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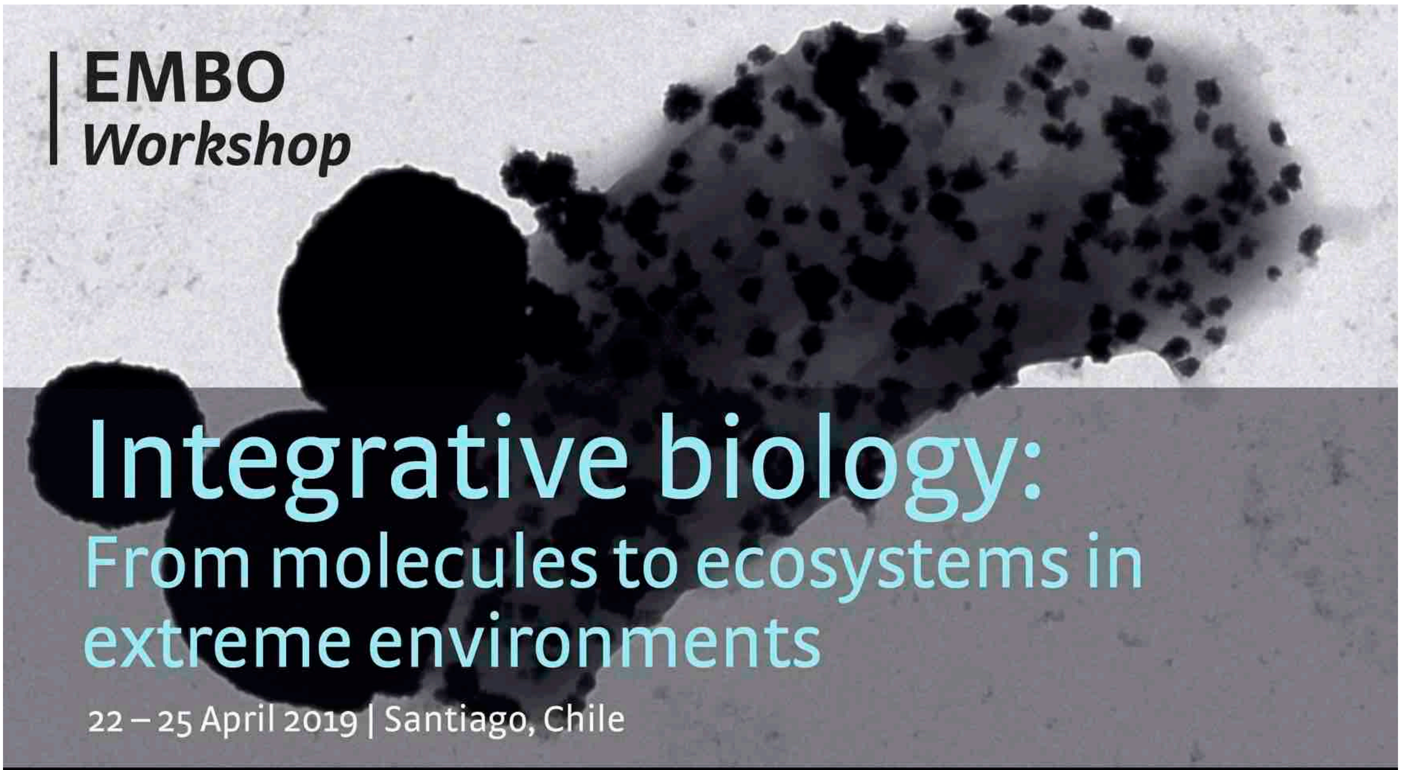

Integrative biology:
From molecules to ecosystems in extreme environments

22 – 25 April 2019 | Santiago, Chile

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Registration deadline
22 March 2019
Abstract submission deadline
15 March 2019

Student/PostDoc	70 EUR
Academic	180 EUR
Industry	700 EUR

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Integrative biology: From molecules to ecosystems in extreme environments (w19-107)

Santiago, Chile, 22 – 25 April 2019

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PLANT BIOLOGISTS

THE UNIVERSITY
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Monday, 22 April 2019

13:30 – 14:00	Registration.	Salon de Honor
14:00 - 14:15	Welcome and Introductory Comments	Salon de Honor
14:15 - 16:25	**Session 1: Diversity in Ecosystems and Communities.** Room: Salon de Honor Chair: Eric Schirmer	
14:15	Session 1---01 **Microbial community in extreme environments** Beatriz Díez, et al.	
14:45	Session 1---02 **Microbial communities composition and activity in different polyextreme environments in northern Chile** Verónica Molina, Martha Hengst, Yoanna Eissler, Cristina Dorador, et al.	
15:15	Session 1---03 **Understanding modern and past dynamics of the Nitrogen cycle in the central Atacama Desert** Claudio Latorre	
15:45	Session 1---04 **Methane Cycle in Maritime Antarctic Lakes** Rodolfo Javier Menes, Diego Roldan	
16:05	Session 1---05 **Versatility in energy dependent metabolism of microbes present in terrestrial hydrothermal environments** Maximiliano Amenabar	
16:25 - 16:55	Coffee break	
16:55 - 19:35	**Session 2: Metadata in New Ecosystems, Aquatic & Extreme Environments, & Evolution.** Room: Salon de Honor Chair: Yves Gibon	
16:55	Session 2---01 **Metabolomics approaches to understand the chemical communication in plant–microbe interactions** Marta-Marina Pérez-Alonso, Stephan Pollmann	

17:25	Session 2---02 **High bacterial species novelty in metagenome assembled genomes from hot springs (32 - 98 °C): metabolic insights of new taxa of thermophilic bacteria** Jaime Alcorta, Oscar Salgado, Beatriz Díez
17:45	Session 2---03 **Biotechnological and bioinformatic advances in conifer research** Cesar Lobato-Fernandez, Francisco Ortigosa, Rafael A. Cañas, Fernando N. de la Torre, Maria Belen Pascual, Concepcion Avila, Francisco M. Canovas
18:05	Session 2---04 **Genetic diversity between criotolerant yeasts with beer fermentation potential** Francisco Cubillos, et al.
18:25	Session 2---05 **Transcriptomic-based analysis of Fischerella thermalis metabolism in a hot spring temperature gradient.** Pablo Vergara-Barros, Beatriz Díez
18:45 - 20:00	Welcome Reception

Tuesday, 23 April 2019

09:00 - 10:30	**Session 3: Adaptation to Extreme Conditions.** Room: Salon de Honor Chair: Rodrigo A. Gutiérrez
09:00	Session 3---01 **Tolerance to temperature shifts in natural environments** Enrico L. Rezende
09:30	Session 3---02 **Plant developmental responses to salt stress** Fernanda Garrido, Daniel San Martín, José O`Brien
10:00	Session 3---03 **Genome sequence and RNA expression profiles of Orestias ascotanensis (Teleostei; Cyprinodontidae): strategies for adaptation to extreme environmental conditions** Martin Montecino

10:30 - 11:00	Coffee break
11:00 - 12:30	**Session 3: Adaptation to Extreme Conditions.** Room: Salon de Honor Chair: Rodrigo A. Gutiérrez
11:00	Session 3---01 **Zinc Finger C2-C2 transcription factors: plant regulators to deal with to adverse environmental conditions** José Dominguez-Figueroa, Laura Carrillo, Begoña Renau-Morata, Rosa-V Molina, Daniel Marino, Javier Canales, Martin Weih, Stephen Pollman, Jesús Vicente-Carbajosa, Sergio G. Nebauer, Joaquin Medina
11:30	Session 3---02 **De novo transcriptome assembly and expression analysis provide insights into the molecular basis of heat response in Nothofagus pumilio** Maximiliano Estravis Barcala, María Verónica Arana, Paula Marchelli, Katrin Heer, Birgit Ziegenhagen, Nicolás Bellora
11:50	Session 3---03 **A reverse genetic approach identifies a novel transcriptional regulator involved in temperature signaling to the Neurospora crassa Circadian Clock.** Felipe Muñoz-Guzmán, Valeria Caballero, Luis F. Larrondo
12:30 - 15:00	**Lunch and Poster Session I:: Lunch and Poster Session I: Extremophiles and Eco-communities. Tuesday 23 April** Room: Zocalo Biological Science Chair:
01	**Bacterial communities associated to Chilean altiplanic native plants from the Andean grasslands soils** Beatriz Fernandez Gomez, Jonathan Mandonado, Dinka Mandakovic, Alexis Gaete, Rodrigo A. Gutiérrez, Alejandro Maass, Verónica Cambiazo, Mauricio González
02	**Bioprospecting of bioactive compounds from rhizosphere actinomycetes of Lupinus oreophilus in the Atacama Desert** Francisca Marchant, Jean Franco Castro, Valeria Razmilic, Diego Lagos, Barbara Andrews, Juan Asenjo

03	**Endophytic fungi and their role in the induction of transcription factors in response to ABA-dependent and independent under drought stress in Colobanthus quitensis** Rasme Hereme, Patricio Ramos, Marco Molina-Montengero
04	**Experimental evolution of Saccharomyces eubayanus in ethanol improve its fermentative capacity** Wladimir Mardones, Carlos Villarroel, Roberto Nespolo, Francisco Cubillos
05	**Depict the biogeographical patterns of microorganisms along the Southern Ocean** Guillaume Schwob, Léa Cabrol, Julieta Orlando, Elie Poulin
06	**Interaction Between Arabidopsis thaliana and Ensifer meliloti for Improved Plant Growth and Nitrogen Nutrition** Grace Armijo, Tatiana Kraiser, María Paz Medina, Javier Santiago, Ana Zúñiga, Bernardo González, Rodrigo A. Gutiérrez
07	**Antarctic microorganisms: key players in the successful colonization of the Antarctic plant Colobanthus quitensis in Antarctica under a climate change scenario.** Andrea Barrera, Ian Acuña-Rodriguez, Cristian Torres-Díaz, Peter Convey, Marco Molina-Montenegro
08	**Systematic review of soil bacterial communities from arid environments at a global-scale.** Javiera Vásquez-Dean, Felipe Maza, Isidora Morel, Rodrigo Pulgar, Mauricio Gonzalez
09	**Hoffmannseggia doelli: Characterization and Propagation of an Extremophile Plant from the Atacama Desert** Melissa Aguilar, Isabel Pochet, Gabriela Carrasco-Puga, Francisca Díaz, Claudio Latorre, Rodrigo Gutiérrez
10	**Ecological genomics in the Atacama Desert: Extreme aridity, low Nitrogen and high radiation as key drivers of natural selection** Soledad Undurraga, Daniela Soto, Carol Moraga, Alejandro Montecinos, Francisca Diaz, Gabriela Carrasco, Viviana Araus, Jonathan Maldonado, Ricardo Nilo, Orlando Contreras-López, Tomás Moyano, et al.

11	**Microbial diversity associated with mineralization in the Nitrate and Iodine Deposits of Northern Chile** Mayra Cortés, Alex Echeverría, Priscilla Avendaño, Olga Encalada, Guillermo Chong, Aliro Ahumada, Cecilia Demergasso, Lorena Escudero
12	**Proteorhodopsin phototropy in Antarctic coastal waters** Jerónimo Cifuentes, María Estrella Alcamán-Arias, Tomás Alarcón-Schumacher, Beatriz Díez
13	**Arsenic resistance/tolerance on the Polyextremophile Exiguobacterium genus: Multi-omics approach on strains isolated from different Salar de Huasco niches.** Juan Castro-Severyn, Coral Pardo-Este, Yoelvis Sulvaran, Carolina Cabezas, Alan Briones, Naiyulin Morales, Laurence Molina, Franck Molina, Francisco Remonsellez, Eduardo Castro-Nallar, Claudia Saavedra
14	**Cytokinin-dependent transcriptional regulation of PIN auxin efflux carriers in response to developmental and environmental cues** Martín Pincheira, José O'Brien
15:00 - 17:30	**Session 4: Rapid Responses to Abiotic or Biotic Stress.** Room: Salon de Honor Chair: Joaquin Medina
15:00	Session 4---01 **Response of nitrogen nutrition to challenging environment in Arabidopsis** Laurence Lejay
15:30	Session 4---02 **Homogalacturonan status modulation through PME/PMEI13 is a key component of Arabidopsis defense during the early stage of infestation by Myzus persicae** Francisca Blanco-Herrera, Christian Silva-Sanzana, Jonathan Celiz-Balboa, Elisa Garzo, Susan Markus, et al.
16:00	Session 4---03 **Hunting temperate viruses in Chilean Patagonia hot springs microbial mats** Sergio Guajardo-Leiva, Oscar Salgado, Beatriz Díez

16:20	Session 4---05 **Cold-shock genes in the adaptation of Antarctic Pseudomonas to different temperature conditions** César X. García-Laviña, Ana C. Ramón, Susana Castro-Sowinski
16:40	Session 4---06 **Regulatory networks underlying differential susceptibility to Botrytis cinerea in tomato plants grown under different nitrogen regimes.** Andrea Vega, Mario Agurto, Paulo Canessa, Gustavo Hoppe, Camila Huidobro, Rodrigo A. Gutiérrez

Wednesday, 24 April 2019

09:00 - 10:30	**Session 5: Physiology & Metabolomics in Normal and Extreme Environments.** Room: Salon de Honor Chair: Laurence Lejay
09:00	**Phylogenomics and Systems Biology approaches reveal conserved adaptive processes in Atacama Desert plants** Rodrigo A. Gutierrez, Soledad Undurraga, Daniela Soto, Kranthi Varala, Gil Eshel, Erika Viviana Araus, Francisca Díaz, Gabriela Carrasco, Chase W. Nelson, Dennis Stevenson, Gloria Coruzzi, et al.
09:30	Session 5---02 **Top-down and bottom-up modelling approaches to link metabolism and plant performance** Yves Gibon, et al.
10:00	Session 5---03 **Nutrient cycling at the extreme; the role of UV radiation on litter mass losses.** Aurora Gaxiola
10:30 - 11:00	Coffee break
11:00 - 12:45	**Session 5: Physiology & Metabolomics in Normal and Extreme Environments.** Room: Salon de Honor Chair: Laurence Lejay
11:00	Session 5---01

	Mining genes for climate change. Using Cistanthe longiscapa to understand stress resilience Ariel Orellana
11:30	Session 5---02 **The RGF1-PLT2 regulatory network maintains primary root meristem activity in low phosphate environments.** Peter Doerner, Xin Tian, Yuanyuan Li, et al.
12:00	Session 5---04 **Analysing changes in assimilate transport and grapevine ripening metabolism induced by the physiological disorder Berry Shrivel.** Sara Crespo, Michaela Griesser, Mirosław Sobczak, Rainer Schuhmacher, Elżbieta Różańska, Markus Walter Eitle, Astrid Forneck
12:45 - 15:00	**Lunch and Poster session II:: Lunch and Poster session II: Synthetic and Systems/Network Biology. Wednesday, 24 April** Room: Zocalo Biological Science Chair:
01	**Natural genetic variation as a tool to study root architecture in response to osmotic and salt stress** Jose O'Brien, Inti Pedroso, Jeremy Gagiano
02	**The influence of FtsZ on the multiseptum formation in filamentous cyanobacteria** Sebastian Velozo, Jorge Olivares, Mónica Vásquez
03	**ψ-trap: Microfluidic platform for long-term phenotyping of plant single cells** Eric Thorand, Teuta Pilizota, Naomi Nakayama
04	**Pairwise Probabilistic Framework to infer functional gene networks and identify key genes in response to perturbations.** Tomás Moyano, Elena Vidal, Eleodoro Riveras, Antoine de Daruvar, Rodrigo Gutierrez
05	**The role of Serendipita indica as a modulator of K+ acquisition in Arabidopsis thaliana**

	Carmen Guerrero-Galan, Raúl Jiménez-Coll, Rosario Haro, Begoña Benito, Stephan Pollmann, Jesús Vicente-Carbajosa
06	**PS-Plant: tracking plant growth traits and leaf movement patterns with a novel low-cost 3D- imaging system** Alistair McCormick, Livia Scorza, Gytis Bernotas, et al.
07	**CyanoGate: A Golden Gate modular cloning suite for engineering cyanobacteria based on the plant MoClo syntax** Alistair McCormick, Grant Gale, et al.
08	**The BST family: incorporating thylakoidal components of the Chlamydomonas CO2-concentration mechanism into higher plants** Alistair McCormick, Liat Adler, Nicky J. Atkinson
09	**Effects of deletion of circadian clock genes in Anabaena sp. PCC7120.** Marcial Silva, Javiera Jiménez Á, Mónica Vásquez
10	**A Multi-Model Framework for The Arabidopsis Life Cycle** Argyris Zardilis, Alastair Hume, Alistair Mccormick, Robert Muetzefeldtd, Gordon Plotkin, Andrew Millar
11	**Being FAIR and Open while being more Productive** Andrew J. Millar, Eilidh Troup, Tomasz Zieliński
12	**Studying the role of soil microorganisms in chickpea root system architecture regulation** Peter Doerner, Cristobal Concha, Thibaut Bontpart, Ingrid Robertson, Valerio Giuffrida, Sotirios Tsaftaris
13	**The Ancient Transcription Factor ZHOUPI Controls development of a novel water transport tissue in liverworts** Justin Goodrich, Yen-ting Lu, Jeanne Loue-Manifel, Gwyneth Ingram, Takayuki Kohchi, Ryuichi Nishihama
14	**Analysis of predicted metabolic pathways based on the genome of the annual killifish Austrolebias charrua** Cristina Muñoz, Miguel Allende, Ricardo Nilo

15	**Metabolomic and transcriptomic approaches reveal new components related to sugar metabolism involved in the protective effect of melatonin on fruit exposed to cold stress** Simon Miranda, Paulina Vilches, Bruno Defilippi, Romina Pedreschi, Talía del Pozo
16	**Ready, steady, go! Kap1/Trim28-dependent release of paused RNA polymerase II is essential for X inactivation** Sara Buonomo, Elin Enervald, Rossana Foti, Gozde kibar, Stefano Gnan, Martin Vingron
15:00 - 17:30	**Session 6: Genome Regulation, Gene Regulatory Networks & Epigenetics.** Room: Salon de Honor Chair: Stephan Pollmann
15:00	Session 6---01 **Transcriptional control in seed development and its connections to stress responses** Jesus Vicente-Carbajosa, et al.
15:30	Session 6---02 **Tissue-specific nuclear membrane proteins direct 3D genome organization changes important for tissue differentiation, disease, and cell environmental responses** Eric Schirmer
16:00	Session 6---03 **Specialized adaptations and rapid genome expansion in a group of South American annual killifish** Miguel Allende, et al.
16:30	Session 6---04 **New tricks for old dogs - domesticated transposases as components of novel plant chromatin modifying complexes** Justin Goodrich, Christos Velanis, Franziska Turck, Frank Wellmer, Bennett Thomson, Perera pumi
16:50	Session 6---05 **Rif1 a hub connecting nuclear architecture and replication timing** Sara Buonomo, Stefano Gnan, Ilya Fliamer, Kyle Klein, David Gilbert, Wendy Bickmore

17:10	Session 6---06 **Mechanistic insights into controlling cell identity by transcription factors** Abdenour Soufi, et al.
Thursday, 25 April 2019	
09:00 - 10:30	**Session 7: Lessons from network structures in natural environments.** Room: Salon de Honor Chair: Francisca Blanco Herrera
09:00	Session 7---01 **Lessons from desert endophytic bacteria to enhance plant growth and crop yield in extreme environments** Heribert Hirt, et al.
09:30	Session 7---2 **Hydro-actuated morphing enables informed dispersal of dandelion diaspores** Madeleine Seale, Cathal Cummins, Enrico Mastropaolo, Ignazio Maria Viola, Naomi Nakayama
10:00	Session 7---03 **Deciphering the cell division in filamentous Cyanobacteria** Mónica Vásquez, Derly Andrade, Carla Trigo, Jorge Olivares, Marcial Silva, Javiera Jiménez, Blanca Aguila
10:30 - 11:00	Coffee break
11:00 - 12:30	**Session 7: Lessons from network structures in natural environments.** Room: Salon de Honor Chair: Francisca Blanco Herrera
11:00	Session 7---01 **Circadian clocks, temperature and Patagonian forest ecology** Maximiliano Estravis-Barcala, Nicolas Bellora, Alejandro Martinez-Meier, Marina Gonzalez-Polo, Julieta Cagnacci, Paula Marchelli, Birgit Ziegenhagen, Lars Opgenoorth, Katrin Heer, Marcelo Yanovksy, Maria Veronica Arana
11:30	Session 7---02

	Plant-microbiome interactions modify the co-occurrence patterns of soil bacterial communities along an altitudinal gradient in the Andes of the Atacama Desert. Dinka Mandakovic, Mauricio González
11:50	Session 7---023 **AMI1 linkes indole-3-acetic acid biosynthesis with plant stress responses** Marta Marina Pérez-Alonso, Beatriz Sánchez Parra, Paloma Ortíz García, Thomas Lehmann, Lucía Jordá, Robert G. Björk, Sazzad Karim, Mohammad R. Amirjani, Henrik Aronsson, Stephan Pollmann
12:10	Session 7---04 **Recent advances in introducing an algal CO2-concentrating mechanism into higher plants.** Alistair McCormick
12:30 - 15:00	Lunch Hall
15:00 - 17:20	**Session 8: Genome Editing & Synthetic Biology for Translation** Room: Salon de Honor Chair: Martin Montecino
15:00	Session 8---01 **Forging a causal chain around the circadian clock, from genome sequence to field traits** Uriel Urquiza, Argyris Zardilis, Nacho Molina, Andrew Millar
15:30	Session 8---02 **Upcycling metals with bacteria** Louise Horsfall
16:00	Session 8---03 **A novel avirulent and exopolysaccharide-producing Bacillus anthracis from Indian hot spring: genomic approach** Aparna Banerjee, Rajib Bandopadhyay, Sara Cuadros-Orellana
16:20	Session 8---04 **Halophilic adaptation of ADP-dependent kinases from Methanosarcinales order of archaea.** Felipe Gonzalez-Ordenes, Pablo Cea, Nicolas Fuentes, Sebastian Muñoz, Victoria Guixé, Victor Castro-Fernandez

16:40	Session 8---05 **Universal Loop assembly (uLoop): open, efficient and agnostic DNA fabrication** Bernardo Pollak, Tamara Matute, Ariel Cerda, Isaac Nuñez, Valentina Vargas, Constanza Lopez, Vincent Bielinski, von Dassow Peter, Dupont Christopher, Fernan Federici
17:00	Session 8---06 **The use of synthetic biology to uncover basic principles of circadian oscillators: from temperature compensation to the processing of environmental cues** Alejandra Goity, Luis Larrondo
17:20 - 18:00	Closing Panel Discussion Salon de Honor
18:00 - 20:00	Closing Reception Salon de Honor

Hoffmannseggia doelli: Characterization and Propagation of an Extremophile Plant from the Atacama Desert

Melissa Aguilar, Isabel Pochet, Gabriela Carrasco-Puga, Francisca Díaz, Claudio Latorre, Rodrigo Gutiérrez

Departamento de Genética Molecular y Microbiología, Facultad de Ciencias Biológicas, Pontificia Universidad Católica de Chile, Santiago, Chile

Under the current global climate change scenario, the discovery and characterization of plant species adapted to extreme environmental conditions has become increasingly important. Hoffmannseggia doelli (“mutukuru”) is an endemic perennial herb of the Chilean Atacama Desert that grows between 2900 and 3800 meters above sea level (m a.s.l.) in the western Andes Mountains. Its growth habitat is characterized by high radiation (≥620 watt/m2), low water availability (~ 76 mm annually) and soils with abundant toxic minerals. Under these adverse conditions, H. doelli has been able to develop a tuberous root that has been used as a food source by Atacama natives over centuries.

This work constitutes the first attempt to establish H. doelli cultures under laboratory conditions. We have optimized these growth conditions as a foundation for future physiological and genetic studies. Under our experimental conditions, H. doelli is capable to germinate and grow. We have also obtained tuberous roots after 45 days of growth those of which were analyzed by optical microcopy finding organelles which structure and morphology are similar to amyloplasts. Furthermore, we have used this tuberous root for clonal propagation of this species.

We established a protocol for in vitro H. doelli micropropagation using axillary buds. We obtained calluses after one month of bud growth in cytokinin-enriched media (20 µM BA). We also regenerated shoots after an additional month under the same conditions. These shoots developed roots when transferred to an auxin-enriched media (10 µM NAA) and grown for one month. Finally, fully-regenerated plantlets were successfully transferred to potting medium and grown in greenhouse conditions. In summary, we established a simple axillary bud regeneration method for H. doelli with two different hormonal concentrations and a total time of four months.

High bacterial species novelty in metagenome assembled genomes from hot springs (32 - 98 °C): metabolic insights of new taxa of thermophilic bacteria

Jaime Alcorta [1], Oscar Salgado [1], Beatriz Díez [1, 2]

[1] *Department of Molecular Genetics and Microbiology, Pontificia Universidad Católica de Chile, Santiago, Chile*
[2] *Center for Climate and Resilience Research (CR)2, Santiago, Chile*

Hot spring microbial mats are composed by diverse bacteria and archaea whose presence and activity are modulated mainly by temperature, pH and geochemistry. The microbial diversity has been addressed lately by metagenomics to mainly report general patterns of taxonomy and metabolic processes. However, metagenome assembled genomes (MAGs) can be used to describe discrete genomic populations to improve our understanding of genomic adaptations of unknown/uncultured taxa that thrive in these extreme systems.

Our aim is to study the taxonomy and codified metabolic processes from high quality MAGs obtained from 21 hot spring illumina metagenomes from Chile (unpublished) and public databases in a wide temperature range (32 to 98 °C). All reads were quality trimmed and de-novo assembled. Contigs were binned into MAGs and their completness/contamination was analyzed with CheckM. High quality MAGs were taxonomically classified with GTDB-tk and their codified metabolic processes were annotated with KEGG.

We obtained 381 high quality MAGs with bacterial predominance (371). The taxonomic novelty of the obtained MAGs was across all levels, being classified in novel phyla (2), class (4), order (26), family (69), genus (171) and species (336). Therefore, a great species novelty (88%) whithin these 21 metagenomes was revealed. The metabolic processes encoded in these MAGs will improve our understanding of the roles of these uncultured microbes, such as the two MAGs from novel phyla potentially involved in nitrogen and methane biogeochemical cycles of these extreme systems.

Specialized adaptations and rapid genome expansion in a group of South American annual killifish

Miguel Allende, et al.

Center for Genome Regulation, Santiago, Chile
Facultad de Ciencias, Universidad de La República, Montevideo, Uruguay

Annualism in killifish has been described in the African and American continents and is likely to have arisen independently at least twice. These animals have adapted to survive in ephemeral ponds that dry out for part of the year, forcing the fish to grow, reproduce and die within a span of a few months. The following generation arises from embryos that are deposited in the susbstrate, surviving in a developmental diapause allowing them to resist desiccation for extended periods. Development resumes and hatching occurs during the following rainy season. Given these specializations, it is of interest to understand the molecular and genomic strategies that have evolved in annual fish. We have sequenced the genomes of two South American annual fish: Austrolebias charrua and Cynopoecilus melanotenia. Despite having a common ancestor between both species dating back less than 15Myr ago, the genome of A. charrua is twice the size (3Gb) of that of C. melanotenia. This rapid genome expansion occurred by the evolutionarily sudden amplification of transposable elements (TEs) and other repetitive sequences. Members of the LINE family of retrotransposons make up about 20% of the genome, a number similar to that found in the human genome. Comparing both genomes, we find that A. charrua has three times more intragenic REs than C. melanotenia. Analysis of coding sequences shows that A. charrua also displays a two-fold expansion in the number of genes showing a paralog rate of 2.2 (compared to 1.58 for C. melanotenia). We provide evidence for neo- and sub-functionalization of duplicated genes by performing tissue-specific transcriptome analysis between both species. Our results suggest that the genome of A. charrua is undergoing dynamic changes that may provide a mechanism for evolutionary innovation and adaptation to a highly unstable and challenging environment.

Versatility in energy dependent metabolism of microbes present in terrestrial hydrothermal environments

Maximiliano Amenabar

Fundación Científica y Cultural Biociencia, Santiago, Chile

Hydrothermal environments such as hot springs, fumaroles, or geysers are dynamic surface features that form as the result of the interaction between water, heat, and rocks. Due to the geological nature of these environments, their physicochemical conditions can change both in space and time, shaping the distribution, composition and activities of microbial communities inhabiting hydrothermal areas. As such, these environments and the communities they support have serve as model systems for addressing key questions in Earth Science, including those aiming to understand the factors that control the distribution of microorganisms and their activities in the environment and those that seek to unravel the mechanisms allowing microbes to deal with fluctuating environmental conditions. Here we report a thermoacidophilic and autotrophic archaeon, designated as Acidianus strain DS80, that exhibit flexibility in its energy metabolism using soluble and insoluble substrates to growth. Strain DS80, isolated from an acidic hot spring from Yellowstone National Park, can grow lithotrophically using hydrogen (H2) or elemental sulfur (S°) as an electron donor, and S° or soluble/mineral forms of ferric iron as electron acceptors. The extent of metabolic flexibility was further studied using genomic and physiological approaches and the ecological consequences of being metabolically flexible discussed. Our results showed that genome-guided predictions of energy and carbon metabolism of organisms may not agree with physiological observations in the laboratory, and by extension, the environment. Here we provide evidence that the availability of electron acceptors influences the spectrum of potential electron donors and carbon sources that can sustain growth. Similarly, the availability of H2 enables the use of organic carbon sources in DS80 cells respiring S°, thereby expanding the ecological niche of these organisms by allowing them to compete for a wider array of substrates that are available in dynamic environments.

Circadian clocks, temperature and Patagonian forest ecology

Maximiliano Estravis-Barcala [1], Nicolas Bellora [2], Alejandro Martinez-Meier [1], Marina Gonzalez-Polo [3], Julieta Cagnacci [1], Paula Marchelli [1], Birgit Ziegenhagen [4], Lars Opgenoorth [4, 5], Katrin Heer [4, 5], Marcelo Yanovksy [6], Maria Veronica Arana [1]

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The Andean-Patagonian region comprises one of the most singular forestry ecosystems of the planet and constitutes one of the last frontier forests of its type. In this region, Nothofagaceae, a monotypical family in the order Fagales, dominates in generally hostile environments, inhabiting almost all the narrow forestry landmass of the Patagonian Andes. This region will be affected by increasing temperatures according to climate change (CC) predictions. In this context, a fundamental question is how trees will cope with these changes, given their low population turnover.

Here we explored the hypothesis that the upper thermal limit for clock functioning influences thermal adaptation in Nothofagus obliqua and N. pumilio. These are two emblematic tree species of the Patagonian forests, which constitute examples of extremes of adaptation of closely related species to altitude, inhabiting non-overlapping thermal niches. We show that the circadian clocks of both species are out of their compensation range at 34°C. In diurnal conditions, at 31°C, daily oscillation in the expression of the homolog clock gene NoTOC1 is maintained in N. obliqua, which inhabits warmer and lower altitudes of the mountains but is lost in N. pumilio, which inhabits higher and colder habitats. Experiments across an altitudinal gradient show that the expression of NpTOC1 in N. pumilio is affected in warmer and lower environments out of its distribution range, and this is associated with reduced accumulation of dry weight, chlorophyll and survival. This behavior is not evident in N. obliqua seedlings grown in higher environments out of their natural range. Taken together, our results provide the first evidences in favor that performance of circadian clock at different temperatures contribute to physiological adaptation to the local thermic environment. This phenomenon might influence the ability of N. obliqua and N. pumilio to respond to increasing temperatures such as those predicted by CC.

Interaction Between Arabidopsis thaliana and Ensifer meliloti for Improved Plant Growth and Nitrogen Nutrition

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Nitrogen (N) is an essential macronutrient whose availability in the soil has a critical role in plant growth and development in natural as well as in agricultural environments.
Plants acquire N directly from the soil and in some cases N can be provided by interacting with N-fixing bacteria. This kind of interactions are well described in legumes, but are also observed in some non-legume plant species, that are unable to form nodules. Understanding these plant-bacteria interaction mechanisms could have important agronomic implications, reducing the use of N-fertilizers in non-legume crops.
Our goal was to evaluate a functional association between a non-legume model plant, Arabidopsis thaliana, and a N-fixing model bacteria, Ensifer meliloti, to study and identify molecular mechanisms underlying this association.
Through genetic and biochemical evidence we found that E. meliloti enhanced A. thaliana growth under N-deficiency conditions. We showed that this growth promotion under N-deficiency is at least partly mediated by bacterial N-fixation and allows the plant to complete the life cycle even under severe N-deficiency. We also determined bacterial root colonization through different types of microscopy, locating this bacterium in the rhizosphere associated to the epidermis of the plant root. Finally, we demonstrated that A. thaliana homologs of key regulatory genes involved in legume:rhizobium interactions are required for growth promotion mediated by E. meliloti.
Our results indicate a non-canonical interaction between A. thaliana and E. meliloti for plant nutrition under N-deficiency with conserved molecular mechanisms of legume:rhizobium interactions for improved growth under N-limiting conditions. We are currently investigating in more detail this last aspect.

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A novel avirulent and exopolysaccharide-producing Bacillus anthracis from Indian hot spring: genomic approach

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Microbe in extreme environments like hot springs are uniquely adapted to high temperature by different cellular modifications like exopolysaccharide production, genomic changes, expression of proteins and many more. Extremophiles also often harbour some industrially important secondary metabolites like enzymes, pigments or polysaccharides that has promising industrial applicability. Indian Himalaya, Deccan region and coal mine sites are home to several unexplored hot springs. A unique avirulent and thermotolerant Bacillus anthracis is recorded from a virgin Indian hot spring, Panifala. Whole genome sequencing has revealed absence of characteristic virulence plasmids and capsule biosynthesis genes in it. Further absence of any complete prophage genes reveals no possible virulent gene transmission event in past. Non-pathogenicity has also been confirmed via in vitro macrophage association/inhibition assay and in vivo mice model. Exopolysaccharide produced by this B. anthracis is structurally elucidated and its functional properties are investigated too. The EPS is found to be a homopolymer of glucose with a molecular weight of 1.103 ×103 Da. Melting transition of the EPS started after 276ºC indicates a good thermal stability of the polymer. The exopolysaccharide biopolymer reveals potent anti-oxidant and emulsification property. Moreover, its excellent shear-thinning behaviour and viscoelastic nature indicates its suitability to be used in food industry. This study reveals occurrence of highly uncommon Bacillus anthracis in hot spring environment which is adapted to high temperature with several genetic modifications and is uniquely avirulent. Also, it is a good producer of glucan-like polysaccharide that could be potentially used as an antioxidant, emulsifier or viscosifier in food industry.

Antarctic microorganisms: key players in the successful colonization of the Antarctic plant Colobanthus quitensis in Antarctica under a climate change scenario.

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For a given plant, the colonization success is mainly limited by the microsite conditions in which its propagules arrive. The microorganis of soil has been recognized fundamental for the ecophysiological performance of almost all plant species, and particularly relevant in harsh environments; here we tackled this question by assessing its role in the colonization success of the antarctic plant Colobanthus quitensis in the Antarctic ecosystem. Taking advantage of the retreat of the Glaciers "Baranowsky" and "Ecology" (King George Island) and Byers (Livingston Island), five groups of five C. quitensis plantlets were transplanted to the field using two soil types (control and sterilized) at 30, 100 and 300 m away from the each glacier, distance that also represented a soil moisture gradient. Complementarily, to understand these dynamics under the context of the predicted global temperature rise, the same experiment was replicated using open top chambers (OTCs), in "Ecology glacier", which increase the annual temperature average as expected on such future conditions. The variables responses analyzed were photochemical efficiency (Fv/Fm) and abscisic acid (ABA) foliar content were assessed one month after establishment as descriptors of performance and drought tolerance, respectively. Furthermore, plant survival was recorded during two growing seasons. Microbiota appeared to be more relevant away from the glacier, showing significant differences for all the analyzed variables between C. quitensis growing with and without them. Interestingly, the increase in temperature derived from the OTCs imposed additional stress for C. quitensis individuals growing away from the glacier. In conclusion, we found that the soil microbiota is determinant for the success of colonization of C. quitensis mainly in microsites where water scarcity prevails. For this reason, under the climate change that is approaching, it is relevant to evaluate symbiotic interactions between soil microorganisms and C. quitensis.

Homogalacturonan status modulation through PME/PMEI13 is a key component of Arabidopsis defense during the early stage of infestation by Myzus persicae

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By sucking the phloem sap and vectoring phytopathogenic viruses, aphids are a worldwide threat to crop yields. Pectic homogalacturonan (HG) has been described as a defensive element for plants during infections with phytopathogens. However, its role during aphid infestation remains unexplored. Using immunofluorescence assays and biochemical approaches, we analyzed the HG methylesterification status and associated modifying enzymes during the early stage of Arabidopsis thaliana infestation with the green peach aphid Myzus persicae. Additionally, the influence of PME activity on aphid settling and feeding behavior was evaluated by free choice assays and the Electrical Penetration Graph technique, respectively. Our results revealed that HG status and its modifying enzymes are significantly altered during the early stage of the plant-aphid interaction. Aphid infestation induced a significant increase in total PME activity and methanol emissions, concomitant with a decrease in the degree of methylesterification of HG. Conversely, inhibition of PME activity led to a significant decrease in the settling and feeding preference of aphids. Additionally, we demonstrate for the first time the defensive role of a PME inhibitor (AtPMEI13) during aphid infestation, since pmei13 mutants are significantly more susceptible to M. persicae in terms of settling preference, phloem access, and phloem sap drainage.

Ready, steady, go! Kap1/Trim28-dependent release of paused RNA polymerase II is essential for X inactivation

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The eukaryotic nucleus is a very busy space, where transcription, DNA replication and DNA repair all take place and influence each other. However, the rules and principles that control these interactions are still unclear. My group is interested in understanding the molecular bases of these relationships. X-chromosome inactivation (XCI) is the process that ensures dosage compensation of the X-linked genes between female and male mammals. This is achieved by transcriptional silencing of the genes on one of the two X chromosomes in females. XCI is a paradigm exemplifying the orchestrated action of nuclear re-positioning, gene silencing and control of DNA replication timing. The major regulator of XCI is the long non-coding RNA Xist, monoallelically upregulated at the onset of XCI from the future inactive X chromosome. Previous studies from our laboratory have identified Rif1 as a key regulator of DNA replication timing and chromatin architecture. Here, we identify Rif1 as an important regulator of Xist expression. We show that XCI is significantly reduced in differentiating Rif1 deficient female mouse embryonic stem (ES) cells as a result of a lack of Xist upregulation. Furthermore, we show that loss of Rif1 leads to lethality in female mouse embryos as a result of defective XCI. Our data reveal a new, previously unknown mechanism of control of Xist, in which the onset of its expression is triggered by the regulated release of the paused RNA polymerase II (Pol2). Our data show that RIF1 is essential for the conversion of paused into processive RNA polymerase II. The onset of XCI can only take place during a very narrow window of time during embryonic development or cell differentiation in vitro. Our work has brought to light a new pathway that ensures the prompt and robust upregulation of Xist in response to differentiation.

Rif1 a hub connecting nuclear architecture and replication timing

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DNA replication is temporally and spatially organized in all eukaryotes, but the function and molecular control the of the replication-timing program are still largely unknown. It has been proposed that three-dimensional chromatin organization could be a key determinant of the timing of activation of origins of replication. We recently identified Rif1 as a protein involved in the regulation of both replication timing and nuclear architecture and we have characterised it as an adaptor for protein phosphatase 1 (PP1). It is however unclear if Rif1 controls both independently of each other or if nuclear architecture per se plays a role in the establishment of the replication timing program. In addition, it is unknown if both processes depend on the interaction between Rif1 and PP1. We have generated mouse embryonic stem cells that express a mutant of Rif1 unable to interact with PP1 (Rif1ΔPP1) as a sole source of Rif1, aiming at possibly generating a separation of function allele. We have analysed the effect of the expression of Rif1ΔPP1 on replication timing and nuclear organisation in these cells and will report on the unexpected results of our analyses.

Halophilic adaptation of ADP-dependent kinases from Methanosarcinales order of archaea.

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Halophilic organisms inhabit hypersaline environments where the extreme ionic conditions and osmotic pressure have driven the evolution of molecular adaptation mechanisms. In Euryarcheota, only the Halobacteria and Methanosarcinales groups have cultivable halophilic organisms and it is the proteins from Halobacteria that have been most widely studied. The main features indicated as responsible for the haloadaptation in these proteins are a reduction of the hydrophobic core and a strongly negatively charged surface. In our work, we addressed the halophilic adaptation of the ADP-PFK/GK from Methanosarcinales, we studied enzymes found either in halophilic or non-halophilic organisms and compared them with Eukarya and Halobacteria proteins. We reported a non-canonical strategy employed by current Methanosarcinales proteins to be functional and stable at high salt concentrations. This strategy differs from the currently proposed models for Halobacteria proteins and it is characterized by a huge increase in the Lys content surface and by no reduction of the hydrophobic core. The resurrection of the last common ancestor of ADP-PFK/GK from Methanosarcinales shows that the ancestral enzyme displays an extremely high salt tolerance and thermal stability. Structure determination by X-ray crystallography of the ancestral protein reveals unique traits such as a 9-fold increase in the Lys content, a huge increase in the Glu content, and yet no reduction in the hydrophobic protein core. Taken together, our results support a non-canonical strategy for adaptation to halophilic environments that differs from the currently proposed models for Halobacteria proteins and the ancestral proteins reconstruction opens up new lines of research to explore the halophilic character of ancestral enzymes as a potential tool in biotechnology and to unveil the molecular evolution of halophilic organisms and their proteins.

Arsenic resistance/tolerance on the Polyextremophile Exiguobacterium genus: Multi-omics approach on strains isolated from different Salar de Huasco niches.

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Exiguobacterium is a polyextremophile genus that thrive in adverse environments. The Salar de Huasco is one of these environments due to its pressure, UV-radiation, temperatures, pH, salinity and presence of toxic compounds like arsenic. However, the physiologic and/or molecular mechanisms that enables them to prosper in these environments have not yet been described. Our research group has isolated several strains from this genus with diverse tolerance levels to As from 5 different Salar de Huasco niches. We set out to describe the bacterial community composition through 16S amplicon sequencing, the environmental conditions that could be affecting this composition and the variation of these between the sites. The five sites presented different concentrations of arsenic in sediment and in all of them we were able to isolate strains of Exiguobacterium with different levels of tolerance to As(III) and As(V). We sequenced the genomes of 14 of these strains to describe, through comparative genomics, the functional potential of these strains that could be explaining their ability to resist global stress and the different levels of tolerance to As. Finally, we choose three of these strains to perform 2D proteomic and gene transcriptional expression to try to clarify the physiological pattern that would be enabling these bacteria to thrive in environments with high concentrations of As. So far we can conclude that the different niches of Salar de Huasco have very particular and contrasting conditions between them and each bacterial communities seem to be shaped and adapted to overcome these conditions. The results of comparative genomics demonstrate that although Huasco strains are grouped with respect to all the available genomes, within this subset there is variability and this is demonstrated with the resulting proteomic profiles between three strains with different levels of resistance, which were validated through transcriptional gene expression.

Proteorhodopsin phototropy in Antarctic coastal waters

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Proteorhodopsin (PR) is a retinal-containing integral membrane protein that functions as a light-driven proton pump with the potential to generate energy for cell growth or maintenance. PR comprises two main families of proteins that absorb light at different wavelength; 525 nm (green) and 490 nm (blue), advantage that makes them able to exploit different spectra of the sunlight. The combination of presence, transcriptional activity and taxonomic affiliation of the PR-gene were investigated for the first time in coastal Antarctic waters during the austral summer in Chile Bay (Greenwich Island, Antarctica).

Trough meta-omics we have identified that during the summer period of 2014 there was a bacterial community represented by alpha-, gamma-proteobacteria and Flavobacteriia that presented, and actively transcribed green-PR and blue-PR during day- and night-time. The PR-bearing bacteria represented on average the 16.7% of the bacterial community, and the transcription of this gene was higher during the day than at night. Also, we determined through qPCR that 13.7 and 27.9% of the bacteria from coastal waters of Chile Bay presented the PR-gene during 2016 and 2017 summers, respectively. The transcription of the PR gene was also evaluated, and we found that as in 2014 the PR-gene was transcribed daily.

Our results show that PR could represent the main molecular strategy used by marine phototrophic bacteria to harvest sunlight energy at these coastal seawaters. This observation gives crucial information respect the prevalence of this mechanism in Antarctic seawater and the significance of this strategy to enter sunlight energy into the Antarctic biosphere.

Microbial diversity associated with mineralization in the Nitrate and Iodine Deposits of Northern Chile

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In the Atacama Desert, northern Chile, they are located the Nitrate and Iodo Deposits (NID). This work is part of a project that studies the microbial diversity present in the NID. It is hypothesized that the saline facies of NID, according to their composition, define specific habitats for microorganisms. In this context, three different areas were sampled, old mines ("Oficinas") Pissis and Savona (PS), Pampa Unión (PU) and the Toco and Zapiga (TZ).
The analysis of the microbial communities was carried out by sequencing the 16S rRNA with Illumina-MiSeq. The study of phylogeny and ecology made through the QIIME, Primer-6 and PiPHillin softwares. Enrichment cultures were performed in modified FTW medium (0.68-20.56 g/l NaNO3). The analysis of nitrate reduction in the cultures was performed by exchange chromatography using the column IonPacTM AS11 and KOH as eluent. The mineralogy was determined by X-ray diffraction (XRD).
The XRD showed the main presence of halite, darapskite, nitratin, quartz and other secondary minerals. In the microbial communities were identified, as dominant phylum, Firmicutes, Proteobacteria, Bacteroidetes and Actinobacteria. The relationship between the relative abundance of sales and the presence of microorganisms makes it possible to hypothesis an association. According to this, the abundance of Firmicutes was associated to the greater presence of halite and Proteobacteria to nitratin.
In addition, the presence of high concentrations of nitratin would increase the presence of Actinobacteria and Bacteroidetes. In sampled sites, nitrate reducing bacteria were found, and the nitrate reduction percentage was 56-68% (PS), 13-31% (PU) and 4.5-24% (TZ). The interaction between hostile conditions for life, microbial diversity and the capacity to reduce nitrate observed provides relevant information for a better knowledge of the microbial participation in the Nitrogen metabolism of these natural reservoirs. An analogy with the processes of evidence in a second hypothesis.

Analysing changes in assimilate transport and grapevine ripening metabolism induced by the physiological disorder Berry Shrivel.

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Berry Shrivel (BS) is a physiological disorder that alters cv. Zweigelt grape berry ripening. The illness affects single grapevine clusters with an irregular incidence between years, fields and plants. Environmental conditions have been related to its incidence but not confirmed. BS grapes are mainly characterized by high acidity, low sugar, K+ and anthocyanin content and loss of turgor. Different studies investigated BS berry nutrient profile, transport capacity and cell viability but the reasons of its causes are still unknown. In this work we aim to shed light over the mechanisms associated with BS initiation to clarify its induction process. Based on previous studies our hypothesis is that nutrient allocation to BS berries is disturbed, we proposed two main reasons: an irregular sink activity and/or degradation of vascular tissues. To examine sink activity and sugar unloading we successfully analysed the transcriptional and enzymatic activity of sugar transporters and invertases. Results show irregular activity of tonoplast transporters from pre-ripening until full-ripe. Furthermore, we hypostatise a relation among irregular sugar content and irregular anthocyanin content, which may not be related with anthocyanin gene activity, in addition, sugar metabolism is disturbed but its role in BS induction is not clear. To examine vascular tissues different microscopic techniques were applied in rachis and pedicel sections at first symptoms appearance (véraison) and late symptoms (full-ripen). Anatomic studies indicated morphologic differences at cambium with reduced cell layers in BS clusters. Further, phloem alterations were quantified as secondary tissue development and reduced phloem conductivity, what may indicate limited assimilate transport capacity in BS clusters. Collapsed sieve plates due to callose and reduced density of sieve plates may exacerbate restricted assimilate conductance. According to our results both physiology and metabolism are disturbed in BS development what enhance the complexity of BS disorder.

Genetic diversity between criotolerant yeasts with beer fermentation potential

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Saccharomyces eubayanus represents the so-long missing cryotolerant ancestor of lager yeast and can be found in the South Hemisphere in association with Nothofagus forests. Despite the commercial relevance of lager beer, little information is available regarding the evolutionary history of the species. In this talk, we will show how we sample the extensive presence of the species in South America and demonstrate the isolation of 160 strains from ten sampling sites in a range of 2,000 km distance. We sequenced the entire genomes of 82 of these strains and, together with other 25 available genomes, obtained phylogenetic data. Our results revealed the presence of four main lineages, together with dozens of admixed strains. The PB-1 lineage isolated from Tierra del Fuego exhibited the highest genetic and phenotypic diversity, lowest LD blocks and highest Fis values compared to the other lineages, suggesting that adaptation to cold temperatures in extreme environments has greatly increased inbreeding rates. Differences between lineages and strains were found in terms of aneuploidy and (pan)genome content, providing evidence of lateral gene transfer from an unknown donor. Furthermore, the greater genetic diversity of PB-1 from Tierra del Fuego supports the hypothesis of a S. eubayanus colonization from peripheral glacial refugia from southern Patagonia and then moved towards northern and western regions, including North America and New Zealand. Interestingly, isolates from northern sites exhibited the greatest tolerance to high temperatures and the best fermentation performance compared to southern isolates, which were comparable to commercial lager strains. Our results highlight the high abundance and extensive genetic diversity of S. eubayanus in Chile and demonstrates the enormous utility of this yeast for wort fermentation.

Microbial community in extreme environments

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Extreme environments represent ideal natural models to understand the principles of microbial ecology and biogeochemistry, and how climate change is affecting them. We investigated the effect of abiotic and also biotic parameters such as interactions with viruses in the taxonomy and function of microbial communities in extreme environments such as hydrothermal and polar marine systems through integrative approaches: metagenomics, metatranscriptomics, metaviromics, proteomics and biogeochemistry.

Our results show that the spatial substitution of microorganisms is due to the niche differentiation caused by changes in environmental conditions. The contribution to the C and N cycles by microorganisms such as filamentous heterocystous cyanobacteria in thermophilic photoautotrophic mats, as well as proteorodopsin-bearing bacteria, and nano- and phytoplankton in Antarctic coastal waters, demonstrated the prevalence and significance of certain strategies to cover the main demands of food webs in these ecosystems. We also discovered new phages and viruses, which are infecting and potentially controlling relevant communities for the biogeochemical cycles, suggesting possible global implications of these viruses for the general maintenance of these extreme ecosystems.

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The RGF1-PLT2 regulatory network maintains primary root meristem activity in low phosphate environments.

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Molecular, biochemical and genetic approaches have revealed the identity and mechanistic interactions between many genes required for the patterning and maintenance of root meristems. Plant growth regulators, particularly auxins have been placed at the centre of meristem maintenance control. However, these are just second messengers. Direct mechanistic links between the environmental and metabolic cues that underpin homeostasis and responsivity in patterning and growth-regulatory mechanisms underpinning stem and transient-amplifying cell activity remain poorly understood.

We have used genetic and molecular approaches to identify the meristem-sustaining RGF1-PLT2 regulatory network as a key target of pathways that enable a marked but temporally limited extension of root growth and foraging capacity when experiencing phosphate limitation. We show how the sulfotransferase activity of tyrosyl protein sulfo-transferase (TPST) on RGF1 and PSK is crucial for extended meristem maintenance to allow foraging for phosphate. But TPST not only regulates root traits by maintenance of the primary meristem, TPST also contributes to emergent root system traits, specifically by indirect regulation of the lateral root network and the spatial extent of the root system. We conclude that by maintaining stem and transient-amplifying cell homeostasis, the RGF1-PLT2 regulatory network underpins the sink strength of the primary root, which in turn tunes the distribution of growth activity across the root system and mediates environmental responsiveness to a key limiting nutrient, phosphate.

Studying the role of soil microorganisms in chickpea root system architecture regulation

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Root phenotyping is important to improve our understanding how root system architecture contributes to resource acquisition in plants. Root growth and root systems adapt to their environment; therefore, plants must grow in soil to provide meaningful information to breeders. Such analyses have previously been possible only with large capital investments and highly-trained operators, and therefore have been out of reach for most stakeholders; specifically, breeders in low-income countries. By contrast, large-scale root phenotyping in controlled conditions is required to identify root system architectures advantageous for desirable resilience and stress tolerance traits related to root systems.

We developed an engineering concept to solve this challenge based on the utilisation of commodity components, standardised, open source software and computer vision and machine learning approaches to put advanced expert tools into the hands of breeders in low-income countries. We are using the system to study the growth of chickpea plants (Cicer arietinum L.), which is an important food security crop in South Asia and Sub-Saharan Africa.

The system consists of three modules: the growth module, the imaging module and the analysis module. The first two modules are physically located on site, the third is on the cloud. The growth module is a simple, commodity component-based box to visualise and document plant root systems growing in soil (the mesocosm). The current setup allows ≥80% of the root system to be visualised. The imaging module is a dark box, with 5 Raspberry Pi devices and cameras and associated software to capture and perform initial processing of images. The posterwill focus on the utility of the data generated, and the use of these tools to address changes of root system architecture in response to interactions with Rhizobia and nodulation.

Microbial communities composition and activity in different polyextreme environments in northern Chile

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The particular and extreme relief of northern Chile is recognized for the 15,000 m difference between the marine Atacama Trench in the Pacific Ocean (maximum depth 8,065 m) and the summit of the Llullaillaco volcano (6,723 m altitude) in the Andes, over a linear distance of less than 300 km. In general, these upland environments exhibit high solar radiation (the highest reported on Earth), fluctuating levels of salinity (dominated by NaCl), cold temperatures, aridity and high levels of minerals due to local volcanism (As, S, Li). This array of environmental conditions has important consequences for the specific biological communities inhabiting different environments. Microbial communities are in general dominated by Bacteria and Archaea. Interestingly, different studies report the presence of unique microbial communities in each of the studied aquatic systems and the presence of multiple bacterial phyla, including a high proportion of rare biosphere. Nevertheless, an important part of the microbial community still remains 'invisible' to modern sequencing techniques based on 16S rRNA gene and it is not yet clear the mechanisms driving diversification. Some systems are microbial dominated and microbial mats have an important trophic role. Here we report the results of a decade of microbial studies in different aquatic ecosystems including their functional role in biogeochemical cycles (C, N) highlighting both freshwater (Lago Chungará (4520 masl) and Lago Llullaillaco (6170 masl)) and saline systems (Salar de Huasco (3800 masl) and Salar de Atacama (2500 masl)). Due to climate warming and anthropogenic intervention these unique environments are under risk and with them, their microbial diversity.

De novo transcriptome assembly and expression analysis provide insights into the molecular basis of heat response in Nothofagus pumilio

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Nothofagus pumilio is an endemic tree of the southern temperate forests of Argentina and Chile. It constitutes a key ecological species, distributed across a wide latitudinal (36 to 55°S) and altitudinal range. Moreover, its wood is appreciated and used due to its high quality. Global Climate Change (GCC) predictions for Patagonia indicate a rise in the daily mean temperatures, which will affect the ecological niches of native species, with tremendous ecological and societal implications. The aim of this study was to gain insight into stress responses induced by heat in N. pumilio, through the generation the first transcriptomic resource with annotations for this species, and the study of changes in protein-coding transcripts in response to heat through differential expression analysis. mRNA libraries from whole leaves sampled after two days at 20°C and 34°C were prepared and sequenced in an ionTorrent Proton device. De novo assembly yielded 81,761 contigs, with a high read utilization rate (93%) and more than 95% Core Eukaryotic Genes present. This constitutes the most complete -omic resource for Nothofagus as of today. Annotation against Arabidopsis thaliana proteome resulted in 36,371 annotated contigs. A total of 1081 contigs were differentially expressed between temperatures according to DESeq software. Among these, at 34°C we observed genes involded in flavonoid and phenylpropanoid biosynthesis, de novo protein folding, and proteasome activity among others. This work provides the first transcriptome data and global profiles of gene expression in N. pumilio, generating a substantial contribution to research related with stress responses of forestry species. The differentially expressed genes identified in this study may provide genetic resources for the improvement of growth and production in N. pumilio and other tree species of economic value in a context of GCC.

Bacterial communities associated to Chilean altiplanic native plants from the Andean grasslands soils

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The rhizosphere is considered the primary place for soil microbiome differentiation and plays a key role in plant survival, especially for those subjected to environmental stress. Using high-throughput sequencing of the 16S rRNA gene, we analyzed and compared soil bacterial communities associated to four of the most abundant high altitude native plant species of the Chilean Andean grasslands. We examined three soil compartments: the rhizosphere (bacteria firmly attached to the roots), the rhizosphere-surrounding soil (bacteria loosely attached to the roots) and the bulk soil (plant-free soil). The rhizosphere microbiome was in all cases the least diverse, exposing that the bulk soil was a more complex environment. Taxonomic analysis revealed an abrupt change between the rhizosphere and the rest of the non-rhizospheric soils. Thus, while rhizobacterial communities were enriched in Proteobacteria (mainly Alphaproteobacteria), Actinobacteria (mostly Blastocatellia) dominated in bulk soils. Finally, we detected certain taxonomic rhizosphere signatures, which could be attributed to a particular genotype. Overall, our results indicate that the thin layer of soil surrounding the roots constitute a distinctive soil environment. This study contributes to expand the knowledge about soil bacterial communities in the Chilean highlands and takes the first step to understand the processes that might lead to the rhizosphere differentiation in that area.

Natural genetic variation as a tool to study root architecture in response to osmotic and salt stress

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Plants being sessile organisms are inevitably affected by multiple environmental factors including salt and drought stress, which are two of the biggest abiotic stresses in agriculture. Plants have the ability to modulate the root architecture upon either one of these stresses. These responses depends on the stress itself and a complex hormonal crosstalk between ABA, cytokinin and auxin among others. Thus, we analysed the root phenotypic responses to salt and drought stress amongst 56 different Arabidopsis thaliana ecotypes. We characterize the primary root length, number of lateral roots and lateral root density in all the ecotypes. We have found an array of differences in root phenotypes amongst ecotypes, from highly sensitive to resistant in either stresses. We identify a differential response in the different ecotypes in the primary root and lateral roots. Moreover, the response to salt stress was somehow different to the osmotic stress, thus ecotypes resistant to salt stress did not have an altered response to osmotic stress. Taking advantage of the availability of all the genomes of the different ecotypes of A. thaliana and previous phenotypic root characterization in response to ABA, cytokinin and auxin, we will perform genome wide association studies which may lead to uncovering significant association amongst ecotypes and perhaps characterize gene families and their role in stress responses.

Cold-shock genes in the adaptation of Antarctic Pseudomonas to different temperature conditions

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Antarctica is one of the harshest and most pristine permanently cold ecosystems in the world where cold-adapted microorganisms thrive. Yet, little is known on how these extremophiles cope with low temperatures. Regarding this, proteomic studies from cold-adapted bacteria have drawn a parallel between the proteins overproduced during growth under sustained cold temperatures with the long recognized “cold-inducible proteins” transiently over-produced during the cold-shock response in mesophilic bacteria.

Our recent work aimed to assess the expression of the seven cold-shock genes (cspA to G) retrieved from a draft genome of the psychrotolerant Antarctic bacterium Pseudomonas sp. strain AU10 with a RT-qPCR approach in mid-log cultures incubated at 4 °C and 30 °C, and in cultures subjected to a cold-shock (from 30 °C to 4 °C, 75 min). Also, we analyzed the expression stability of eight candidate reference genes for the proper normalization of RT-qPCR data. Four genes were validated as suitable reference genes, but only recA with ftsZ were selected for normalization. From the seven csp paralogs, only cspA, cspB, cspC, and cspG showed significant differences in expression in the conditions assayed. Among them, only cspA was over-expressed during cold-shock when compared with the 30 °C growth condition (4 fold), but its expression was not transient since the largest expression levels were observed at sustained cold temperatures (7 fold at 4 °C compared with 30 °C). In addition, cspB and cspC were only over-expressed when cells grew at 4 °C, but in a lesser extent. Interestingly, cspG showed the opposite expression behavior, being 18 times over-expressed at 30 °C compared with 4 °C growth temperature. Our results suggest that Antarctic Pseudomonas may have adapted the regulation of different csp genes to cope with the extreme temperature conditions found in the Antarctic continent.

Nutrient cycling at the extreme; the role of UV radiation on litter mass losses.

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Microbial communities play key roles in maintaining multiple ecosystem functions like nutrient cycling. Identifying which factors regulate diversity and community composition is key to understanding ecosystem functioning. At local scales vegetation type as well as soil moisture, pH, and nutrient availability are determinants of soil microbial communities composition. In some resource-limited ecosystems, ultraviolet radiation not only regulates soil microbial composition, but also leads to shifts in microbial communities with concomitant effects on nutrient cycling via reduced rates of litter decomposition. We present results of a series of litter decomposition experiments along a UV-radiation gradient in Chile and show how differential exposure to UV-radiation alters litter decomposition through different mechanisms. At the highest UV-radiation site litter mass loss was decoupled from nitrogen dynamics and microbial extracellular enzyme activity was very low. UV exposure decreased litter lignin and hemicellulose fractions, suggesting that photodegradation plays a key role on nutrient cycling this site. Finally, we found significant changes in fungal-to-bacterial ratios as a function of UV exposure. In contrast, at the lowest UV-radiation site litter mass loss was correlated to both, nitrogen dynamics and photodegradation. Indeed we found significant litter mass losses as a function of UV exposure and microbial enzyme activity. In these sites fungal-to-bacterial ratios did not change, this may indicate the existence of UV-radiation threshold above which relative abundances within microbial communities do not change significantly. Our results suggest that, to an extent, UV-radiation could actually “facilitate” microbial activity and litter decomposition. Therefore, soil microbial communities may be adapted to some levels of UV-radiation. However, in some of our sites UV radiation is extremely high and seems to alter soil microbial communities. Results are discussed in light of the extremely high levels of UV-radiation often recorded in Chilean ecosystems and its potential impact on carbon and nutrient cycles.

Top-down and bottom-up modelling approaches to link metabolism and plant performance

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A key goal for plant sciences is to understand how metabolism participates in plant performance. Metabolism, which is engine of the construction and maintenance of biomass, is indeed at the heart of many trade-offs between growth and defence against biotic and abiotic stresses. However, metabolism is extremely complex, with its many intricate pathways that undergo significant reprogramming throughout the development of plant organs, making it difficult to identify the mechanisms responsible for these trade-offs. Systems biology, which can be defined as an iterative theory and experimentation approach, represents a great opportunity to deal with this complexity. On the one hand, newly emerging top-down approaches have been shown to provide highly predictive statistical models linking metabolome and plant performance. On the other hand, mechanistic modelling of metabolism has never been so easy thanks to significant advances in analytics and computing power.

The use of synthetic biology to uncover basic principles of circadian oscillators: from temperature compensation to the processing of environmental cues

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Circadian rhythms are self-autonomous rhythms generated at the cellular level with a period close to 24 hours in constant conditions. They are present in diverse organism, from bacteria to mammals. Although they appeared independently throughout evolution, the molecular bases governing them are conserved. The central circadian oscillator is composed of a transcriptional-translational feedback loop (TTFL), where the negative element directly inhibits the positive element, which promotes its transcription.

In Neurospora crassa the negative element is the protein FREQUENCY, encoded by the gene frq, and the positive element the White Collar Complex (WCC). In addition, the rhythmic information is transmitted through a transcriptional cascade causing the rhythmic expression of genes controlled by the clock (ccgs).

To improve our knowledge in the genetic topological plasticity of the clock, we used transcriptional rewiring technics, a synthetic biology approach, to generate new circuitry topologies of the central clock. We generated Hybrid Oscillators (HOs) changing the promoter of frq with the promoter of a ccg and evaluated the capacity of the system to generate and sustain rhythms even when the TTFL architecture is modified. Using this approach, we demonstrated the ability of the core oscillator to sustain rhythms, even when the evolutionary conserved core oscillator is dramatically modified. The HO with better performance displays circadian oscillations that are temperature compensated. Interestingly, the light response and phase determination are different in the HO. Finally, we confirmed that this HO has an extended functional TTFL architecture where at least five additional transcriptional regulators are now part of the core circadian oscillator.

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New tricks for old dogs - domesticated transposases as components of novel plant chromatin modifying complexes

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Transposons comprise a large fraction of plant genomes and are intimately linked with epigenetic regulation by their hosts. Typically hosts monitor tranposon activity by producing small RNAs with homology to transposon transcripts leading to the recruitment of repressive DNA and histone modifications. However, transposons are not merely passive victims, but can encode proteins that inhibit the host surveillance mechanism. In some cases these transposases have become domesticated, and may serve roles in host gene regulation or even in host tranposon regulation. We identified the Arabidopsis ALP proteins genetically, as suppressors of Polycomb group (PcG) mutant phenotypes, suggesting that they act by antagonising PcG action . The PcG were identified as key regulators of developmental patterning in animals and plants, although more recently they have also been linked to transposon silencing. The PcG proteins repress their target genes, in part by directing histone methylation through the activity of a well conserved enzyme complex, the Polycomb Repressive Complex 2 (PRC2). Suprisingly we found that the ALP proteins encode domesticated transposases distantly related to those of Harbinger class transposons. Using a proteomics approach we found that the ALP proteins are components of a novel, variant PRC2 complex. We and others have recently found that several other domesticated Harbinger transposases are also components of chromatin modifying complexes in plants. Currently we are conducting a range of biochemical and genomic assays to test whether the ALP transposases alter the enzyme activity or targetting of the PRC2 histone methyltransferases and to determine whether they have a role in host gene or transposon regulation.

The Ancient Transcription Factor ZHOUPI Controls development of a novel water transport tissue in liverworts

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When land plants evolved from aquatic ancestors, various key innovations were necessary for survival in a more arid environment. These include development of a waterproof cuticle, presence of gas exchange pores such as stomata, production of a multicellular embryo able to produce numerous spores from a single fertilisation event, and efficient water transport systems. In Arabidopsis, the seed-specific gene ZHOUPI (ZOU) regulates several of these pathways, for example it controls cuticle formation in the embryo, and cell separation and death of the endosperm tissue to allow growth of the embryo. ZOU protein interacts with another bHLH transcription factor ICE1, which is expressed more broadly and required for stomatal formation. Since the ZOU and ICE1 genes are ancient and found in plants lacking seed or even stomata, this raises the question as to their role in early land plants. We are using the model liverwort to find out the role of ZOU and ICE genes in this early diverging land plant lineage,. Using yeast two hybrid and complementation assays we find that the molecular activity of ZOU and ICE genes is conserved between Arabidopsis and Marchantia. To determine MpZOU biological function in Marchantia we characterised the expression pattern of the Marchantia ZOU and ICE1 orthologues, inactivated them using CRISPR/Cas9 genome editing, and mis expressed them. We found that in additon to a role in cuticle formation, ZOU controls the development of a novel, external water conduction tissue (pegged rhizoids) characterised by peg like cell wall thickenings and programmed cell death. We recently conducted RNA seq to identify ZOU/ICE targets in pegged rhizoid formation and test whether there are any common pathways for cuticle and peg formation. We conclude that the ZOU/ICE1 partnership was likely present in earliest land plants and important for several adaptations to life on land.

Hunting temperate viruses in Chilean Patagonia hot springs microbial mats

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Viral infections can vary from productive to lysogenic dependent on multiple factors such as virus genetics, host genetics, virus host ratio, host physiological state and obviously environmental conditions. Even when lysogenic to lytic viral switch is central to viral ecology, temperate viruses have been much less studied than their lytic counterparts. Inherent difficulty issues with estimating the rates of lysogeny in natural viral communities have obscured the attempts to assess these populations.

Here we used a multi-omic approach to study lytic and lysogenic viral communities in highly under-sampled environments as there are hot spring phototrophic microbial mats. Metagenome assembled genomes (MAGs) from Porcelana hot spring microbial mats (Northern Patagonia, Chile) were interrogated for the presence of integrated temperate viruses. Viral metagenomes of natural and mitomicyn C treated/induced microbial mats were analyzed to study differential abundance of viral genomes and proteins (functions), as well as community parameters such as α and β diversities. Our results suggest that lysogenic and lytic viral populations are strongly associated to specific hosts and consequently to environmental features that determines the host community structure. Furthermore, dominant bacterial taxa showed the presence of abundant CRISPR-Cas systems with spacers against the most abundant and diverse viral populations, allowing us to propose that lytic lifestyle is prevalent in hot springs phototrophic mat and that lytic viruses and their hosts were under an active diversification through co-evolutive forces.

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The role of Serendipita indica as a modulator of K+ acquisition in Arabidopsis thaliana

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The interaction of plants with symbiotic fungi enhances their acquisition of nutrients, particularly when they are scarce in the environment. This benefit could be achieved by direct uptake and apoplastic release by the fungus or through the modulation of plant transport systems in the root. In Arabidopsis thaliana, K+ absorption depends on the Shaker-like channel AtAKT1 at moderate to high concentrations (over 0,1 mM K+) and the transporter AtHAK5, whose role becomes more important at low K+ concentrations (under 0,1 mM). They depend on different regulation mechanisms, the first being modulated at the protein level and the second mainly through overexpression under K+ deficiency. Recent transcriptomic analyses have highlighted that the symbiosis of Arabidopsis thaliana with Serendipita indica upregulates AtHAK5, together with some Ca2+-related signaling proteins, belonging to the CBL and CIPK families, that could modulate the function of both AtHAK5 and AtAKT1 through phosphorylation. Our current goal is to identify the molecular interactions between CBL and CIPK candidates with both transport systems to understand the mechanisms triggered by Serendipita indica that could lead to an improved plant K+ nutrition.

Phylogenomics and Systems Biology approaches reveal conserved adaptive processes in Atacama Desert plants

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The Atacama Desert in Chile is the oldest and driest desert on Earth. Despite being one of the harshest environments in the world, plants have colonized and adapted to its extreme abiotic conditions. In order to identify genes underlying the adaptive traits of these “extremophile” plants, we developed a systems biology and phylogenomics pipeline that uses transcriptome data to annotate genes, determine evolutionary relationships, identify orthologues, and measure natural selection. Our approach identifies the evolutionary divergence of “extremophile” Atacama plants by comparing their sequences to publicly available phylogenetically-related (“sister”) species, which are not adapted to Atacama’s extreme conditions. We identified, collected, and sequenced the transcriptome of 32 plant species within an altitudinal transect that spans the limits for life in Atacama. All these species are seed plants, with a preponderance of Angiosperms. An overall set of 70 species (32 from Atacama, 32 sisters, and 6 model plants) was processed, generating nearly 1.7 million predicted proteins and over 30 thousand orthologue families. The resulting phylogenomic tree contained twenty nodes that account for the divergence of extremophile Atacama plants from their non-Atacama sister species. We identified thousands of genes that provide support for independent origins of environmental adaptation. We identified a subset of genes that gave recurring support (independent origins). This subset was enriched ($p\text{-value} < 0.05$) in processes related to response to stress, response to radiation, photosynthesis, and nitrogen compound metabolic processes, among others. Data were further used to identify key genes involved in adaptation to marginal soils. Functional characterization of key candidate genes is ongoing in selected plant model systems.

Endophytic fungi and their role in the induction of transcription factors in response to ABA-dependent and independent under drought stress in Colobanthus quitensis

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Symbiosis is considered one of the successful mechanisms that allows plants to improve their ability to tolerate different types of stress. This interaction has been described in Colobanthus quitensis, a vascular plant that inhabits environments as limiting as Antarctica, which stands out for its extreme dryness. Among the mechanisms that plants have to tolerate water stress conditions, is the induction of the pathway dependent and independent of ABA, being key in the induction of these pathways, the expression of transcription factors (TFs). However, there is no information on the role of endophytes (E) on the expression of TFs involved in the responses under water stress conditions. In these work, we evaluate the induction of TFs-mediated drought-responsive genes of the dependent (ABF and MYC2) and independent (DREB1 and DREB2) pathway of ABA, in plants with endophytic fungi (E+) and without endophytic fungi (E-) of Colobanthus quitensis, as well as biochemical and physiological responses, under condition of hydric stress, which represents 50% of water availability respect to the current availability. The results of Efficiency of Photosystem II (Fv/Fm) and Level of membrane lipid peroxidation (TBARS) both, a stress proxy, showed significant differences between individuals E+ and E-, observing in individuals E-, higher levels of TBARS and lower Fv/Fm. In addition, these differences were even more evident under condition W- (more water limiting), compared to condition W (current water availability). Regarding the expression of genes, only significant difference was observed between individuals E+ and E-; however, no difference was observed between the induction of the pathways. Furthermore, under condition W- the relative expression levels were lower, compared to condition W. In conclusions, the induction of TFs would be mediated by the presence of endophytes, however, there would be no inclination to induce one path over the other.

Lessons from desert endophytic bacteria to enhance plant growth and crop yield in extreme environments

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We currently have more than 1 billion of undernourished people worldwide. This situation is not going to get better, unless we can increase food production by 50 % in the next decades. However, drought, salt and heat stress make up to more than 60 % of crop losses, so that improving abiotic stress resistance is one of the most important factors in securing food production. In the DARWIN21 project (http://www.darwin21.org), we isolate and employ endophytic desert microbes to enhance stress tolerance of crops in open and covered desert agriculture. I will present the results from our molecular genetic approaches to uncover the molecular processes of these beneficial plant-microbe interactions. Our work allowed the identification of highly conserved bacterial metabolites that induce plant tolerance to multiple abiotic stresses. Our results provide an immediately applicable low cost strategy to achieve the 2050 food production aims in an organic and sustainable manner

Upcycling metals with bacteria

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Synthetic Biology has given us the tools to engineer bacteria for the repurposing of waste streams and the chance to move towards a more sustainable and circular economy. A limiting factor in using waste in this way is the presence of minor amounts of metal contaminants, which inhibit bioprocesses and kill bioremediating microorganisms. There are, however, bacteria that are tolerant to high concentrations of metal ions due to a resistance mechanism that involves metal reduction and nanoparticle formation, and they may provide the key to including inorganic components within this alternative, biologically-catalysed cycle. These microorganisms have the potential to manufacture metallic nanoparticles, irrespective of the source of metal cations, and provide us with new particles with novel functions. To exploit this we are identifying and optimising genetic elements with an aim to increase nanoparticle production and control nanoparticle size and homogeneity; in effect standardising nanoparticle samples by using biology. Whilst developing this process we are exploring its application in the treatment of contaminated waste, water and land. To demonstrate these applications we are working to remove copper from whisky distillery by-products, examining how we can recover valuable metals from spent lithium ion batteries, and aiming to financially incentivise land decontamination by combining phytoremediation, bioprocessing and bacterial nanoparticle synthesis.

The T1 generation tobacco adaptation research to cold stress that expresses the desC gen

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The study of mechanisms of plant resistance to abiotic stress is one of the most important trends at present. In particular, much attention is paid to the adaptation of plants to lower temperatures and frosts. One of the mechanisms that reduce the sensitivity of plants to hypothermic stress is to increase the viscosity of membranes, which is ensured by increasing the proportion of unsaturated fatty acids in their composition. Desaturases are enzymes that promote the formation of double bonds in fatty acids and thus convert them from saturated to unsaturated. T1 generation tobacco plants that experiments with the desC gene encoding Δ9-acyl-lipid desaturase of cyanobacteria Synechococcus vulcanus were used for research. To determine the resistance of plants to stress of reduced temperatures and frosts, the plants were exposed to cold stress 0°C - 20 minutes, then -5°C - 80 min. How control was the use of wild-type tobacco plants and transgenic tobacco that expresses the gfp::licBM3 gen. The loss of electrolytes, the level of accumulation of malondialdehyde, the activity of the superoxide dismutase enzyme was checked after stress. Less damage was detected in tobacco plants with a desC gene relative to control.

Understanding modern and past dynamics of the Nitrogen cycle in the central Atacama Desert

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Revealing links between biogeochemical cycles and climate are fundamental for understanding the functioning of the earth system. We have been working on understanding the modern and past nitrogen cycle in the hyperarid central Atacama Desert with particular emphasis on N using stable isotope analyses. Over our 4500 m gradient, we find that δ15N tracks moisture as expected but only where plant cover is >10%. Below this amount, δ15N values shift towards lighter values, decreasing until reaching the coast where values are again much higher (>20 ‰). A 50,000 yr record of δ15N values from individually 14C-dated fossil rodent middens reveals that during the last glacial period, δ15N values were 20 ‰ higher compared to present values, with strong oscillations in δ15N values (7 – 24 ‰) as regional temperatures began to increase at the onset of the current interglacial. Changes in δ15N over the last 17,000 years are mostly linked with precipitation and we show that the %extralocal flora (a proxy for rainfall) correlates with δ15N. Yet, this does not explain the large 8 ‰ shift at the interglacial onset or the extremely high values seen in full glacial middens. Furthermore, our midden δ15N record inversely tracks a marine sediment δ15N record off coastal northern Chile, which also reveals a large shift towards positive δ15N values at 17 ka marking the onset of ocean stratification and the development of an intense oxygen minimum zone. Long-distance nitrogen transport and fertilization of terrestrial ecosystems by marine N ventilation could in part explain the large N shift seen in our fossil middens as oxygen minimum zones began releasing large quantities of N2O through denitrification. These biogeochemical changes reveal a dynamic N cycle linked to both marine and terrestrial processes.

Response of nitrogen nutrition to challenging environment in Arabidopsis

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Because of the dramatic effects of nitrogen on growth and development, plants have evolved to adapt to a challenging environment. At the level of root nitrate uptake it results in a highly integrated process, which is determined by nitrate availability, the nitrogen demand of the whole plant and the carbon produced by photosynthesis. This last regulation enables plants to adjust nitrogen acquisition by roots and carbon acquisition by shoots, which is necessary for the incorporation of inorganic nitrogen into amino acids and proteins. The results we obtained revealed that the control of root nitrate uptake by carbon signalling depends on a signal coming from the Oxidative Pentose Phosphate Pathway (OPPP). Interestingly, OPPP is a major source of NADPH and is critical to maintain redox balance under stress situation. This led to the hypothesis of an OPPP-related redox regulation of root nitrate uptake. This hypothesis is supported by recent data showing that root nitrate transporters in Arabidopsis are also regulated by the redox status of the plant. Furthermore, preliminary data indicate that the signalling mechanism is linked to the first step of the OPPP, coded by G6PDH and involved in the production of NADPH. Finally, it seems that oxidative stress could be a more general hidden player in the regulation of nitrogen nutrition. Indeed, recent results suggest that at least part of the regulation of root nitrate transporters by N signaling is also link to the redox status of the plant. In this context, further developments, in collaboration with the group of Yves Gibon in Bordeaux and Rodrigo Gutierrez in Chile, will concern the implication of such signalling pathways for plants adaptation to extreme environment in the Atacama desert.

Biotechnological and bioinformatic advances in conifer research

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Conifers are species with a great economic and ecological value that are present in many different landscapes. The current technological and methodological advances allow a better understanding of the conifer's development and adaptation, but also these advances can be used to solve practical problems in forestry with important applications at industrial level. In our laboratory, we are developing a variety of genomic resources in maritime pine (Pinus pinaster Aiton), one of the best experimental models for genetic and molecular studies in conifers [1, 2]. The adaptation and response of trees to environmental cues have been investigated by performing transcriptomic and metabolomic profiling over a year in 25-year-old pines using the latest biotechnological and bioinformatic advances [3]. RNA-Seq studies are being used to determine changes in the transcriptome in response to different nitrogen nutrition conditions, during embryonic development and gene expression atlas in the different tissues from seedlings [4]. The availability of a first draft of the Pinus pinaster genome will be a key tool to identify and annotate long and small non coding RNAs associated to nutritional changes. New platforms of third generation sequencing will have a great technological impact in the characterization of conifer megagenomes. We are currently using the Oxford Nanopore technology, MinION device, for the detection of post-transcriptional modifications, nuclear, mitochondrial and plastidial genome sequencing, as well as for metagenomics studies.

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Plant-microbiome interactions modify the co-occurrence patterns of soil bacterial communities along an altitudinal gradient in the Andes of the Atacama Desert.

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Co-occurrence networks have been used to examine putative ecological interactions among microbial OTUs or ‘nodes’, as well as their associations to physicochemical and nutritional variables. These network associations provide a graphic visualization of potential relationships between microorganisms (positive and negative interactions, representing co-presences and mutual exclusions, respectively), providing a starting point for further investigations on the ecological mechanisms underlying the establishment and maintenance of microbial structures. Here, we analyzed the bacterium-bacterium interactions from six microbial co-occurrence networks representing bacterial soil communities from three vegetation zones along an altitudinal gradient in the Andes of the Atacama Desert: the “Andean steppe” between 4,500–4,000 m a.s.l; the “puna” zone, between 4,000–3,300 m a.s.l; and the lowermost vegetation belt, the “prepuna”, from 3,300 to 2,500 m a.s.l., in two different compartments according to their proximity to the roots: the rhizosphere-surrounding soil (bacteria loosely attached to the roots; “RSS”), and the bulk soil (plant-free soil, “BS”). Analysis of BS and RSS co-occurrence networks showed that the most connected OTUs from the six networks, which are often proposed to be critical components of bacterial community for network stability, were not dominant in abundance, indicating that some of the low abundant but highly connected ‘species’ may play a keystone role in network dynamical properties. Also, RSS communities of the prepune and steppe plants showed a clear bias toward positive interactions in comparison to BS microbiome, which could be the result of functional interdependencies among taxa of soil bacterial communities associated to plants growing under the most extreme conditions of the altitudinal gradient. We believe that our research program is essential to understand the relationship of plant-soil microbiome, especially for plant survival under extreme environmental stress, and to develop biotechnologies that could be used to improve crops in an era of climate change.

Bioprospecting of bioactive compounds from rhizosphere actinomycetes of Lupinus oreophilus in the Atacama Desert

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The World Health Organization has announced that antimicrobial resistance has expanded faster than the incorporation of new antibiotics, which will have a major impact on health and the economy worldwide. Due to the high rate of rediscovery of known compounds, the search for potential bioactive compounds from unexplored environments is required. Although rhizosphere actinobacteria have been recognized as a promising biotechnological source of new bioactive compounds with plant growth-promoting and antimicrobial activities, few have been studied from extreme environments. In this work, actinobacteria isolated from rhizosphere of Lupino (Lupinus oreophilus) from the Atacama Desert were characterized by bioassay, molecular techniques and enzymatic tests. A total of 139 actinobacteria were selectively isolated using different pre-treatments and culture media. Of the total, 74 were subjected to antimicrobial tests against a set of bacterial and fungal pathogens, and to detection of biosynthetic genes of specialised metabolites (PKS-I, PKS-II, NRPS and AHBA) by PCR. Sixty-two percent of the isolates showed potential to produce bioactive compounds. Based on 16S rRNA sequences analysis, the isolates were taxonomically grouped with the genera Streptomyces or Micromonospora. The analysis by BOX-PCR fingerprinting revealed genetic variations among the isolates. Furthermore, the production of industrially important hydrolytic enzymes such as amylase, cellulase, chitinase and protease was observed. Overall, these results indicate that rhizosphere actinobacteria from the Lupino plant represented an important source of bioactive compounds with antibacterial, antifungal and enzymatic properties.

Key words: actinobacteria; unexplored extreme rhizosphere; screening bioactive compounds; antimicrobial and enzymatic activity.

Experimental evolution of Saccharomyces eubayanus in ethanol improve its fermentative capacity

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The Lager beer yeast S. pastorianus is a hybrid between S. cerevisiae and the cryotolerant yeast S. eubayanus. The latest was recently found in Patagonia, however only a limited number of studies have evaluated its potential for beer production. Recently, our group isolated hundreds of S. eubayanus strains from west Patagonia (Chilean territory), showing a broad range of fermentative capacities and low ethanol production. To improve their fermentative capacity and ethanol tolerance, we adopted an experimental evolution strategy. Ten genetically identical groups combining 30 different strains from different isolation localities (Villarrica, Puyehue and Coyhaique) were incubated during 260 generations in a restrictive ethanol containing media (9% v/v). After 50 generations a sustained increase on ethanol tolerance was detected, showing a maximum fitness after 150 generations. Whole-genome sequencing of three ethanol-evolved lines showed that a single genetic background prevailed after 260 generations, while the control lines (evolved solely under glucose) showed different backgrounds at the end of the experimental evolution assay. Moreover, 164 new mutations were detected in the ethanol evolved lines, likely explaining the adaptation to ethanol. Additionally, the best resulting ethanol evolved strains showed a 143% increase in their fermentation capacity in beer wort (similar to commercial lager strains). This represents the first step to obtain genetically improved wild yeasts for produce novel beers with unique organoleptic characteristics.

PS-Plant: tracking plant growth traits and leaf movement patterns with a novel low-cost 3D- imaging system

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Image-based phenotyping is a powerful tool for tracking plant dynamic growth, allowing the evaluation of plant performance under different environment and/or genetic backgrounds. Despite the increasing availability of different plant phenotyping tools, the field continues to evolve, and several outstanding issues still need to be addressed, including accuracy, robustness, affordability and ease-of-use. Here we present PS-Plant, a novel three-dimensional (3D) phenotyping system based on the photometric stereo technique. PS-Plant can estimate surface inclination angles for each pixel in an image, allowing plant shape reconstruction in 3D, which generates more accurate projected area estimations than two-dimensional (2D) approaches and provides the quantification of leaf angle estimations. PS-Plant is relatively low-cost (c.a. £2,000), highly portable and can be adapted for different plant growth environments. Detailed validation analysis of the system using know-sized objects and Arabidopsis plants produced comparable results to expensive state-of-the-art 3D plant phenotyping systems in terms of area and angle estimations. We then used PS-Plant with near-infrared (940 nm) LEDs as illumination sources to track the growth of plant phenotypes under different combinations of light and temperature throughout the diel cycle. To automate the segmentation and extraction of basic growth features, we developed bespoke machine learning models combined with post-processing computer vision algorithms. This allowed us to extract phenotypic differences for the different treatments, such as total rosette and individual leaf areas, rosette compactness, rosette diameter, leaf movement patterns and individual leaf architecture. Such features can be used, for example, to predict plant resilience to stress. With PS-Plant we hope to deliver an adaptable and low-maintenance platform to ensure maximum accessibility to the research community, particularly for low-income or developing countries.

The BST family: incorporating thylakoidal components of the Chlamydomonas CO2-concentration mechanism into higher plants

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Food security is a pressing global issue that must be addressed if we are to meet the demands of our growing population. Photosynthetic efficiency and growth in most plants (i.e. C3 plants) are restricted by the poor catalytic characteristics of the CO2 assimilating enzyme Rubisco. Several photosynthetic organisms have evolved CO2-concentrating mechanisms (CCMs) to overcome the limitations of Rubisco. Introducing a CCM into a C3 crop (e.g. rice or wheat) is predicted to increase photosynthesis by up to 60%. We aim to engineer a single cell CCM based on the green alga Chlamydomonas reinhardtii into higher plants. Algal CCMs contain a unique organelle within the chloroplast called the pyrenoid, wherein Rubisco is localised when the CCM is active. Rubisco in the pyrenoid is believed to be fed CO2 via a series of bicarbonate pumps in the traversing thylakoid. This process increases the concentration of CO2 in the pyrenoid, leading to high rates of CO2 assimilation. It is still unclear how CO2 is initially pumped into the thylakoid lumen. Recently three new bestrophin-like proteins (BSTs) have been identified as potential candidates involved in lumenal CO2 transport and pyrenoid assembly. All three BST proteins (BST1, BST2 and BST3) are expressed under low CO2 conditions and localise at the periphery of the pyrenoid. We have successfully expressed GFP-fusion proteins for each BST in planta and have confirmed they localise to the chloroplast in Nicotiana benthamiana. The BST family could play an important role in our efforts to build the pyrenoid in a higher plant chloroplast.

Recent advances in introducing an algal CO2-concentrating mechanism into higher plants.

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Meeting the food demands of the rising global population is one of the most pressing challenges for Plant Science. Much research is focused on overcoming the limitations of C3 photosynthesis, which is the most common form of CO2 assimilation in higher plants, including critical staple crops. Unlike C3 plants, many photosynthetic organisms have evolved CO2-concentrating mechanisms (CCMs) that actively increase CO2 concentrations near the primary carboxylase enzyme, Rubisco, thus enhancing the rate of CO2 assimilation and suppressing photorespiration. Eukaryotic microalgae, such as Chlamydomonas reinhardtii, possess highly efficient biophysical CCMs that involve HCO3- pumps to elevate CO2 in the chloroplast and mechanisms to constrain CO2 leakage, and the aggregation of Rubisco in a fascinating organelle called the pyrenoid. I will discuss current work towards understanding how the pyrenoid functions and progress towards building a biophysical CCM in the model plant Arabidopsis, with the goal of enhancing photosynthesis and potentially improving productivity in C3 crops.

CyanoGate: A Golden Gate modular cloning suite for engineering cyanobacteria based on the plant MoClo syntax

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Cyanobacteria are ancient photoautotrophic prokaryotes that are considered to be the ancestral source of chloroplasts in higher plants. The ability to synthesise complex molecules using captured light energy and fixed atmospheric carbon dioxide has made cyanobacteria a promising platform for the renewable production of high value chemicals. Several new tools and parts are currently being developed for cyanobacteria to advance metabolic engineering to levels commensurate with other model cell factories (e.g. yeast, E. coli). We have developed a cloning system which includes a suite of new vectors and modular parts called CyanoGate, which is compatible with the syntax of the Golden Gate Modular Cloning (MoClo) Toolbox for plants. Here we present 33 synthetic promoters and 5 native promotors, one new origin of replication, transformation plasmids for chromosomal integration or self-replication, and CRISPR interference tools for gene repression. We have characterised these parts in two separate cyanobacterial species, Synechocystis sp. PCC 6803 and the more recently described fast-growing strain Synechococcus elongatus UTEX 2973. The system will soon be publicly available on Addgene and can be readily expanded to accommodate other standardised MoClo parts to accelerate the development of reliable synthetic biology tools for the cyanobacterial community.

Zinc Finger C2-C2 transcription factors: plant regulators to deal with to adverse environmental conditions

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In natural environments, plant species have to deal with multiple nutrient stress conditions simultaneously. During the last few years, research has been mainly focus the study of plant responses to specific stresses, and understanding of adaptation to multiple and combinative stress conditions is reduced, but indicative of complex interactions. In fact, several multi-omics analyses and functional studies of specific genes have discovered a crosstalk of signaling pathways for nutrient stress adaptation. We are interested in re-construct the underlying structure of the regulatory networks and signaling pathways involved in plant responses to limitation of water and nutrients, but also to discover the functional links between the genes.

In this work, we identify the roles of ZF1 and ZF3, Arabidopsis Zn Finger C2-C2 transcription factors in nitrate responses that were identified by forward genetic screenings. The zf3-1 KO mutant and knockdown zf1R lines exhibit nitrate-dependent root phenotypes, whereas ZF1 and ZF3 overexpression lines showed increased biomass and changed root architecture. In addition, transcriptomic analyses of overexpression lines indicated that both factors regulate the expression an important set of carbon and nitrogen regulated genes. Consistently, metabolite profiling revealed that the total amount of key nitrogen metabolites including glutamate and glutamine were higher in ZF1/3-overexpressing plants in N-sufficient and limiting conditions. By contrast, zf3-1 and zf1R mutants exhibited lower amounts of those metabolites. Interestingly, the overexpression of ZF1 and ZF3 genes in tomato modified amino acid and sugar content, improving biomass and yield. All these results identify ZF1 and ZF3 as important regulatory factors of the nitrate responses in Arabidopsis.

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Methane Cycle in Maritime Antarctic Lakes

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Cold environments are recognized as important contributors to methane biogeochemical cycle, however only limited knowledge is available on the contribution of Antarctic ecosystems to this process. With the aim of exploring the possible influence of Maritime Antarctica ecosystems on methane cycle, five lake sediments of King George Island (South Shetland Islands) were studied. This island harbors many freshwater lakes, which are frozen most of the year but during austral summer they could became a source of methane emission. A microcosm-based approach was used to investigate the effects of temperature and exogenous methanogenic substrates on methanogen activity. Methanotrophic activity was also determined. The Bacterial and Archaeal community structure was investigated by 16S rRNA gene sequencing (Illumina MiSeq platform). Endogenous methanogen activity (without substrate amendment) was negligible in all sediments except meltwater lake sediment, due to the low level of organic carbon available. Hydrogenotrophic methanogenesis were detected in all sediments (up to 8.5 µmol CH4.day-1.g-1) and prevailed over aceticlastic methanogenesis in each sediment. The range of temperatures assayed (2 to 15°C) had a strong influence on methanogenic activity (increase up to 70-fold at 15°C). Methanogenesis from methanol was insignificant below 15°C. Potential methanotrophic activity varied from 0.4 to 21 µmol CH4.day-1.g-1. The five studied sediments had different microbial community structure, according to the diversity indices. Proteobacteria, Bacteroidetes, Firmicutes and Acidobacteria predominated in all sediments (71-85% of all Bacteria sequences). Type I methanotrophs, particularly Methylobacter, dominated all communities. Methanoregula (hidrogenophilic) and Methanosaeta (aceticlastic) were the most abundant methanogens in all sediments (52-71% of all Archaea sequences) with the exception of meltwater lake sediment in which Methanosphaerula palustris predominated.

These results indicate that freshwater lake sediments of King George Island may not represent important potential reservoirs for methane emissions. Moreover, since most of the sediments showed potential methanotrophic activity methane emission could be mitigated.

Forging a causal chain around the circadian clock, from genome sequence to field traits

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The 24-hour circadian clock is a tractable biological process, where we are linking our understanding of molecular regulation from the lab to the field (Millar, Annu. Rev. Plant Biol., 2016; J. Exp. Bot. 2019). We built mechanistic, mathematical models of the clock gene circuit and its outputs between germination and flowering, and linked them in a Framework Model for Arabidopsis growth (Chew, Seaton et al. bioRxiv 2017; https://doi.org/10.1101/105437). Here, we move beyond this genotype-phenotype to smaller scale and to genome sequences. Uriel Urquiza used absolute clock RNA and protein levels (LHY, CCA1, PRR7, TOC1 copy numbers per cell) to replace the models' arbitrary units. Combining biophysical data and binding models, he shows how to use genome sequences as an input to predict timing function. The models were tested using novel NanoLUC reporter fusions in vivo. At larger scales, Argyris Zardilis (see poster; J. Exp. Bot. 2019) has linked upwards to the whole Arabidopsis lifecycle, across years and locations. These are steps towards a 'crops in silico' approach, starting from increasingly-available crop genome sequences and reaching up to field traits. In future, such models might test the full causal chain of Genetics, from genome sequence via gene circuit and plant phenotypes, to fitness, selection of sequence variants and hence evolution of the genome sequence.

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A Multi-Model Framework for The Arabidopsis Life Cycle

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The Framework Model (FM) [1] provides a bridge in the genotype-phenotype gap with a mechanistic representation of Arabidopsis vegetative growth starting from the circadian clock, linking cellular to organismal processes. Can we go a step further, to connect organismal phenotype to eco-physiological outcomes, in other words to evolutionary adaptation? The FM only represented the vegetative stage, and was calibrated to lab growth conditions. For any meaningful ecological experiments we need natural environmental conditions, the whole life cycle and a means to represent plant populations. Here we present an extension to the FM that addresses the above problems and allows the study of ecological outcomes starting from genetic and (natural) environmental inputs [2]. First, the original FM is simplified, creating the FM-lite model. This is then adapted for natural environmental conditions, and finally extended with seed maturation and reproductive growth models that we refactored from the literature, creating the FM-life model. We present representative simulations of plant populations over decades, showing ecological outcomes from different location (environment) / genotype combinations (G x E). We envision this to be a framework where the constituent models can be replaced or extended to facilitate further research, for example, representing selection in the population.

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Being FAIR and Open while being more Productive

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Open research, data sharing and data re-use have become a priority for publicly- and charity-funded research. In particular, principles of Findable, Accessible, Interoperable and Re-usable (FAIR) data are being increasingly adopted. However, data re-use requires a detailed description of the experimental conditions, biological materials used, handling procedures, analysis methods: the metadata. Gathering so many details at the time of final data deposit is a tiring and time-consuming process, an extra burden that negatively impacts on productivity. Unless it is enforced, this leads to poor metadata quality and undermines the whole idea of data re-use.

The collection of detailed metadata could be facilitated (and enforced) by customized tools that are integrated with research workflows. Such tools must provide immediate value to the researchers – data producers, by solving their particular problems or facilitating their research. This approach transforms data sharing into a "side effect" of routine scientific activity rather than requiring separate, specific work. However such customizations are highly field-, and topic-specific and cannot be provide in a centralised way.

SynthSys is testing sustainable but effective and tailored ways of incorporating data management into individual research. For this aim, we leverage existing University infrastructure and general Biological Data Repositories, such as the FAIRDOM toolset (https://fair-dom.org/) and public, self-service FAIRDOMHub (https://fairdomhub.org).

Metabolomic and transcriptomic approaches reveal new components related to sugar metabolism involved in the protective effect of melatonin on fruit exposed to cold stress

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Melatonin (MEL) is a well-known animal hormone, recently discovered in plants playing an important role in regulating plant development and abiotic stress response. In plants, studies have reported the protective effect of MEL during abiotic stresses, focusing on the relationship between MEL and antioxidant metabolism. Additionally, other reports mainly in climacteric species have addressed how MEL affects fruit ripening and senescence. However, the mechanisms by which MEL exerts its protective effect in a non-climacteric fruit is not deeply understood. In order to identify potential candidates that may account for MEL effect in a non-climacteric model, we exogenously applied MEL to sweet cherry and performed transcriptomic and metabolomic analyses in a short time-course. By metabolomic analysis, we found that soluble sugars, such as arabinose, turanose, talose and mannobiose correlate with MEL-treated fruit. Accordingly, transcriptomic analysis showed that MEL modulates sugar pathways after 24 h and 72 h post-treatment. In a second experiment, we explored the effect of MEL on sweet cherry during cold stress (CS). Our results indicate that MEL protects sweet cherries from CS, by transcriptionally modulating aquaporins and fruit cuticle, along with antioxidant metabolism. Furthermore, candidate genes identified by the integrative approach were validated by qPCR in sweet cherries during CS. Beyond redox-related genes, our results indicate that pathways related to sugar metabolism are triggered by MEL during CS. In addition, phenotypic analysis shows that MEL improves the tolerance of fruit to stressful conditions. Further studies are required to get deeper insight into the interplay between MEL effect on sugar metabolism and the antioxidant regulation and/or cell wall rearrangement.

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Genome sequence and RNA expression profiles of Orestias ascotanensis (Teleostei; Cyprinodontidae): strategies for adaptation to extreme environmental conditions

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Orestias ascotanensis (Cyprinodontidae) is a teleost pupfish inhabiting springs in the Ascotan saltpan in the Chilean Altiplano (3,700 masl) and is subject to extreme environmental challenges. This species is part of a genus inhabiting both freshwater and salt lake environments distributed along the central Andes range which shows multiple allopatric speciation events, most notably in the southern part of its distributional range. We have de novo assembled the genome of O. ascotanensis at high coverage, representing the first sequenced teleost from a desert environment. Comparative analysis of the O. ascotanensis genome sequence to those of other previously sequenced teleosts, identifies potential adaptive mechanisms in this species including paralog expansion in families of genes that have been associated with stress resistance to metals ions, salinity and DNA repair after UV exposure, a set that partially overlaps with genes that are under positive selection pressure. We also provide evidence supporting a role for miRNAs expressed in this species, which are predicted to target mRNAs coding for proteins classified in these same categories. Together, our results shed light on the mechanisms operating during adaptive evolution of Andean fishes in response to environmental stress conditions. Furthermore, we propose that these inter-Andean basin lakes represent new natural laboratories suitable for exploring the adaptive strategies developed by their inhabitant species.

Pairwise Probabilistic Framework to infer functional gene networks and identify key genes in response to perturbations.

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It is second nature nowadays to use changes in gene expression to identify relevant genes in response to a perturbation or in a developmental transition. However, many key genes for an organism's response are not regulated at the gene expression level (e.g. early genes in signaling pathways). These genes are currently hidden to transcriptome-based approaches. Here we sought to address the problem of finding functionally relevant genes for a condition "A" regardless of whether they change at the gene expression level under contrasting experimental conditions to evaluate "A". In order to identify these genes, we first determined transcriptome states and boundaries using large expression databases and a novel entropy-based framework in two popular model organisms Arabidopsis thaliana and Saccharomyces cerevisiae. We uncovered inherent restrictions in gene expression at the genome-wide level, that reveal novel functional relationships for genes that are not obtained by widely used methods such as correlation networks. Moreover, our approach allowed us to identify novel genes in response to perturbations, some of which are and some of which are not regulated in response to the perturbation. Our conceptual framework to analyze transcriptome data provides new insights into gene regulatory networks that cannot be attained with existing methods. This approach can be easily applicable to any organism with large transcriptome databases.

Analysis of predicted metabolic pathways based on the genome of the annual killifish Austrolebias charrua

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Background: The comparison of genomic sequences between species, allows the identification of genes and proteins selected during evolution which allow species to adapt to their environment. To identify these differences, the metabolic pathways deduced from the repertoire of genes can be studied in the species of interest. Recently we have sequenced the genome of Austrolebias charrua (Cyprinodontiformes), whose eggs have the unique ability to survive the drying of their habitat by an adaptation in embryonic development.
We aim to compare the genome of Austrolebias with other fish species inhabiting less extreme environments. In particular, the metabolomic signature of these fish could reveal some of the mechanisms that these species would use to survive in fluctuating environments.
Methods: To determine a metabolic comparison between fishes, we developed a protocol, using existing bioinformatic tools such as E2P2v3, which allows us to recover enzymes from the sequenced genome information and contextualize them within metabolic pathways using Pathway Tools. In addition, to identify genes that could explain the biology of A. charrua, we used a comparative approach to identify genes under positive selection. We collected highly conserved proteins encoded by genes of teleost species and compared them to those of annual fish.
Results: Our findings reveal that, metabolically, A. charrua is more directly related to fish that share the same type of life histories, and are even more closely related to species that share the same type of habitat. We are in the process of identifying genes under positive selection in A.charrua.
Conclusion: A. charrua has a metabolic signature that is consistent with its life history and environment, though it also shows features in common with all teleosts.
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A reverse genetic approach identifies a novel transcriptional regulator involved in temperature signaling to the Neurospora crassa Circadian Clock.

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One of the most pervasive environmental perturbations imposed to living organisms are the constant light/dark transitions product of the Earth's rotation around its own axis. Yet, organisms have evolved molecular strategies, such as circadian clocks, to anticipate these transitions. Such clocks exhibit a common molecular circuit, which is based on a positive element able to activate the expression of a negative one that then represses the action of the former, inhibiting its own expression. This system is capable of sustaining oscillations under several external perturbations, but the compensation mechanisms to maintain these periodic rhythms remain largely unknown. Studies in mammals, Drosophila and Arabidopsis have shown some additional transcriptional inputs that support the central molecular circadian circuit, by modulating the expression of core-clock components. In Neurospora crassa the clock central circuit has been well characterized but the participation of other transcriptional networks in this system are still unknown. Here, we identify novel transcriptional regulators controlling the clock in N. crassa through a reverse genetic approach, utilizing the existing knockout collection for every transcription factor described in Neurospora and bioluminescent circadian reporters. Thus, we have defined a set of transcriptional regulators that modulate circadian features in our experimental conditions, which falls in a broad range of function or processes. Among these candidates we identified the KO for the transcription factor KPR-16, which exhibits a remarkable period lengthening of ~2 hours. Interestingly, KPR-16 homologues have been associated to temperature sensibility. We demonstrated that in the absence of this transcription factor the Neurospora clock was unable to respond to temperature changes over the compensation temperature range, unveiling unexpected aspects of temperature sensing by circadian systems. iBIO, FONDECYT 1171151 and HHMI International Research Scholar grant.

ψ-trap: Microfluidic platform for long-term phenotyping of plant single cells

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Synthetic biology strives to genetically engineer cells through the design-construct-test cycle. Our capability to test predicted functions can be enhanced by accurate and large-scale cell phenotyping platforms. Currently, the effects of genetic constructs in plant cells are often measured at the cell population level, which by averaging out characteristic cell to cell distribution of a given behaviour, can lead to misleading conclusions. In order to capture the stochasticity and heterogeneity of individual cell behaviours important for cell function, we need to characterise a population at the single cell level.

We employ microfluidic techniques to immobilise single plant cells and to subsequently manipulate their environment. The goal of the cell trapping is long-term monitoring of single plant cells with constant exchange of nutrients and oxygen. We designed a microfluidic single plant cells trap (ψ-trap) which uses the hydrodynamic trapping principle. The design consists of 3072 individual cell traps in which each single trap connects the upstream side with the downstream side of the main channel. We can routinely trap more than 2000 single cells and follow their dynamic behaviours over the course of 3 days. Depending on the flow rate, we can introduce compressive mechanical forces and predictable deformations to the cells. By exchanging the medium chemical stimuli can be applied, the cells' dynamic responses can be quantitatively monitored using visible reporters and phenotyping.

Hydro-actuated morphing enables informed dispersal of dandelion diaspores

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The common dandelion can pioneer new habitats as far as hundreds of kilometres away, thanks to the pappus, a bundle of bristles that resembles a parachute. Pappus is however over 90% empty space, and thus the flight mechanism of a parachute doesn't apply to the dandelion diaspore. In order to understand the aerodynamic underpinnings of the flight of the dandelion, we set-up a bespoke wind tunnel with which the fluid dynamics around the pappus was visualized. A previously unobserved flow behaviour was found downstream of the pappus, in which stable circulation of air creates a halo-like ring vortex. This ring vortex is separated from the pappus but stays at a constant distance, creating a domain of low pressure toward which the pappus tries to move. This previously unknown type of flight is enabled by the high porosity of the pappus, owing to the hairy design that can act partially like a solid body. The pappus is not a fixed structure; it closes when the moisture level is high in the air, for example with fog or mist. This morphing is due to the changes in the shape of the receptacle tissue called pulvinus, and it is reversible and takes less than an hour to shift between the open and closed configurations. When closed, the vortex above the pappus becomes broken, shedding in oscillation and making the flight unstable. In addition, the wet and closed diaspores do not take off from the capitulum as readily as open ones. There is an inverse correlation between the air moisture level and wind speed. We hypothesize that moisture-dependent morphing of the pappus enables informed dispersal of the dandelion seeds, such that they are released preferentially when there is stronger wind to uplift the seeds for dispersal over a longer distance.

Plant developmental responses to salt stress

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High salt concentration in soil modulates in a negative manner plant growth and development due to an increase in osmotic stress and ion toxicity. In roots, high soil salinity causes inhibition of both primary root elongation and number of lateral roots. Auxin has a key role in the modulation of root architecture throughout the life cycle and in response to environmental stresses. To achieve this, auxin has a complex signaling pathway that involves the perception of the hormone, degradation of a repressor complex and the transcriptional expression of auxin-responsive genes. Auxin F-box 3 receptor (AFB3) is one of the four auxin receptors described in Arabidopsis thaliana. It has been found that this receptor is involved in the modulation of root architecture, depending on the availability of nutrients in the soil. The putative downstream regulatory network in this context has previously been proposed, identifying NAC4 and OBP4. Here we showed that over-expression of AFB3 exhibited increased resistance to salt stress in terms of lateral root density and germination rate. We also studied the downstream signaling components to further characterize the role of auxin in response to salt stress. These results give lights of the possible mechanism that leads to the modulation of the root system architecture in response to salt stress. The effect on root plasticity commanded by the auxin signaling pathway could then be modulated to give a tolerant phenotype under stress conditions allowing better performance in unfavorable environments. Soil salinity has been a key problem for crops production worldwide.

Mining genes for climate change. Using Cistanthe longiscapa to understand stress resilience

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The Atacama Desert is one the oldest and driest places on earth, with high radiation levels and precipitation levels that range from 100mm to less than 10 mm per year at the hyperarid core. Episodes of rainfall exceeding these levels occur few times every decade and are responsible for triggering the rise of a rich community of plant species in a phenomenon known as "blooming of the desert". Cistanthe longiscapa, an annual species, is the most abundant sighted species during this phenomenon and can withstand a prolonged period (3-4 months) without further precipitations. We found that this species exhibits eco-physiological adaptations that are probably related to the high irradiation dry environment it inhabits. To better understand how these adaptations and to detect molecular mechanisms related to its resilience to high irradiation and water scarcity, the genome of this species was sequenced (739 scaffolds and N50= 2.7 Mbp) predicted genome size was of nearly 800 Mbp and a gene number estimated of 37.716. Both karyotype and kmer analysis suggest that the species is diploid, even though some level of duplication typical of polyploid species was found. Interestingly, some biological processes exhibit a great number of genes, in some cases up to several hundreds, that fall into categories that could be seen as a response of the genome to the extreme environment where this plant lives. Transcriptomic analyses of plants living in different sites revealed differences in their repertoire of expressed genes, indicating their plasticity to cope with differences in the environment.

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AMI1 linkes indole-3-acetic acid biosynthesis with plant stress responses

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The evolutionary success of plants relies to a great extent on their extraordinary ability to adapt to changes in their environment. These adaptations require that plants balance their growth with their stress responses. Plant hormones are crucial mediators orchestrating the underlying adaptive processes. However, whether and how the growth-related hormone auxin and the stress hormones jasmonic acid (JA), salicylic acid (SA), and abscisic acid (ABA) are coordinated remains largely elusive. Here, we report on the physiological characterization of AMIDASE 1 (AMI1) from Arabidopsis thaliana, a homolog of the auxin synthesis-related iaaH gene from Agrobacterium. We provide evidence for the contribution of AMI1 to cellular auxin homeostasis. Moreover, microarray analyses disclosed that a considerable number of stress-related genes, including JA and ABA biosynthesis genes, are differentially expressed in the ami1 mutant. The ami1 mutant exhibits moderately repressed growth, but enhanced JA and ABA accumulation, which underlines the role of AMI1 in the crosstalk between auxin and JA as well as ABA. Thus, AMI1 is a coordinator in the trade-off between plant growth and stress responses, balancing auxin with JA and ABA homeostasis.

Cytokinin-dependent transcriptional regulation of PIN auxin efflux carriers in response to developmental and environmental cues

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PIN-FORMED (PIN) transporters are key components of the polar transport of the phytohormone auxin. Its polar transport is essential for the proper development of the plant since it drives the auxin accumulation in specific cells and tissues. This accumulation, known as auxin maxima, is then necessary for the physiological outcome of auxin, such as root growth and the development of lateral root primordia among many others. It have been shown that the expression of different PIN transporters is modulated under cytokinin and also stress responses such as salt. In response to cytokinin, this modulation takes place in a regulatory element in the PIN promoter denominated PIN CYTOKIKIN RESPONSE ELEMENT (PCRE). Thus, we identify the transcription factor PinR4 that is expected to bind to the PCRE domain and could be a component of the crosstalk between this two phytohormones in root development and stress responses. We studied the root architecture -root length and lateral root density- in two mutant lines for PinR4 in response to cytokinin, auxin and salt stress treatments. Our preliminary results show that the pinr4 mutants are resistant to cytokinin treatment in terms of lateral root density when compared to wild type. Moreover, under auxin treatment the mutant lines showed a reduced density of lateral roots in comparison to wild type. For the salt treatment the mutant lines showed an increase sensitivity as they have shorter roots and had less density than wild type. This result suggests that PinR4 plays a role in the auxin-cytokinin crosstalk in the regulation od root architecture and in response to salt stress response.

Universal Loop assembly (uLoop): open, efficient and agnostic DNA fabrication

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Standardised approaches for DNA fabrication such as Golden Gate and Gibson assembly are playing an important role in the development of systematic strategies for studying, reprogramming and engineering biological systems. Here, we present “universal Loop assembly” (uLoop), a simple, recursive, open source and species-agnostic method for DNA assembly that enables hierarchical fabrication of large DNA constructs (> 30 Kb) with high efficiency (> 85 %) and fidelity. The system is intuitive, versatile and abstracts technical details from assemblies, enabling its use by non-specialists. Assembly is conducted iteratively alternating between two levels, determining an exponential increase of assembled genetic modules by a factor of 4 in each assembly, with no theoretical limit on the number of genetic modules that can be composed. We have generated 4 versions of plasmids from well-established backbones with diverse origins of replication (pBR322, p15A, pSC101). Furthermore, uLoop uses the common syntax for the assembly of standardised DNA parts into transcription units and enable interoperability with alternative syntaxes (e.g. CIDAR MoClo, Loop, GoldenBraid) and techniques such as 3G assembly. We show the use of uLoop to introduce host-specific elements during the assembly routine and its application in eubacteria and three kingdoms of eukarya. Our plasmids will be made available to the community through the OpenMTA for unrestricted sharing and open-access.

Metabolomics approaches to understand the chemical communication in plant–microbe interactions

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The global climate change is arguably one of the biggest threats of our times that has already led to a wide array of impacts on the environment, the economy, and society. The expected heat, drought, floods, and unpredictable growing seasons are thought to have detrimental effects on the agricultural production system, causing immense economic losses and insecurity of food supply. To mitigate the risks provoked by the climate variability, agricultural innovations counteracting these changes need to be embraced and accelerated.

In order to achieve maximum improvements, the required agricultural innovations must go beyond the focus on the crop side only, but rather pursue a holistic approach including the entire ecosystem. Over millions of years, plants have evolved in close vicinity with other organisms, in particular with soil microbes that shaped their evolution and contemporary ecology. Interactions among community members can be beneficial, pathogenic, or have little to no functional impact. In any case, they are assumed to change with environmental stress conditions. Soil microorganisms regulate nutrient transformations and, thus, provide plants with nutrients. This has a direct impact on plant fitness mostly by improving nutrient uptake from the soil through the interaction with, e.g., root-nodulating bacteria or mycorrhizal fungi. Given this co-evolution and the pivotal importance of plant–microbial interactions, it is not astonishing that a growing body of recent publications report on the existence of extraordinary reciprocal influences that chemically regulate not only plant–microbial interactions, but also the composition of the rhizosphere. However, how this chemical cross-kingdom communication is achieved is far from being fully understood. Here, we will report on how different metabolomics approaches can be used to deepen our insight into the chemical crosstalk between plants and their microbial symbionts.

Tolerance to temperature shifts in natural environments

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During the last century global temperatures have increased at an unprecedented rate, posing a threat to many ecosystems across the planet. Understanding how these systems will respond remains a major challenge because ongoing climate change involves not only a general rise in average temperatures, but also an increase on the frequency and magnitude of extreme thermal events. This problem is exacerbated because temperature impacts organisms at many different levels, from energy expenditure to ranges of thermal tolerance, and these attributes tend to vary across lineages adapted to different conditions. In this seminar, I will discuss the different frameworks employed to quantify thermal tolerance and review the main findings of recent large-scale studies. Analyses employing critical thermal limits as surrogates for thermal tolerance indicate that there is substantial adaptive variation for cold tolerance across lineages, and very limited potential in heat tolerance to respond to warming conditions due to physiological constraints. Unfortunately, empirical and theoretical evidence suggests that the estimation of critical thermal limits may be unreliable for multiple reasons, and therefore many of the conclusions stemming from these studies are presently open to debate. Furthermore, distribution models based on critical thermal limits exhibit very low predictive power, which drastically limits our abilities to forecast which specific lineages and/or ecological communities might be more threatened by global warming. Consequently, I will discuss some alternative venues to quantify thermal tolerance that take into consideration both the intensity and the duration of the thermal stress, which are not only more realistic but also open the venue to study how organisms with different tolerance estimates may respond to changing average temperatures and thermal extremes in natural settings.

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Tissue-specific nuclear membrane proteins direct 3D genome organization changes important for tissue differentiation, disease, and cell environmental responses

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Tissue-specific nuclear membrane proteins direct 3D genome organization changes important for tissue differentiation, disease, and cell environmental responses

Different tissues have specific 3D genome organization patterns and it is clear that disruption of genome organization can lead to changes in gene regulation and even to human disease. In fact it has been suggested that a majority of the disease alleles remaining to be identified likely occur in non-coding regions where they could disrupt spatial contributions to genome regulation. Moreover, rapid gene and chromosome repositioning has been demonstrated in response to environmental or pathogenic stimuli. Despite this there is very little understanding of how 3D genome organization patterns, and particularly tissue-specific patterns, are established. We have found several nuclear envelope transmembrane proteins (NETs) preferentially expressed in muscle, fat, liver and blood that are each important for establishing genome organization patterns in their respective tissues. Each affects the positioning and expression of distinct sets of important genes for tissue functioning and/or differentiation. Mutations in widely expressed nuclear envelope proteins cause a wide range of human diseases that tend to have tissue-specific pathologies, so we postulated that tissue-specific NETs might mediate these pathologies through disruption of genome organization or even directly cause disease. Compellingly, we found mutations in muscle gene repositioning NETs PPAPDC3, Tmem38a, Tmem201 and Tmem214 in previously unlinked Emery-Dreifuss muscular dystrophy patients. In addition to providing tight temporal regulation of genes in differentiation these NETs can also participate in faster responses to environmental stimuli, both recruiting genes to and releasing genes from the nuclear membrane with consequences for gene expression directing regulatory switching.

Depict the biogeographical patterns of microorganisms along the Southern Ocean

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The Southern Ocean and Antarctica are pristine ecosystems and also ones of the most brittle in regard to the current global warming. Understanding the current organisms biogeography in these areas has become a major issue in order to predict the future patterns of distribution in response to global changes. Microbes that represent the dominant biomass in these ecosystems, and control most of the biological flux, are often involved in close associations with macro-organism affecting each other's growth, metabolism, and fitness. However, while the biogeography of macro-organisms is already well described, little is known so far about the biogeographic patterns of micro-organisms, particularly in the case of symbiotic microbes that are supposed to share a common evolution history with their hosts.

In that regard, one of the aims of the ongoing project « Genomics Antarctic Biodiversity » (GAB) is to describe the holobiont among 3 sea urchin species belonging to the Abatus genus distributed along the Southern Ocean, and to investigate a possible co-evolution of the intestinal microbiota and the host.

As a starting point of this project, gut microbial composition of the sea urchin species Abatus cordatus was surveyed in the Kerguelen Islands (French Southern and Antarctic Lands) by next generation sequencing of 16S rDNA amplicons, along with surrounding sediments.

The first results revealed that sediments contained in the A. cordatus gut and from the surrounding habitat exhibit the same dominance of Pirellulaceae and Thermoanaerobaculaceae, respectively belonging to the Planctomycetes and Acidobacteria phyla, representing up to 60% of the sequences obtained. Despite this homogeneity, the microbial composition is clearly distinct between the two biological compartments, with about 45% of the OTUs exclusive to either. The putative functional implications and the use of these OTUs as biogeographic marker of the holobionte have been discussed.

Effects of deletion of circadian clock genes in Anabaena sp. PCC7120.

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The circadian clock influences in Cyanobacteria the timing of certain cellular processes such as photosynthesis, cellular respiration and cellular division. This regulation requires the presence of the central oscillator KaiABC which control the system and allows to predict and anticipate environmental changes to optimize the cellular response adapting for example its chromosome topology, transcriptome, proteome and metabolism.

Studies on unicellular organisms proved the inhibition of Z-ring formation by the circadian central oscillator KaiABC, controlling in this way the timing of cell division. The Z-ring is a structure formed by Fts-Z that acts as a scaffold for the divisome and is the key of cytokinesis. Despite the advances in understanding the factors that orchestrates cellular division on cyanobacteria, the proteins that participate and how the process actually happen in multicellular cyanobacteria is still unknown. In order to explore the effects of circadian clock in filamentous cyanobacteria in this study we generate a mutant of Anabaena sp. PCC7120 by deletion of kaiABC cluster through homologous recombination.

The polyploid characteristic of filamentous cyanobacteria makes the process of mutagenesis long and complex in order to obtain a fully segregated mutant. Unexpectedly, during the segregation of the kaiABC cluster deletion mutant, the filaments morphology were not linear straight filaments as the wild type, instead branched filaments which is characteristic of the Stigonematales order, were observed. When the segregation was complete the phenotype was morphology similar to the wild type. All the segregation process was followed by optical, confocal and electron microscopy. The transient branched phenotype suggests that branching morphologies in cyanobacteria is not depending on the presence of particular genes but controlled by differential expression of cellular division genes, in this case, influenced by the KaiABC oscillator.

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Mechanistic insights into controlling cell identity by transcription factors

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The endogenous expression of the transcription factors (TFs) Oct4, Sox2, Klf4, and c-Myc (OSKM) is essential for maintaining pluripotency in embryonic stem (ES) cells. Most strikingly, the ectopic expression of OSKM can reprogram somatic cells to become induced pluripotent stem (iPS) cells. As OSKM were originally chosen based on their role in maintaining pluripotency, it is often thought that reprogramming is a reversal process of embryonic development. Unlike maintaining pluripotency however, reprogramming is highly inefficient, and little is known about how OSKM functionally-contribute to inducing pluripotency as compared to maintaining pluripotency. We have previously mapped of the interactions between OSKM factors and the human genome during the first 48 hr of cellular conversion to pluripotency. We have shown that OSK, but not Myc, act as pioneer TFs by targeting distal enhancers within closed chromatin. We have also revealed that the pioneer activity of reprogramming factors relates to the basic ability of TFs to adapt their DNA-binding domains (DBDs) to target partial motifs exposed on the surface of nucleosomes. Here, I will present new evidence showing that inducing pluripotency is functionally distinct from maintaining pluripotency using a systematic comparison between the essential functions of Oct4 during reprogramming and maintaining pluripotency. I will also present detailed biochemical analysis defining the structural features of Oct4 that impart the pioneer function. Altogether, our findings provide new insights into the basis of controlling cellular identity by transcription factors.

Ecological genomics in the Atacama Desert: Extreme aridity, low Nitrogen and high radiation as key drivers of natural selection

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Understanding biological processes that underlie plant resilience to extreme abiotic conditions is a major challenge for plant biologists. This knowledge is essential to develop biotechnologies that could be used to improve crops in an era of climate change or to expand the limits of agriculture to marginal lands. We characterized plants from three pristine and extreme ecosystems from Atacama Desert in Northern Chile. In the central Atacama Desert, the western slopes of the Andes provide a natural altitudinal gradient of environmental parameters, such as rainfall and temperature. As a consequence, various plant communities succeed each other at different elevations: the pre-puna (2400 – 3300 m a.s.l), the puna (3300 – 4000 m.a.s.l.), and the high Andean steppe (4000 – 4500 m.a.s.l.). In order to find underlying genetic mechanisms supporting plant survival in these extreme environments, we sequenced the transcriptome of the 32 most abundant and ecologically important species. Our studies provide new insights into mechanisms for evolution of plant abiotic stress tolerance, and improve our understanding of the highly unique ecosystem of the Atacama Desert.

Deciphering the cell division in filamentous Cyanobacteria

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Filamentous cyanobacteria with heterocyst cells are present in a wide type of environments in the earth: marine, freshwater, sediments, lands, etc. But also can dominate extreme environments and provide nutrients and support for crusts formations. Filamentous cyanobacteria can also interact with plants, fungi, and other eukaryotes. Its origins in the Earth are from one billion years ago. Despite its importance, we know very little about essential processes such as cell division.

Applying Anabaena sp. PCC7120 as a model, by genomic analysis we found a new cell division protein that participates in the septum localization: CyDiv. Our results showed that CyDiv interacts with itself and with other components of the divisome, in a similar way of FtsB in E. coli. We also demonstrated that cell division in filamentous cyanobacteria is not a binary process. Therefore, mother and daughter cells are generated during the cell division, incorporating the ageing concept in the filament development.

There are still numerous genes uncharacterized and processes poorly understood in cyanobacteria despite its key importance in the Earth.

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Systematic review of soil bacterial communities from arid environments at a global-scale.

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Recent advances in genomics and informatics tools have expanded our ability to characterize the soil microbiome from extreme environments. Data is accumulating rapidly, yet, a complete state of the art report/systematic review in bacterial communities reported from arid soils hasn't been performed. That information is required to initiate a comparative analysis of soil bacterial communities in desert environments, aiming to: identify similarities between bacterial communities from arid environments and compare the bacterial communities found by our group in the Atacama Desert with other arid environment microbiomes. In this context, we conducted a systematic review including 70 articles reporting arid soil bacterial communities and analyzed the characteristics of these articles, to evaluate how are we approaching the environmental microbiology of arid soils and contribute to summarize the body of knowledge accumulated. The systematic review was performed based on the PRISMA statement. We conducted a search in three scientific databases: PubMed, SCOPUS and Web of Science (WOS) between Dic-2017 and March-2018. 70 articles reporting bacterial communities using 16S rRNA described using NGS from un-manipulated desert soil were selected to be included in the analysis. Independent collection of data from articles was performed by three authors using predefined data fields. We used basic statistic tools to analyse different aspects of the reports including editorial, environmental and bacterial community features. Our results show a global-scale insight of researchers studying arid soil microbiology, the common environmental features of these soils, bacterial communities harboured in them as well as unveiling biases in this area.

Regulatory networks underlying differential susceptibility to Botrytis cinerea in tomato plants grown under different nitrogen regimes.

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Nitrogen (N) is one of the main limiting nutrients for plant growth and crop yield. Despite its role as a nutrient, N plays an important role acting as a signaling molecule that modulates gene expression of a wide range of plant processes. Indeed, N availability also influences plant ability to cope with pathogen attacks. Since plant defense is a complex biological process and energetically costly response mechanism, it is expected that the metabolic state of the plant plays a fundamental role in the outcome of the plant-pathogen interaction. In the case of Botrytis cinerea, the role of N on disease development in different plants appears to be variable and the molecular mechanism underlying this interaction is poorly understood. In this work, we analyzed the global gene expression response of Solanum lycopersicum against infection by the necrotrophic fungus Botrytis cinerea, under contrasting nitrate conditions. Our results indicate that defense responses to B. cinerea infection are affected by N availability, showing more susceptibility in nitrate-limiting conditions. Using dual RNA seq temporal transcriptional analysis, we identified 307 tomato genes that display expression profiles affected by Botrytis depending on N status and 99 Botrytis genes that were expressed in planta differently depending on the plant N status. Gene expression analysis revealed trends in nutrient, hormonal signal and plant defense. Our results provide insights into potential crosstalk mechanisms between necrotrophic defense response and N status in plants.

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The influence of FtsZ on the multiseptum formation in filamentous cyanobacteria

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Raphidiopsis raciboskii (in the past Cylindrospermopsis raciborskii) species belongs to order Nostocales, is a filamentous diazotrophic cyanobacterium. Along the filament, the multiseptum formation can be observed. However, the cause of this phenotype is still unknown. In this study, we explored the role of FtsZ, a key protein involved in cell division, over the septum formation and other cellular features. Within the bacterial cytoskeleton, FtsZ protein plays a crucial role during cellular division, where this protein serves as a scaffold to the process of cytokinesis and septum formation. In silico analysis of FtsZ from R. raciboskii showed an increase in proline frequency of 8% approximately in this variable region respect to the FtsZ of Anabaena sp. PCC7120 (that do not present this multiseptum formation). To evaluate the effect of FtsZ from R. raciborskii in Anabaena sp. PCC7120 we replaced the gene in Anabaena with the one from R. raciborskii by homologous recombination. Preliminary results gave a statistically significant reduction of 30.8% on cellular size on Anabaena sp. PCC7120, suggesting a faster contraction on the cytokinesis or a higher frequency of this process. This feature is coherent with the phenotypes observed in R. raciborskii.

Transcriptomic-based analysis of Fischerella thermalis metabolism in a hot spring temperature gradient.

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Cyanobacteria are bacterial organisms characterized by their ability to obtain their energy from the sun, fix carbon dioxide to organic carbon compounds and, in some cases, fix N2 to ammonium. However, it has been reported that some cyanobacteria can grow in media supplemented with sugar under conditions of photosynthesis inhibition such as darkness or chemical inhibition, behaving as mixotrophs instead of strictly photoautotrophic organisms. In environments such as microbial mats of neutral pH hot springs, Cyanobacteria are one of the most important primary producers, since eukaryotes primary producers cannot grow. In Porcelana hot spring, the cyanobacterium Fischerella thermalis uses photosynthesis as the main energy source, becoming the main primary producer and nitrogen fixer in the thermal gradient of ~40ºC to 58ºC. Our metatranscriptomic data, and in a manner consistent with previous studies, also indicate that most of the Fischerella thermalis genes, such as those associated with photosynthesis and nitrogen fixation, were repressed at a temperature higher than 58ºC. These results strongly suggest that temperature is limiting the autotrophic activity of Fischerella thermalis at transcriptional level in this system. In addition, our data also indicate that Fischerella thermalis is still active at high temperatures, such as 66ºC. At that temperature, stress response genes and carbohydrate metabolism genes such as sugar channels and glycolysis-associated genes as well as genes related to the metabolism of amino acids were induced. Some of those results were confirmed by RT-qPCR experiments. The latter suggests that Fischerella thermalis changes its energetic metabolism in response to high temperatures.

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Transcriptional control in seed development and its connections to stress responses

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Research activities in our group relate to the study of seed gene regulation. We have identified transcription factors (TFs) that control the expression of genes associated to maturation and germination phases in seed development. Functional characterization of conserved cis-regulatory elements, localized in the promoters of maturation and germination specific genes, and TFs interacting with them allowed the inference of regulatory networks. In the last years we have extended these studies into the characterization of stress responses associated to seed development (i.e. dehydration, hypoxia, endoplasmic-reticulum (ER-) stress, etc.), the identification of the underlying TFs involved and their participation in abiotic stress responses in vegetative tissues. We are also investigating the origin and evolution of these gene networks is in non-seed plants like Physcomitrella patens.