranes of the endoplasmic reticulum, Golgi apparatus and vacuoles of plant cells. In *Arabidopsis thaliana* root hairs, ECAS regulate calcium homeostasis, favoring the polarized growth of these cells. Studies with different simple mutants for each of them, showed that some of these ECAS have redundant functions and that the deficiency of others produces a decrease in the length of the root hairs. On the other hand, a pharmacological inhibition study was carried out with CPA (cyclopiazonic acid), which is an inhibitor of the homologous protein in mammalian cells, and hair shortening was observed. Low temperature conditions generally promote greater growth of root hairs, so it might be thought that in plants inhibited with CPA and subsequently subjected to low temperatures, hair growth would be at least partially rescued.

Keywords: ECAs, calcium homeostasis, root hairs, low temperature.

P. 14

COP1 as a key redox-controlled regulator of hypocotyl growth under shade in plants

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Shade from neighbours enhance hypocotyl growth in *Arabidopsis thaliana* to increase the access to light. Reactive oxygen and nitrogen species (ROS and RNS, respectively) can function as signalling molecules in growth adjustment processes. However, it was suggested that shade could reduce the generation of ROS by the photosynthetic apparatus, alleviating their growth inhibitory effect. In contrast, we observed that shade triggered a more oxidative redox status in hypocotyl cells associated to the accumulation of superoxide anion, hydrogen peroxide and nitric oxide and the reduction in the glutathione pool. Seedlings affected in ROS and RNS accumulation genetically or pharmacologically, reduced the promotion of hypocotyl growth by shade, a response that required the E3 ubiquitin ligase CONSTITUTIVELY PHOTOMORPHOGENIC 1 (COP1). Due to their reactivity, cysteine (Cys) residues are targets of a variety of post-translational oxidative modifications, including S-nitrosylation consolidated as a novel mechanism in physiological processes requiring a rapid and versatile regulation. Shade-mediated redox changes favoured COP1 S-nitrosylation. Mutation of a S-nitrosylated Cys reduced COP1 stability and capacity to interact with its targets, causing reduced biological activity under shade. Under field conditions, contrasting neighbour cues reach the plant from different angles. When exposed to these conflicting cues, COP1 mutant in S-nitrosylated Cys lost their vertical orientation making shade avoidance less efficient. These results place a COP1 as a key redox-controlled regulator cell growth promotion in an eco-physiological context.

Keywords: Arabidopsis, redox regulation, hypocotyl growth, shade.

P. 15

RS31: a novel player involved in the regulation of light-induced seed germination and flowering in *Arabidopsis thaliana*

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Seed dormancy is a developmental checkpoint that prevents mature seeds from germinating under conditions that are otherwise favorable, allowing plants to regulate when and where they grow. Primary dormancy refers to the innate dormancy possessed by seeds when they are dispersed from the mother plant. Temperature and light are the most relevant environmental factors that regulate seed dormancy and germination. These environmental cues, that can trigger molecular and physiological responses (including ABA and GA signaling), induce a massive reprogramming of gene expression, and shape the seed transcriptome by affecting each possible level of gene expression such as *mRNA* splicing, translation, and stability. The expression of many genes that regulate dormancy, germination and flowering can be modulated by alternative splicing (AS, a co-transcriptional mechanism that generates transcriptome diversity) in response to the environment. We have previously shown that when *Arabidopsis* seeds receive a pulse of Red light, the AS pattern of the splicing factor RS31 is drastically changed. Here, we show that seeds overexpressing the RS31 coding isoform (namely *mRNA1*) do not show primary dormancy and germinate even under suboptimal light conditions, suggesting that *mRNA1*, ergo the RS31 protein, has a key role during the establishment of primary dormancy and functions during light-induced seed germination. Accordingly, ABA- and GA-related genes have altered expression levels. We also show that overexpression of the *mRNA1* delays flowering under SD and LD conditions when compared to the wild type, suggesting that RS31 is also involved in the regulation of this process. Overall, affecting alternative splicing may also alter key physiological traits.

Keywords: dormancy, germination, flowering, seeds, light.

P. 16

Abscisic acid and ABI4 appears to be involved in *Arabidopsis thaliana* gamma carbonic anhydrases regulation during embryogenesis

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Abscisic acid (ABA) is a hormone involved in many plant's processes, among which seed development and germination. ABA signaling pathway requires the action of ABSCISIC ACID INSENSITIVE (ABI) transcription factors. In particular, ABI4 has been shown to regulate the expression of cytochrome c 2, a member of the mitochondrial electron transport chain (mETC), during germination in *Arabidopsis*. However, it is unknown if this and other members of mETC are regulated by ABA during embryogenesis. *Arabidopsis thaliana* gamma carbonic anhydrases (At γ CA) form a heterotrimeric domain (CA1-CA2-CAL2, named CA domain) that is part of the mitochondrial Complex I and it is essential for its assembly. Transcript levels of some At γ CA family members increase during the maturation phase of embryo development and reach a peak at the end, as do ABA levels, whereas other members show an opposite trend, according to RNAseq publicly available data. In addition, *in silico* analysis of the promoter regions of At γ CAs show putative binding sites for ABI transcription factors. In order to determine whether ABA regulates At γ CA expression by ABI4, their transcript levels were determined by RT-qPCR in immature seeds of *Arabidopsis* WT and *abi4* mutant plants treated with ABA. Preliminary results indicate that ABA induces At γ CA2, while it represses At γ CA1 expression in WT plants. On the contrary, At γ CA1 levels are increased in *abi4* mutants whereas At γ CA2 are reduced. Taken together, results suggest that ABA is involved in At γ CA regulation through ABI4 during embryogenesis. This differential regulation may have an impact on the composition of the CA domain affecting complex I function. Future experiments will be directed to study GUS activity in pCA::GUS reporter plants in response to ABA treatment.

Keywords: abscisic acid, carbonic anhydrases, embryogenesis.

P. 17**DNA methylation regulates thermoresponsive growth in Arabidopsis by modulating CRY1 expression**

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Plants adapt to warm environments through physiological and morphological changes termed thermomorphogenesis, which involve transcriptional reprogramming exerted mainly by PHYTOCHROME INTERACTING FACTOR 4 (PIF4). Fluctuating temperatures can also influence the patterns of cytosine DNA methylation, and thus gene expression. However, whether these epigenetic changes provide an adaptive advantage remains unclear. Here, we provide evidence that DNA methylation is required to regulate thermomorphogenesis. Hypomethylated *drm1 drm2 cmt3* mutant seedlings show impaired hypocotyl elongation at mildly elevated temperatures. In agreement, blocking DNA methylation with the reagent 5-azacytidine impairs hypocotyl elongation in response to warming in three different Arabidopsis accessions, independently of SUPPRESSOR OF DRM1 DRM2 CMT3 expression. Additionally, treatment with 5-azacytidine decreased the expression of the auxin response reporter *DR5::GUS* during warming. At the molecular level, the lack of DNA methylation abolished the warming-mediated induction of *PIF4* target genes, while up-regulation of *PIF4* expression remained unchanged. Finally, DNA methylation impairs blue light inhibition of hypocotyl growth during thermomorphogenesis by repressing the expression of the blue-light receptor *CRY1*. Together, our findings provide evidence of the epigenetic regulation of a photoreceptor to control plant responses to warm environments.

Keywords: DNA methylation, thermomorphogenesis, hypocotyl elongation, warming.

P. 18**A role for a CONSTANS gene homolog in Arabidopsis thaliana development**

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The BBX transcription factor family in plants has been characterized due to its importance in the regulation of photomorphogenesis, flowering, shade avoidance and response to biotic and abiotic stresses. One of the most described members of this 32 genes family is *CONSTANS* (*CO*, *BBX1*) which has a key role in the photoperiodic control of flowering. *CO* has 5 related homologs (*BBX2-6*) which have not been extensively studied. Here, we managed to obtain *Arabidopsis thaliana* mutants of *CO* and its homologous genes by using the CRISPR/Cas9 system and evaluated their role in different physiological processes. We found that under red light conditions photomorphogenesis was altered in the mutants and that its gene expression was down-regulated. Overall, these results contribute to our understanding of the BBX gene family and its crucial role in Arabidopsis development.

Keywords: Photomorphogenesis, BBX, red light, Arabidopsis.

P. 19**Pleiotropic effects associated with the expression of a recombinant fibroblast growth factor in transplastomic plants**

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Transformation of the plastid genome is a widely used method for the generation of transgenic plants, with the potential to accumulate high levels of recombinant proteins. However, foreign transgenes may cause unintended pleiotropic effects affecting plant development and physiology. The mechanisms underlying these effects are dependent on the heterologous protein and remain to be elucidated. In this study, we examined the phenotypes of transplastomic tobacco plants that express a recombinant human fibroblast growth factor (hrFGFb), a protein used for the maintenance of embryonic stem cells *in vitro*. The transplastomic lines (UTR-FGF) exhibited slower growth rate and delayed flowering compared to non-transformed tobacco plants (NT). In addition, UTR-FGF lines showed a chlorotic phenotype which correlated with a reduction in chlorophyll fluorescence levels (SPAD). To study whether photosynthesis is affected in UTR-FGF lines, we analyzed different chlorophyll fluorescence parameters using the pulse-amplitude modulated (PAM) technique. Analysis on dark-adapted plants revealed that the maximum quantum yield of PSII (FV/FM) was almost two-times lower in transplastomic lines compared to NT, indicating an important reduction in their photosynthetic capacity. We measured photosynthetic parameters in light-adapted leaves and obtained a significant reduction of the PSII efficiency (ϕ PSII) and an increased NPQ (non-photochemical quenching) rate in UTR-FGF lines compared to NT. These results suggest that UTR-FGF lines have an impaired capacity to conduct photochemical reactions and likely to generate ATP and reducing equivalents by photosynthesis. The high fraction of quenching based on heat dissipation might be indicating profound perturbances in antennae complexes in the transplastomic lines. Taken together, these results demonstrate that the transformation of the plastome with hrFGFb transgene has pleiotropic effects, causing both developmental and physiological impairments.

Keywords: transplastomic plants, pleiotropic effects, photosynthesis.

P. 20**Interactions of Phytochromes B and C fine tune the response to ambient light signals**

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Plants employ photoreceptors to continuously monitor and respond to changes in environmental light parameters such as intensity, duration and spectral quality. A specific group of photoreceptors, known as phytochromes, plays a significant role in regulating responses to red and far-red light. The genome of *Arabidopsis thaliana* encodes five distinct phytochromes (phyA to phyE), which have both specific and overlapping physiological roles. The spectrum of responses is increased by the ability of phytochromes to form heterodimers. phyB and phyC form heterodimers and phyC is nonfunctional in the absence of other phytochromes; we have shown that phyB and phyC must act together to trigger a flowering response to photoperiod. Here, we report on the roles of phyB phyC heterodimers. We used physiological and genetic approaches to uncover responses in which phyB phyC heterodimers show additional and more important roles than phyB phyB homodimers. The hypocotyl responses to light quality were highly dependent on phyB phyC heterodimers, as well as a blue light signal. Leaf shape and petiole length were also highly dependent on phyB phyC. Our data indicate that a day-light-generated blue light signal interacts with active phyB phyC heterodimers during the night period to fine tune the responses to shade.

Keywords: phytochromes, light quality, Arabidopsis thaliana.

P. 21**Unraveling differential roles of ATG14 and VPS38 in *Physcomitrium patens* apical growth**

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PI3P is a key regulator of membrane dynamics and trafficking processes, synthesized by VPS34. This kinase associates with VPS15 and ATG6, and forms two complexes (C) that differ in one subunit: C-I, with ATG14, participates in autophagy, and C-II, with VPS38, is involved in endosomal trafficking. In plants, the function of ATG14 and VPS38 has not been assessed in the context of apical growth, nor in evolutionarily distant organisms such as bryophytes. Herein, we use *Physcomitrium patens* protonemata, an apical-growing tissue comprising two functional and morphologically different cell types (chloronema and caulonema), as a model to address these areas.

We first compared gene expression in chloronemata- and caulonemata-rich media, revealing distinct patterns for VPS38 and ATG14 in each cell type. Subsequently, we examined changes in *PpVPS34pro*: *PpVPS34-citrine* expression during caulonemata induction (exogenous auxin or nitrogen deficiency). Our results indicated increased fluorescence intensity in chloronemal cells, which then differentiated into caulonema.

To discriminate whether the induction of caulonema development is associated with PpVPS34 function in autophagy or endocytic trafficking, we generated moss *atg14* and *vps38* knock-out lines. The *atg14* mutants exhibited an early-senescence phenotype, similar to *atg5* mutants, while the *vps38* lines showed a marked reduction in gametophore size and rhizoid development without early senescence symptoms. Moreover, the percentage of caulonemal filaments decreased in *atg5* and *atg14* lines, suggesting that autophagy participates in caulonemata development, although it is not essential.

Overall, *atg14* and *vps38* phenotypes suggest that C-I and C-II participate in different aspects of apical growth and development, promising to be useful tools to dissect the autophagic and endocytic trafficking roles of PI3P. In addition, results indicate the participation of autophagy in apical growth and caulonemata development.

Keywords: *Physcomitrium patens*, development, phosphoinositides, Atg14, Vps38, autophagy.

P. 22**Deciphering dependent and independent roles for the families of circadian clock coactivators: what can we learn from high-order null mutants?**

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Throughout evolution plants have developed sophisticated systems to stay in sync and even predict daily and seasonal cycles. This is possible thanks to an endogenous time-keeping mechanism known as the circadian clock. At the center of this system there is a network of proteins interconnected by transcriptional feedback loops that regulate the expression of ~30% of the transcriptome in Arabidopsis, rice, maize, papaya, poplar, and soybean. Most core clock components are negative regulators of the expression, but there are two families termed REVEILLE (RVE) and NIGHT LIGHT-INDUCIBLE AND CLOCK-REGULATED GENE (LNK) that act as positive co-regulators. Our group along with others have identified and characterized these families, and found that both have relevant roles in plants' life. Null mutants for these genes have shown similar phenotypes in many clock-controlled traits, still, there are some relevant processes such as the regulation of flowering time in which lacking LNK or RVE components doesn't seem to have the same effect. In this study, to further understand the role of these families in the regulation of circadian outputs, we performed a side-to-side comparison of higher-order null mutants for each clade (*rve3/4/5/6/8* and *lnk1/2/3/4*). By analyzing new available high-throughput transcriptomic data, and combining it with physiological assays we studied the impact each of these mutations have on processes such as flowering time, hypocotyl elongation, and stress responses. As a result, we were able to evaluate to what extent these mutants share common features, and how overlapping is the role of LNK and RVE genes in the regulation of circadian outputs. In the past, the selection of natural allelic variants of clock components, such as LNK2 in tomato, has allowed the expansion of crops to new territories. Thus, we believe that a better understanding of these families could be useful in the development of novel strategies for further crop improvement.

Keywords: Chronobiology, Circadian clock, Plant physiology, Transcriptional regulation

P. 23**Connection between AtSINA-L7 and auxin metabolism**

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The gene Seven in absentia like 7 (At5g37890, SINA-L7) encodes a RING finger protein displaying E3 ubiquitin ligase activity. This protein is implicated in radiation response and is expressed across various developmental stages in nearly all plant tissues. Auxins hold a pivotal role in initiating and shaping the growth of leaves, flowers, and roots, primarily through cell division, with a notable emphasis on indole-3-acetic acid (IAA). Additionally, auxins possess the capability to coordinate a wide array of developmental responses within distinct tissue types.

Within plants, SINA-T5, a paralog of SINA-L7, actively facilitates ubiquitination-mediated degradation of NAC1, thereby exerting a negative regulatory influence on auxin signals. Notably, there are reports indicating that SINA-T5 (the homolog of SINAL7 in *Arabidopsis thaliana*) is intricately involved in the regulation of flowering processes. This involvement stems from its promotion of ubiquitin-mediated degradation of NAC1, ultimately leading to the attenuation of auxin signals.

The aim of this study is to comprehensively characterize AtSINA-L7 by utilizing two homozygous mutant lines of SINA-L7 sourced from *A. thaliana* plants (SALK_096989 and CS833574), and to explore its relationship with auxin metabolism. For the experimental phase, the application of the phytohormone AIA via spraying [10⁻⁸ M] over a period of 6 consecutive days was proposed. The preliminary results acquired demonstrated an approximate 15% reduction in aberrant siliques and a noteworthy 30% increase in seed count, among other observed outcomes. These findings underscore the substantial role of AtSINA-L7 in modulating developmental responses and governing auxin metabolism within plants.

Keywords: Arabidopsis thaliana, auxins, metabolism, developmental responses.

P. 24**Cell architecture during plant growth and development**

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The size and shape of plant organs are mainly determined by the timing, the duration and the directionality of cell growth. Each plant cell must integrate endogenous and external signals from neighbouring cells in order to execute coordinated decisions for growth and finally shape cell architecture. We use *Arabidopsis*' early development as a model for studying signal coordination for differential cell growth, from seeds germinating and developing in darkness (skotomorphogenesis) until they reach the light and change to an autotrophic lifestyle (photomorphogenesis). Photoreceptors, different factors acting as master regulators and many phytohormones like auxins or ethylene, among others, have a great impact on early development and growth's decisions. Cortical microtubules (cMTs), as an integral component of cytoskeleton, also play key roles in determining growth directionality, and their intrinsic dynamics nature needs synchronization with the external and internal signals. Despite its importance, the precise coordination of these signals for cell growth in early development remains poorly understood. In this work we analyse the physiology and cMTs dynamics of the marker line GFP-MAP4 in different photo and skotomorphogenic mutant backgrounds. We evaluate microtubule array patterns in hypocotyl and apical hook cells during skotomorphogenic growth in photomorphogenic mutants in the dark, such as *cop1*, *pif1pif3pif4pif5*, and *hyl1*, and in a skotomorphogenic mutant in light (*hy5*). By examining these results and considering the dependency of cMTs dynamics on light/dark signalling regulators, we aim to get insights into the coordination of cell growth in early development.

Keywords: microtubules, cellular growth, cell biology, skotomorphogenesis.

P. 25**The ecophysiology of seedling recruitment during floods: The case of *Echinochloa colona*, a harmful arable weed of extensive crops**

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In the Pampas, the transition of floodplains to agriculture has facilitated the encroachment of hydrophyte weeds. Our objectives were: (i) to investigate whether flooding controls or promotes *Echinochloa colona* spread and, (ii) to explore environmental cues that can stimulate underwater germination of its seeds. To address (i), we conducted two flooding experiments (flood level: 10-15 cm) in soil mesocosms obtained from floodplain crops in the Province of Buenos Aires (corn/wheat-soybean/sunflower rotation) and taken to FAUBA experimental field. We simulated the seasonal decrease in floodwater levels throughout the growing season by draining mesocosms monthly starting from winter (year 1). In year 2, we simulated intermittent flood and drainage conditions of varying monthly durations. Experiments included mesocosms constantly flooded and drained to field capacity (controls). We weekly monitored seedlings emergence and recorded established plants, as well as their biomass and fecundity. Significant interactions between treatment and time were observed for emergence in both years ($p < 0.05$). The peaks of emergence coincided with drainage periods, indicating that floods shifted emergence timing towards the summer. Underwater emergence (< 100 seedlings m^{-2}) occurred, producing few yet prolific plants even in constant flooding. The results from both years demonstrate that floods delayed *E. colona* emergence causing it to occur later in the growing season. For objective (ii) we did lab experiments following these hypotheses: 1) High-amplitude daily alternating temperatures (AT) promote underwater germination, 2) Osmopriming under drained conditions promote later underwater germination. Results indicate that both high-amplitude AT and KNO_3 osmopriming were promoted *E. colona* underwater germination in hypoxia. This research highlights the influence of environmental factors on subaquatic germination in *E. colona*, which could have implications for its population dynamics.

Keywords: seedling emergence, establishment, flooding, recruitment, seed germination, submersion, Junglerice.

P. 26**Morphological diversity, selective signals and evidence of local adaptation in Argentinean maize landraces**

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The northern region of Argentina is home to more than 60 native maize landraces, with two main genetic groups of high phenotypic variability: the high-altitude Andean landraces, present in northwestern Argentina (NWA), and the flouly landraces of the northeast (NEA). This work evaluated 9 accessions from each region by means of reciprocal transplant gardens (Maimará, Jujuy & Cerro Azul, Misiones) in order to demonstrate their local adaptation. The variability of 14 agro-morphological and 6 phenological and yield characters was studied using general linear mixed models. NEA landraces showed higher mean phenotypic values, while the NWA ones showed the highest variation in both environments, with a negative correlation between collection altitude and most of the traits. Morphological structuring assessed by a discriminant analysis of principal components (DAPC) revealed the existence of groups unique to each region and a high degree of admixture, with each accession consisting of more than one of the inferred groups. The Andean NWA group was the most consistently recovered in cluster analyses, while NEA maize was divided into two groups not concordant with prior divisions. The search for selective signals used PST - FST comparisons, representing morphological and molecular neutral divergence, respectively. Directional selection signals were detected both within and between regions at most traits, being strongest at the region level and varying in magnitude between gardens. Moreover, fitness values in the NEA garden, measured as the number of plants with good seed quality per plot, showed maladaptation and low yields of NWA maize outside its native range.

Taken together, our analyses suggest that several traits mediate local adaptation in maize landraces from northern Argentina. From a broader perspective, the extensive variability found within regions highlights the need to consider this source of variation in the design of in situ and ex situ conservation programs.

Keywords: fitness, landrace, local adaptation, phenotype, population genetics, reciprocal transplant, *Zea mays* ssp *mays*.

P. 27**Altitude-plant density interaction on Andean maize: contributions to decision making**

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In the Northwest of Argentina, yields are limited by a progressive decrease in temperature with increasing altitude, but also by a lack of specific management strategies to underpin traditional practices. Our hypothesis is that increasing plant densities could compensate for the delay in planting date and phenological development at higher altitudes. The landrace "Amarillo de ocho" was grown at two densities (5.71 pl m⁻² –conventional for this area- and 8.57 pl m⁻²) in two field trials conducted during 2021-22 in Hornillos (HOR), Jujuy (23°39'S, 65°25'W, 2300 masl), and El Rosal (ERO), Salta (24°23'S, 65°46'W, 3350 masl) without water or nutrients limitations. Additionally, samplings in 8 farmer's fields spanning from 2400 to 3400 masl were carried out during 2022-23 growing season where plant density and yield were registered. Average temperature during the crop cycle was 39% lower at ERO compared with HOR, but thermal time requirements from emergency to reproductive stage decreased by 30% at ERO, partially compensating for the phenological delay. Increasing altitude resulted in 50% lower biomass at harvest and 86% lower yields (1107 Kg ha⁻¹ at ERO vs. 7912 Kg ha⁻¹ at HOR). Higher plant densities improved yield at HOR (+29%), related with 37% higher kernel number m⁻² together with a slight reduction in kernel weight (-7%) whereas at ERO, a higher yield improvement (+44%) was related with a higher increase in kernel number m⁻² and a larger decrease in kernel weight (-20%). Across farmer's fields, yield per plant negatively related with increasing plant densities (from 6 up to 16 pl m⁻²), with a trend towards higher improvement in kernel number m⁻² and larger decrease in kernel weight in the highest altitude sites (>3000 masl). Thus, increasing plant density could improve yields in high altitude environments especially due to increased kernel number m⁻².

Keywords: Andean maize, Plant density, altitude, landrace, Northwest of Argentina.

P. 28**Dormancy release or viability loss? The fate of *Lolium multiflorum* Lam. seeds depends on temperature and seed water content.**

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Primary dormancy release and gradual viability loss occur simultaneously in *Lolium multiflorum* seeds, resulting in transient seed-banks. The rate at which both processes occur is regulated by temperature and seed water content. The objective of this work was to quantify the effect of seed water content and temperature on the rate of primary dormancy release and viability loss in *L. multiflorum* seeds. For this purpose, seed water content at harvest was modified by drying or wetting the seeds for increasing times. Six seed water content (SWC) conditions were obtained: 8, 10.5, 13.3, 18, 20.6, and 23.5%. The seeds were then placed in airtight cryovials and stored in the dark at: 15, 20, 25, 30, 35, 40°C (for seeds of 8, 10.5, 18, 20.6 and 23.5% SWC) and 5, 10, 15, 20, 25, 30, 35, 40 and 50°C (for seeds of 13.8% SWC). Every 30 days during a 3-month storage period, the following were quantified: a) seed water content, b) seed dormancy level by germination tests at 15 and 20 °C, and c) viability of non-germinated seeds by tetrazolium test. The results showed that *L. multiflorum* seeds maximized primary dormancy release at low SWC (<10.5%) and high temperatures (>25°C). On the other hand, temperatures >25°C and SWC >18% caused viability loss of 20 to 100% of the seeds in a short period of time (30 to 90 days). The information generated in this work can be used to improve the predictive capacity of emergence models of this weed by including the effect of temperature and seed water content on two key processes that regulate seed emergence (seed dormancy and seed viability). Furthermore, this knowledge may be useful in developing agronomic practices that promote *L. multiflorum* seed-bank viability loss (i.e., seed-bank depletion practices).

Keywords: Italian ryegrass, seed longevity, seed-bank, predictive models of emergence.

P. 29**Critical periods for the expression of vegetative-reproductive plasticity in maize**

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In maize, low plant densities can trigger vegetative and reproductive plasticity mechanisms (i.e., tillering and prolificacy) with positive impacts on grain yield. We evaluated the effect of growth restrictions during the crop cycle to define the critical periods for the expression of plasticity mechanisms. Field studies were carried out in the experimental field of FAUBA during the 2021-2022 and 2022-2023 seasons. Four commercial hybrids with contrasting plasticity mechanisms (phenotypes) were evaluated (T: tillering; P: prolific; PT: prolific+tillering; F: non-tillering non-prolific or flex). Each phenotype was planted at 3 plants per square meter and growth restrictions were imposed with shading during some stages of the crop cycle (S1: V3-V7; S2: V7-V13; S3: V13-R1 and S4: R1-R2), and an unshaded control. In both years, S1 canceled tiller production in all phenotypes except for T in the second year, where tillering was reduced by 40% compared to the control. S2 consistently reduced tiller fertility. Consequently, the number of ears per plant differed among phenotypes (higher in PT due to the contribution of sub-apical and tiller ears) and shading periods. In the controls, the plastic phenotypes showed a higher number of ears and grains per plant than F. In S1 and S2, the number of grains per plant for the prolific phenotypes was higher than for T and F due to shading effects on tiller ears. Kernel weight differed among phenotypes and shading periods, with the highest weights recorded in T under the control, S1 and S2 and the lowest in the prolific phenotypes under S2. When compared with the control, grain yield decreased depending to the shading time and phenotype: S1: -45% and -30% for T and the rest; S2: -40% and -30% for T or PT and the rest; S3: -35% and -55% for P and the rest and S4: -45% for P, -55% for PT or F and -65% for T. In conclusion, there are different critical periods for grain yield depending on the phenotype's plasticity.

Keywords: vegetative-reproductive plasticity; critical period; grain yield; maize.

P. 30**Yield and quality of buckwheat (*Fagopyrum esculentum* Moench) at different sowing dates and nitrogen fertility conditions.**

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Buckwheat is widely cultivated throughout the world due to its high nutritional value and its suitability for celiac diets, as it is gluten-free. Argentina has excellent agroecological conditions for its expansion; however, ecophysiological and agronomic knowledge is scarce both locally and globally. This study aimed to develop ecophysiological bases to optimize the agronomic management of buckwheat and to determine its adaptability in different environments. It focused on predicting its phenological stages to adjust the crop cycle and optimize yield and quality according to environmental conditions. Two field experiments were conducted at FAUBA, with different sowing dates from October to February and nitrogen (N) fertilization levels. Phenology, radiation interception, aerial biomass, yield and grain quality were analyzed. It was found that the total length of the crop cycle was reduced by delaying sowing at a rate of 60 °Cd/day, with the grain filling stage being the most sensitive to shortening. Yields were higher at earlier sowing dates, associated mainly with changes in the number of grains set per m². Nitrogen availability did not affect phenology or yield at the different dates explored. Total aerial biomass decreased, and harvest index increased with delayed sowing. No relationship was found between harvest index and nitrogen levels. Protein content increased with N availability from 50 to 75 kgN/ha, saturating the response from this value. In conclusion, the study demonstrated the importance of adjusting the sowing date to optimize buckwheat yield in different environments, highlighting the relevant role of the length of grain filling in the duration of the crop cycle. Nitrogen availability did not affect phenology or yield but modified grain protein content. These findings could encourage the expansion of the crop in Argentina, considering its nutritional value and its potential in agricultural rotation schemes.

Keywords: phenology, yield, grain quality.

P. 31

Sensibility of seed yield and quality traits of rapeseed to increased temperature and reduced source-sink ratio in different phases of grain filling

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In the last years, climate change has increased mean temperature and reduced solar radiation in southern Chile. However, little is known about the sensitivity of grain yield, its components and quality traits to heat stress (HS) and source-sink (S-S) reduction at flowering and during grain filling. The objective of this study was to evaluate the key physiological mechanisms of rapeseed yield and oil concentration under both HS and S-S reduction at different phases of grain filling.

Rapeseed spring hybrids Lumen and Solar CL (NPZ-Lembke) were sown in four experiments carried out at field conditions in Valdivia, Chile (39°47'S, 73°14'W). HS was evaluated in Exp. 3 and 4, sowing the experiments in years 2019 and 2020, respectively, while S-S reduction was evaluated in Exps. 1 and 2 in 2018 under two sowing dates. Across experiments, three abiotic treatments were carried out: (1) a control without manipulation, (2) HS or S-S reduction from the 0 to 15 days after flowering (DAF) and (3) from 15 to 30 DAF. The HS was induced using portable greenhouses to increase 5°C over the ambient, while S-S reduction was achieved by shading with black nets (75% solar radiation interception).

HS and S-S reduction treatments affected ($p < 0.05$) grain yield, grain number and weight being Lumen less affected than Solar CL. The impact on grain yield and components was higher during 0-15 DAF than during 15-30 DAF. In both stresses, significant reductions were found in grain yield due to grain number reduction ($p < 0.05$). However, differential responses were found in grain weight depending on the timing and type of stress. S-S reduction increased grain weight only in the 0-15 DAF, while HS no affect grain weight in both timing windows. Grain oil concentration was more stable than protein concentration across treatments. Therefore, these findings suggest that grain weight resilience in rapeseed is greater in early grain filling, at least in the high yielding environment of southern Chile.

Keywords: climate change, heat stress, source-sink ratio, grain weight, grain number.

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Zinc, aminoacid and algae extract application seed treatments effect on growth and yield of *Triticum aestivum* with different predecessor herbicides.

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The use of biostimulants in seeds has emerged as a promising strategy to enhance crop yield and quality. Seed application of Zn can fill the deficiency, and improve abiotic stress resistance (herbicide persistence, carry over), nutrient uptake and disease tolerance. Amino acids (AA) can increase the speed and uniformity of germination, improving the number of plants achieved. The objective was to evaluate the additional effect of the combined application of Zn, AA and algae extract (AE) in seed on growth and final yield on *T. aestivum*, with different predecessors: chemical fallow (Glyphosate and 2,4D) (CF) and soybean (Sulfentrazone and Fomesafen) (HS). A field trial was conducted in 2022 at the Facultad de Ciencias Agropecuarias-Universidad Nacional de Entre Ríos (Colonia Ensayo, Argentina). The treatments evaluated were control, Zn, AA and AE (0+0+0; 3+0+0; 3+3+0; 2+2+2+2 cc kg⁻¹), applied to the seed before sowing, in a randomized complete block design with four replications. Samples were taken at 21 and 42 days after emergence (DAE), stages Z2.2 and Z3.1, respectively, determining the dry weight of aerial biomass. In addition, the number of tillers was counted at 21 DAE. The plots were harvested at 140 DAE (Z9) and the final yield was quantified. CF showed significant differences in the number of tillers with respect to HS ($p < 0.01$), for the rest of the variables analyzed the same trend was not statistically significant. For each predecessor, the addition of Zn, Zn+AA and Zn+AA+AE, showed a cumulative increase with respect to the control, for the variables analyzed with respect to the control. The use of biostimulants such as those tested is a tool to improve the initial growth conditions of *T. aestivum* and their evaluation under different conditions is required.

Keywords: Triticum aestivum, biostimulants, seed treatments, herbicide persistence.



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