

ABSTRACT BOOK

INDEX

Organizing committee and acknowledgements 2
Welcome message 3
General information for conference participants 4
Program 7
Abstracts 12
Session 1: BIOTECHNOLOGY 13
Opening oral presentation (BIOop) 14
Oral presentations (BIOo01 – BIOo04) 15
Posters (BIOp01 – BIOp10) 19
Session 2: DIVERSITY AND EVOLUTION 29
Opening oral presentation (EVOop) 31
Oral presentations (EVOo01 – EVOo04) 32
Posters (EVOp01 – EVOp15) 36
Session 3: DEVELOPMENT 51
Opening oral presentation (DEVop) 52
Oral presentations (DEVo01 – DEVo04) 53
Posters (DEVp01 – DEVp12) 57
Session 4: NETWORKS OF METABOLITES, GENES AND ORGANISMS 69
Opening oral presentation (NETop) 70
Oral presentations (NETo01 – NETo04) 71
Posters (NETp01 – NETp08) 75
Session 5: STRESS BIOLOGY (BIOTIC AND ABIOTIC) 83
Opening oral presentation (STRop) 85
Oral presentations (STRo01 – STRo04) 86
Posters (STRp01 – STRp31) 90
Session 6: BREEDING (TECHNOLOGIES AND TRAITS) 121
Opening oral presentation (BREop) 123
Oral presentations (BREo01 – BREo05) 124
Posters (BREp01 – BREp26) 129
List of Attendants 155

ORGANIZING COMMITTEE

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- Bombarely, Aureliano. Universita degli Studi di Milano, Italy.
- Bryan, Glenn. The James Hutton Institute, UK
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- Strickler, Susan. Boyce Thompson Institute, USA.
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- Van Der Knaap, Esther. University of Georgia, USA
- Van Eck, Joyce. Boyce Thompson Institute, USA

Special thanks to:

The organizing would like to acknowledge Drs. Lukas Mueller and Naama Menda from the Boyce Thompson Institute (USA) for the advertising and posting of the conference information at the SOL Genomic Network page. We would like to thank also Mr. Aaron Callahan and Mr. Joie Nguyen, the Boyce Thompson Institute IT team for their technical support during the meeting as well as the Cornell IT for the use of the Zoom license.

WELCOME MESSAGE

Dear member of the Solanaceae Community,

It is our pleasure to welcome you to our first online Solanaceae workshop. Since the first Solanaceae workshop, held in Wageningen in 2004, the Solanaceae community has met in person every year, fostering an atmosphere of collaboration and inclusiveness. This year, due to the COVID pandemic, the Solanaceae 2020 meeting in Thessaloniki was postponed to 2021 and as a consequence we had two options: either skip one year, or go online. We opted for the second. The first meeting of the organizing committee was held in mid- September, and the whole procedure (announcement, registration and abstract submission, selection of abstracts and organization of the oral and poster sessions) was completed in around one month and a half, based exclusively on voluntary work of the organizing committee. We had an overwhelming participation (929 registrations and 137 abstracts from 50 countries) and the extremely high quality of the abstracts submitted made the choice of the ones to include in the oral sessions extremely difficult. This quality and diversity is reflected in the abstracts that you find in this book, and is the best reward for our efforts. We are aware that there may be organizational glitches here and there, but this is a learning experience for all of us. We especially want to thank Aureliano Bombarely and Susan Strickler for their hard work making this happen.

We hope that you will enjoy the meeting as we enjoyed organizing it.

SOL International Online Meeting Organizing Committee

GENERAL INFORMATION FOR CONFERENCE PARTICIPANTS

The most recent version of this document may be viewed on Google Docs: https://docs.google.com/document/d/1hRgut-LCT8J2vBjLDMSNxtvMs5DEwwebyZxUTzwrmPA/edit?usp=sharing

How to participate

ORAL PRESENTATIONS

The oral presentations will be broadcasted with Zoom. Please be sure that you have the **latest version** of Zoom installed on your computer.

- Everyone will be muted except the host and the speakers.
- The recommended duration is 20'+5' discussion (plenary talks) or 12'+3' discussion (all other talks). The moderator will be responsible for keeping the time.
- Questions can be asked in the Zoom chat box and these will be addressed at the end of each talk by the moderator, on a first comes/first served basis
- Talks will be recorded by the moderator and posted to YouTube with the permission of the presenter.
- Participants can attend the oral presentations by going to the following link:
    a. https://cornell.zoom.us/webinar/register/WN_6KjW8BRUTbuPIo6rUemd5Q
    b. Password: 073902
- You can download Zoom at: https://zoom.us/download

If you are an oral presenter, please check the "Instructions for Oral Presenters" document for more details. If you have not received this document yet. Please contact us (you can find the contact information at the end of this email).

POSTERS

The posters will be presented with **Virtual Poster Session** (https://virtualpostersession.org). You don't need a special software to visit the posters, just your web browser. Nevertheless if you want to chat with the poster presenter, you will need to check which platform they will be using and the time in which they will be available.

- Posters can be viewed at the following link: https://app.virtualpostersession.org/e/766d4366c148c0065a11593034b9f7a4

If you are a poster presenter, please check the "Instructions for Poster Presenters" document for more details. If you have not received this document yet. Please contact us (you can find the contact information at the end of this email).

VIRTUAL MEETING ROOMS

Discussions on each session will continue after the session finishes for 30 minutes. We have created **Zoom Meeting Rooms** for each session (max 300 participants). You can access them at the following links:

a. November 9, 2020

i. 15:25 - 15:55 CET, Biotechnology Meeting Room - https://cornell.zoom.us/j/91296568322?pwd=SXo3bGlkc3liMjBDR29kRS9aWHlLQT09
ii. 17:25 - 17:55 CET, Diversity and Evolution Meeting Room - https://cornell.zoom.us/j/94441376981?pwd=eElLQUJuYlRJRmNlcHQzRDhsNVRzdz09

b. November 10, 2020
i. 15:25 - 15:55 CET, Development Meeting Room - https://cornell.zoom.us/j/91837571109?pwd=SXhOOVEwSGx5U0F0RURmTjZVc1NHUT09
ii. 17:25 - 17:55 CET, Networks of Metabolites, Genes, and Organisms Meeting Room - https://cornell.zoom.us/j/99669357428?pwd=T295YVU1a2xHQnFyWjcxRkEwS3ZzUT09

c. November 11, 2020
i. 15:25 - 15:55 CET, Stress Biology Meeting Room - https://cornell.zoom.us/j/96781911728?pwd=V09nZ28yQnVxWnBvM0ZUTVVpdXU3Zz09
ii. 18:25 - 18:55 CET, Breeding Meeting Room - https://cornell.zoom.us/j/91589548226?pwd=Rk9JcW9CZVlScHdrYkdJeVRBRFJpUT09

CHAT CHANNEL

We have created a conference Slack workspace (Solanaceae2020). Slack can be used to text chat within channels and individual conference participants that have signed up.

- You can join this by going to the following link: https://join.slack.com/t/solanaceae2020/shared_invite/zt-ipxynqkj-RKiyQBnojIVZnw_OOL8z_w
- To download and install Slack: https://slack.com/. It is also available as an app. for most of the smartphone operating systems.
- For issues connecting to the conference platforms, please post a message on the conference slack “issues” channel.

TWITTER

The official tag for this conference will be #SOLIOM2020.

When to participate

You can find the program at: https://solgenomics.net/sol2020

The meeting will happen from 13:40 to 18:30 Central European Time (CET) on November 9th, 2020 (Monday), 12:55 to 18:30 CET on November 10th, 2020 (Tuesday) and 12:55 to 18:15 CET on November 11th, 2020 (Wednesday).

- If you need to convert the sessions to your time zone you can use online tools such as: https://www.timeanddate.com/worldclock/converter.html
- You also can add this Google Calendar (https://calendar.google.com/calendar/u/0?cid=dXU5N2YxNTh2dWdmZm12MDFsODBiMjhnZ2tAZ3JvdXAuY2FsZW5kYXIuZ29vZ2xlLmNvbQ) to your Google Calendar or export to any application that you may be using like iCal. The calendar will change the times according the time zone in which it has been set up.

Do you have questions? Contact us:

- General inquiries about registration: Aureliano Bombarely (aureliano.bombarely@unimi.it).
- For issues connecting to the conference platforms, please post a message on the conference Slack "issues" channel.

PROGRAM

CET Time	Nov. 9th , 2020	Nov. 10th , 2020	Nov. 11th , 2020
12:55		Poster session 2 BIO2, EVO2, DEV2	Poster session 4 NET2, STR2, BRE2
13:40	SOLIOM opening	Break	Break
13:55	Session 1 opening	Session 3 opening	Session 5 opening
14:00	BIOop	DEVop	STRop
14:25	BIOo1	DEVo1	STRo1
14:40	BIOo2	DEVo2	STRo2
14:55	BIOo3	DEVo3	STRo3
15:10	BIOo4	DEVo4	STRo4
15:25	Session 1 closing	Session 3 closing	Session 5 closing
15:30	Break	Break	Break
15:55	Session 2 opening	Session 4 opening	Session 6 opening
16:00	EVOop	NETop	BREop
16:25	EVOo1	NETo1	BREo1
16:40	EVOo2	NETo2	BREo2
16:55	EVOo3	NETo3	BREo3
17:10	EVOo4	NETo4	BREo4
17:25	Session 2 closing	Session 4 closing	BREo5
17:30	Break	Break	Questions BREo4-5
17:35			Session 6 closing
17:45 18:00	Poster session 1 BIO1, EVO1, DEV1	Poster session 3 NET1, STR1, BRE1	SOLIOM closing
18:15			Closing Day 3
18:30	Closing day 1	Closing Day 2	

Keep in mind that all the times are Central European Time (CET).

You can add the program to your Google Calendar using the following link:
https://calendar.google.com/calendar/u/0?cid=dXU5N2YxNTh2dWdmZm12MDFsODBiMjhnZ2tAZ3JvdXAuY2FsZW5kYXIuZ29vZ2xlLmNvbQ

November 9th, 2020

13:40 – 13:55 CET – SOLIOM Meeting opening.

Session 1: BIOTECHNOLOGY

Session opens at 13:55 and closes at 15:30

- 14:00-14:25 CET – BIOop: **Alain Goossens**, VIB-Ghent University, Belgium. *Unravelling the regulation of tomato metabolism through interactomics analyses.*
- 14:25-14:40 CET – BIOo01: **Peter Waterhouse**, Queensland Univ of Technology, Australia. *Genetic, epigenetic and metabolomic insights from reference level genome assembly of a wild and a laboratory strain of Nicotiana benthamiana.*
- 14:40-14:55 CET – BIOo02: **Johan Hunziker**, University of Tsukuba, Japan. *Improvement of carotenoid accumulation in tomato fruits by CRISPR-Cas9 Cytidine Deaminase system.*
- 14:55-15:10 CET – BIOo03: **Eva Knoch**, RIKEN, Japan. *The third DWF1 paralog in Solanaceae, sterol D24-isomerase, branches withanolide biosynthesis from the general phytosterol pathway*.
- 15:10-15:25 CET – BIOo04: **Lorena Ramirez**, Wageningen University, The Netherlands. *A new insight of StCDF1 under drought stress in potato*.

15:30-16:00 CET - Break

Session 2: DIVERSITY AND EVOLUTION

Session opens at 15:55 and closes at 17:30

- 16:00-16:25 CET – EVOop: **Chris Martine**, Bucknell University, USA. *Sexual fluidity among the bush tomatoes: Prickly solanums of the Australian Monsoon Tropics.*
- 16:25-16:40 CET – EVOo01: **Matthew Gibson**, Indiana University, USA. *Reconstructing the history and biological consequences of a plant invasion on the Galápagos islands*
- 16:40-16:55 CET – EVOo02: **Pasquale Tripodi**, CREA Research Center for Vegetable and Ornamental Crops, Italy. *Genebank genomics highlights novel centres of diversity and routes of migration in pepper (*Capsicum *spp.).*
- 16:55-17:10 CET – EVOo03: **Andrea Coccuci**, Instituto Multidisciplinario de Biología Vegetal (IMBIV-UNC), Universidad Nacional de Córdoba, Argentina. *Flower color evolution in the florally diverse genus* Salpichroa *(Solanaceae) seen through the eyes of its pollinators.*
- 17:10-17:25 CET – EVOo04: **Remco Stam**, Technical University of Munich, Germany. *Using wild tomato species to study diversity and evolution of biotic stress responses.*

17:30 – 17:45 CET: Break

17:45 - 18:30 CET: Poster session 1 (BIO1, EVO1, DEV1)

November 10th, 2020

12:55 – 13:40 CET: Poster session 2 (BIO2, EVO2, DEV2).

13:40 – 13:55 CET: Break

Session 3: DEVELOPMENT

Session opens at 13:55 and closes at 15:30

- 14:00-14:25 CET – DEVop: **Sebastian Soyk,** University of Lausanne, Switzerland. *Dissecting cryptic genetic variation with impact on tomato domestication and breeding*.
- 14:25-14:40 CET – DEVo01: **Glenn Philippe**, Cornell University, USA. *Elucidating the mechanisms of plant cuticle deposition and restructuring using tomato fruit development as a model.*
- 14:40-14:55 CET – DEVo02: **Bruno Silvestre Lira**, Universidade de São Paulo, Brazil. *Light and ripening-regulated B-BOX protein-encoding genes in Solanum lycopersicum.*
- 14:55-15:10 CET – DEVo03: **Matthias Benoit**, CSHL, USA. *Contribution of Transposons to Structural Variation and Phenotypic Diversity in Tomato.*
- 15:10-15:25 CET – DEVo04: **Ashley Snouffer**, University of Georgia, USA. *Regulation of cell division and cell shape by tomato OFPs and TRMs to control early ovary shape.*

15:30-16:00 CET - Break

Session 4: NETWORKS OF METABOLITES, GENES AND ORGANISMS

Session opens at 15:55 and closes at 17:30

- 16:00-16:25 CET – NETop: **Asaph Aharoni**, Weizmann Institute of Science, Israel. *The Bitter - Sweet Sides of Solanaceae-Specialized Metabolism*
- 16:25-16:40 CET – NETo01: **Luisa Fernanda Bermudez Salazar**, IABIMO, INTA-CONICET, Argentina, *Deciphering the epigenetic variability in S. lycopersicum accessions and their influence on hybrid vigor*.
- 16:40-16:55 CET – NETo02: **Lara Pereira**, University of Georgia, USA. *Natural genetic diversity in tomato flavor genes*.
- 16:55-17:10 CET – NETo03: **Gustavo A. Silva-Arias**, Technical University of Munich, Germany. *Ecological genomics in wild tomatoes to reveal mechanisms of adaptation to living in the driest region of the world*.
- 17:10-17:25 CET – NETo04: **Salvador Torres Montilla**, CRAG, Spain. *A novel system for the artificial differentiation of chromoplasts from pre-existing chloroplasts in leaves*

17:30 – 17:45 CET: Break

17:45 - 18:30 CET: Poster session 3 (NET1, STR1, BRE1).

November 11th, 2020

12:55 – 13:40 CET: Poster session 4 (NET2, STR2, BRE2).

13:40 – 13:55 CET: Break

Session 5: STRESS BIOLOGY (BIOTIC AND ABIOTIC)

Session opens at 13:55 and closes at 15:30

- 14:00-14:25 CET – STRiop: **Parvinderdeep Kahlon**, TUM School of Life Sciences, Technical University of Munich, Germany. *Population studies of the wild tomato species Solanum chilense reveal geographically structured major gene-mediated pathogen resistance*
- 14:25-14:40 CET – STRo01: **Andrea Schrader**, RWTH Aachen University, Germany. *Resilience to salinity in tomato – root transcriptome data analyses.*
- 14:40-14:55 CET – STRo02: **Aymeric Goyer**, Oregon State University, USA. *StPIP1, a predicted PAMP-induced peptide in potato, elicits plant defenses and is associated with disease symptom severity in a compatible interaction with potato virus Y*
- 14:55-15:10 CET – STRo03: **Saloni Mathur**, National Institute of Plant Genome Research New Delhi, India. Decoding the regulatory networks of diverse coding and noncoding RNAs towards heat stress response in tolerant and sensitive tomato cultivars from Indian sub-continent
- 15:10-15:25 CET – STRo04: **Golam Jalal Ahammed**, Henan University of Science and Technology, China. *Nitric oxide is involved in the SlWRKY81 transcription factor-regulated stomatal movement and drought tolerance in Solanum lycopersicum L.*

15:30-16:00 CET - Break

Session 6: BREEDING (TECHNOLOGIES AND TRAITS)

Session opens at 15:55 and closes at 17:30

- 16:00-16:25 CET – BREop: **Dani Zamir,** Hebrew University of Jerusalem, Israel. *Exotic Genetic Libraries' map resistance to Tomato Brown Rugose Fruit Virus (ToBRFV) to the Tobacco Mosaic Virus locus, TM1.*
- 16:25-16:40 CET – BREo01: **Sean Fenstemaker**, Ohio State University, USA. *Using Solanum galapagense to achieve tolerance to water deficit through introgression breeding and grafting*
- 16:40-16:55 CET – BREo02: **Yury Tikunov**, Wageningen University & Research, The Netherlands. *The genetic and functional analysis of flavor in commercial tomato: a novel FLORAL4 gene underlies a QTL for floral aroma volatiles in tomato fruit*
- 16:55-17:10 CET – BREo03: **Jaime Prohens**, Universitat Politècnica de València, Spain. *Towards the development of the first eggplant MAGIC population and QTL analysis of selected morphological traits*

Diploid potato inbreeding mini-session:

- 17:10-17:20 CET – BREo04: **Ernst-Jan Eggers**, Wageningen University & Research, The Netherlands. *The S-Locus Inhibitor gene encodes an F-box protein with a Lectin domain and crucially enables hybrid potato breeding*
- 17:20-17:30 CET – BREo05: **Nathalie Kaiser**, Michigan State University, USA. *Assessing the contribution of Sli to self-compatibility in North American diploid potato germplasm using KASP markers*

- 17:30-17:35 CET – Joint Question period for diploid potato inbreeding talks

17:45-18:15 CET – SOLIOM Meeting closing

ABSTRACTS

Session 1: BIOTECHNOLOGY

Oral presentations

- **BIOop:** Ceulemans *et al*. *Unravelling the regulation of tomato metabolism through interactomics analyses.*
- **BIOo01:** Horizon2020 *N. benthamiana* Sequencing Consortium. *Genetic, epigenetic and metabolomic insights from reference level genome assembly of a wild and a laboratory strain of Nicotiana benthamiana*.
- **BIOo02*:** Hunziker *et al. Improvement of carotenoid accumulation in tomato fruits by CRISPR-Cas9 Cytidine Deaminase system*.
- **BIOo03:** Knoch *et al*. *The third DWF1 paralog in Solanaceae, sterol Δ^{24}-isomerase, branches withanolide biosynthesis from the general phytosterol pathway*.
- **BIOo04:** Ramirez Gonzales *et al. A new insight of StCDF1 under drought stress in potato*

Poster Presentations

Note: Oral presentations marked with a * will be presented also a poster. Their abstract will have a oral presentation ID (BIOo).

- **BIOp01:** Alonge *et al. Towards ultra-accurate and complete chromosome-scale Solanaceae reference genomes*.
- **BIOp02:** Arruabarrena *et al. CYC-B gene edited tomato elite breeding lines created to improve lycopene content in fruits*.
- **BIOp03:** Averello *et al. Modifying Cholesterol Biosynthesis to Accumulate Vitamin D in Tomato*.
- **BIOp04:** Li *et al. CRISPR/Cas9 targeted mutagenesis of the susceptibility gene PMR4 in tomato 'San Marzano' and 'Oxheart'*.
- **BIOp05:** Maioli *et a. CRISPR/Cas9-mediated genome editing in Solanum melongena to reduce fruit flesh browning*.
- **BIOp06:** Molina-Hidalgo *et al. Transcriptomic and phenotypic analysis of engineered tobacco (Nicotiana tabacum) editing the last steps of the alkaloid biosynthesis by CRISPR-Cas9.*
- **BIOp07:** Munir *et al. Tomato, A symbol of food security for developing world.*
- **BIOp08:** Orso et al. *Evaluating biochemical and physiological effect of CRISPR/Cas9-mediated HQT gene editing in S. lycopersicum*.
- **BIOp09:** Takova *et al. Nicotiana benthamiana plants produced recombinant Hepatitis E virus ORF2 capsid protein suitable as a diagnostic reagent and vaccine*.
- **BIOp10:** Vazquez-Vilar *et al. Edition of complex gene families in tobacco with GoldenBraid 4.0, a multipurpose web-based platform for plant genome engineering*.

BIOop

Unravelling the regulation of tomato metabolism through interactomics analyses

E. Ceulemans[1,2], J. Di Sora[1,2], L. Gryffroy[1,2], A.C. Jaramillo Madrid[1,2], A. Ritter[1,2], J. Venegas Molina[1,2], A. Goossens[1,2].

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*Presenting author (alain.goossens@ugent.vib.be)

Abstract
Interactions among and between small molecules and macromolecules drive virtually all cellular regulatory processes within any organism as well as the interaction between different organisms. This is particularly applicable to the regulatory networks that control plant metabolism and have been installed by nature to safeguard plant fitness in a continuously changing environment. To unravel these networks, we have installed different cutting-edge platforms to study interaction between proteins and between proteins and metabolites in tomato. More specifically, this concerns a yeast two-hybrid (Y2H)-Seq and a TurboID platform for protein-protein and a limited proteolysis-coupled mass spectrometry (LiP-MS) for protein-metabolite interaction analyses. I will present these platforms and illustrate how they are being applied in my group to understand several aspects of plant metabolism including:
(1) How the phytohormone jasmonate steers the delicate balance between growth and defence programs, such as the production of bioactive specialized metabolites,
(2) How rhizogenic Agrobacteria metabolically reprogram plant roots to the so-called 'hairy roots', highly proliferating root cultures that are attractive options for the mass production of high-value plant metabolites, and
(3) Which hitherto unknown proteins are targeted by plant metabolites with a signalling function or a yet unknown mode of action.

BIOo01

Genetic, epigenetic and metabolomic insights from reference level genome assembly of a wild and a laboratory strain of *Nicotiana benthamiana*.

Horizon2020 *N. benthamiana* Sequencing Consortium

Horizon2020 N. benthamiana Sequencing Consortium

*Presenting author (peter.waterhouse@qut.edu.au)

Abstract
Nicotiana benthamiana is a member of the Solanaceae family and an ancient allotetraploid. One isolate of *N. benthamiana*, collected from an arid habitat of central Australia, is used in ever-increasing numbers, in laboratories around the world. It has been instrumental in aiding revolutionary discoveries about RNA interference, plant–pathogen interactions and metabolic pathway engineering. We have collected accessions representative of the species' natural distribution and analysed them, alongside the laboratory isolate. Chromosome level genome assemblies were made, using PacBio and Illumina sequencing and Bionano and Hi-C mapping, from the laboratory strain and a wild strain with contrasting phenotypic characteristics, collected from a less harsh environment in Queensland, Australia. Epigenetic states were analyzed using ChIP-seq and bisulfite sequencing. The two subgenomes within these allotetraploids were identified, along with evidence of recombination and rearrangement between them. The LAB strain appears to have undergone more rearrangement and has lost several functions during its adaptation to the arid habitat. For example, in contrast to QLD, LAB is impaired in its defence against viruses, and unable to produce pollinator attracting volatiles, or the potent insecticide nornicotine, or anthocyanin pigments. These and other features appear to confer qualities on the LAB strain that make it attractive as a biofactory and research resource.

BIOo02

Improvement of carotenoid accumulation in tomato fruits by CRISPR-Cas9 Cytidine Deaminase system.

J. Hunziker[1*], K. Nishida[2], A. Kondo[2], S. Kishimoto[3], T. Ariizumi[4] H. Ezura[4, 5]

1- Graduate School of Life and Environmental Sciences, University of Tsukuba, Tsukuba, Japan.
2- Graduate School of Science, Technology and Innovation, Kobe University, Kobe, Japan.
3- Institute of Vegetable and Floricultural Science, NARO, Tsukuba, Ibaraki, Japan.
4- Faculty of Life and Environmental Sciences, University of Tsukuba, Tsukuba, Japan.
5- Tsukuba Plant Innovation Research Center, University of Tsukuba, Tsukuba, Japan

*Presenting author (s1830250@u.tsukuba.ac.jp)

Abstract
Tomato is one of the major crops over the world for its commercially value and health benefit. Because of the convenience of handling, and the relatively small genome size compared to other species of the Solanaceae family, tomato genome has been regarded as the reference among Solanaceae genomes.
The tomato fruit is known as a good source of lycopene, vitamin C, and β-carotene. Carotenoids play an important role in human nutrition because of their pro-vitamin A activity.
Several mutations which affect the accumulation of carotenoid contents in tomato fruits, such as old gold crimson (ogc)[1] or hp family mutants [2-3] have been identified. They have been currently used in traditional breeding to increase the contents of lycopene in commercial cultivars.
The aim of this study is to develop with the single base editing technology by Target-AID, and new breeding materials with a higher carotenoid content, by multiple targeting in a single transformation. For this, transformation on Micro-Tom, using a vector construction including 3 gene targets and a nickase CAS9 (nCas9) protein fused with a Cytidine deaminase (CDA) protein, was done. Although this technology uses transgene for targeting genes, transgenic components can be removed in the next generation. This results in an edited plant, carrying multiple mutations without the presence of transgene. In conclusion, it can be used as a fast tool in gene edition to create new breeding materials without the need of gene introgression by crossing, and results in dramatically reducing the time and cost to provide a new cultivar on markets.

References
[1] Mustilli AC, Fenzi F, Ciliento R, Alfano F, Bowler C. Phenotype of the tomato high pigment-2 mutant is caused by a mutation in the tomato homolog of DEETIOLATED1. Plant Cell. 1999;11(2):145–157. doi:10.1105/tpc.11.2.145
[2] Ronen G, Carmel-Goren L, Zamir D, Hirschberg J. An alternative pathway to beta -carotene formation in plant chromoplasts discovered by map-based cloning of beta and old-gold color mutations in tomato. Proc Natl Acad Sci U S A. 2000;97(20):11102–11107. doi:10.1073/pnas.190177497
[3] Lieberman M., Segev O., Gilboa N., Lalazar A., Levin I. The tomato hortolog of the gene encoding UV damaged DNA binding protein 1 (DDB1) underlined as the gene that causes the high pigment 1 mutant phenotype. Theor Appl Genet (2004) 108: 1574. https://doi.org/10.1007/s00122-004-1584-1

BIOo03

The third DWF1 paralog in Solanaceae, sterol Δ^{24}-isomerase, branches withanolide biosynthesis from the general phytosterol pathway

E. Knoch[1*], S. Sugawara[1], T. Mori[1], C. Poulsen[2], A. Fukushima[1], Y. Fujimoto[3], N. Umemoto[1] and K. Saito[1,4].

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4- Graduate School of Pharmaceutical Sciences, Chiba University, Chiba, Japan.

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Abstract
Withanolides are a large group of structurally-diverse C28 steroidal lactones derived from 24-methylenecholesterol. These compounds are found in the Indian medicinal plant Withania somnifera, also known as Aswagandha, and other members of the Solanaceae. The pathway for withanolide biosynthesis is largely unknown, restricting sustainable production via biotechnology and downstream pharmaceutical usages.
Based on genome and transcriptome data we identified a key enzyme in the biosynthesis of withanolides; a DWF1 paralog encoding a sterol Δ^{24}-isomerase (24ISO). 24ISO originated from DWF1 after two subsequent duplication events in Solanoideae plants. Withanolides and 24ISO appear only in the medicinal plants in the Solanoideae, not in crop plants such as potato and tomato, indicating negative selection during domestication. 24ISO is a unique isomerase enzyme evolved from a reductase, and as such has maintained the FAD-binding oxidoreductase structure and requirement for NADPH. Using phylogenetic, metabolomic and gene expression analysis in combination with heterologous expression and virus-induced gene silencing, we showed that 24ISO catalyzes the conversion of 24-methylenecholesterol to 24-methyldesmosterol. We propose that this catalytic step is the committing step in withanolide biosynthesis, opening up elucidation of the whole pathway and future larger-scale sustainable production of withanolides and related compounds with pharmacological properties.

BIOo04

A new insight of StCDF1 under drought stress in potato

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Abstract
Potato is considered susceptible to drought. Water limitation affects tuber yield, size, and shape of tubers. Therefore, it is essential to understand genes involved in drought tolerance. CDFs genes belong to DOF (DNA-BINDING ONE ZINC FINGER), transcription factors they are involved in several biological functions including abiotic stress response. In potato, vegetative reproduction via tuberization is known to be regulated by diurnal regulation. Here, we show that StCDF1 negatively regulates an antisense lncRNA called StFLORE and genes related to nitrate assimilation such as a nitrate transporter (NRT). This regulatory network is involved in the improvement of controlling stomata closure and nitrogen assimilation throughout the diel cycle during drought. Our results show that elevated expression of StFLORE both by overexpression of StFLORE or down regulation of StCDF1, results in an increased tolerance to drought by reducing water loss through stomatal closure. Conversely, both natural allelic variants of StCDF1 and CRISPR-Cas9 mutations in the StFLORE promoter produce plants with increased sensitivity to water limiting conditions. Furthermore, from DAPseq data of overexpressing and knocking down StCDF1 transgenics plants, we found that StCDF1 protein represses a nitrate transporter gene. This result was corroborated by sequence analysis of potato cultivars where interestingly tolerant drought cultivars have higher expression of nitrate transporter gene and lower expression of StCDF1 during the day. In this study, we contribute to deciphering the role of StCDF1 under drought conditions in potato plants through different molecular approaches including a construction of CRISPR-cas9 cassettes and DAPseq data.

BIOp01

Towards ultra-accurate and complete chromosome-scale Solanaceae reference genomes

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Abstract
Despite recent advances in long-read sequencing technologies, plant genome assembly remains challenging. In particular, modern assemblies often fail to accurately reconstruct genomic repeats that are pervasive in plant genomes. Large initiatives such as the Vertebrate Genomes Project and the Human Telomere-To-Telomere (T2T) consortium have established best practices and industry standards for assembling animal genomes, but it remains unclear how these approaches translate to plant genomes.

Here, we use PacBio Circular Consensus accurate long-reads (CCS), Oxford Nanopore ultra-long reads, and chromatin conformation capture (Hi-C) to establish two platinum-level Solanaceae genome assemblies. We first demonstrate the efficacy of this approach on the widely used tomato reference genotype M82, for which we report substantial improvements in accuracy, contiguity, and completeness compared to previous long-read assemblies. We then apply this approach to establish a new reference genome for the orphan crop *Physalis grisea* (groundcherry). This highly repetitive 1.3 Gb diploid genome also resulted in an ultra-accurate and complete chromosome-scale assembly using our innovative combination of sequencing data types and bioinformatic approaches. Using specific examples from these assemblies, we highlight new methods and best practices for plant genome assembly and scaffolding. We also discuss potential applications in pan and "personalized" genomics for tomato, as well as implications for cross-species functional studies for orphan crops and wild nightshades.

BIOp02

CYC-B gene edited tomato elite breeding lines created to improve lycopene content in fruits

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Abstract
Tomato's red fruit lycopene content is controlled, among other factors, by the decrease in Lycopene Beta Cyclase (CYC-B) gene expression. Spontaneous mutations like old gold (og) and old gold crimsom (ogc) generate non-functional CYC-B enzymes. These variants are used in breeding to increase red color. Since these mutations originated in genotypes carrying the sp mutation and CYB-B and SP genes are linked on chromosome 6, og and ogc mutants have, in consequence, determinate growth. The goal of this work is to generate novel mutations in the CYC-B gene directly into indeterminate growth tomato lines using CRIPR/Cas9. Tomato elite breeding lines 'LT16' and 'LT46', parents of a modern hybrid cultivar, were transformed with a construct containing Cas9 and specific sgRNAs expression cassettes, targeting the coding sequence of CYC-B. Transgenic regenerated plants (resistant to kanamycin) were screened for Cas9-induced mutations in the CYC-B locus using High-resolution fragment analysis and Sanger sequencing. Mutant phenotypes similar to old gold and old gold crimson phenotypes were observed in flowers and fruits of T0 plants. The progeny of one edited line was screened for plants with different combination of the mutant alleles and for T-DNA free plants. Novel CYC-B alleles were characterized by Sanger sequencing. Selected plants will be used to evaluate a new version of the indeterminate hybrid cultivar, free of T-DNA and with different allele variants of the CYC-B gene.

BIOp03

Modifying Cholesterol Biosynthesis to Accumulate Vitamin D in Tomato.

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Abstract
Approximately 30% of people in the United States report using Vitamin D supplements, increasing to 49% of men and 59% of women over 60. Vitamin D is needed for good skeletal health but has also been connected to improved cancer outcomes, better cardiovascular health, and good mental health. Sources of vitamin D include cod liver oil, dairy products, wild mushrooms, and UVB. There is no plant source of dietary vitamin D. Members of genus Solanum contain 7-dehydrocholesterol (7-DHC). When exposed to UVB, this begins the production of vitamin D. 7-DHC serves as the substrate of 7-Dehydrocholesterol Reductase-2 (7-DR-2) in tomato, which produces cholesterol that is used to produce **α**-tomatine. If 7-DR-2 is knocked out it will cause an increase in the amount of 7-DHC. Here we report our pilot research aiming to increase Vitamin D production in tomato by altering its cholesterol pathway. Two sites were selected using CrisprP 2.0 based on the lowest likelihood to produce off-target effects. The sequences to produce sgRNAs were cloned into pDIRECT_21C. This carries AtCas9 driven by the 35S promoter, sites to receive RNA sequences driven by CmYLCV promoter, bacterial kanamycin resistance, and plant hygromycin B. Two tomato lines were chosen for gene editing, MTX-851 because it was bred specifically for Minnesota's growing conditions, and M82 because it established to be transformable by Agrobacterium. Preliminary work has shown that MTX-851 is able to regenerate through tissue culture and at least one line of M82 has been regenerated after Agrobacterium mediated transformation..

BIOp04

CRISPR/Cas9 targeted mutagenesis of the susceptibility gene PMR4 in tomato ‘San Marzano’ and ‘Oxheart’.

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Abstract
Late blight (LB), caused by *Phytophthora infestans*, and powdery mildew (PM), caused by species within the Erysiphaceae family, are the most destructive and widespread diseases in tomato (Solanum lycopersicum L.). The control of these pathogens extensively relies on fungicide application, leading to economic losses and environment impact. The disabling of susceptibility (S) genes, which facilitate pathogen infection, may provide a broad-spectrum and durable type of resistance. To this purpose, the CRISPR/Cas9 gene editing represents the most suitable and fast strategy.
We selected the Powdery Mildew Resistant 4 (PMR4) gene, whose disabling has been shown to confer PM resistance in Arabidopsis and in the tomato variety ‘Moneymaker’. In order to verify whether the effect of disabling S genes is background-dependent, we knocked-out the PMR4 gene in two widely cultivated varieties, ‘San Marzano’ and ‘Oxheart’. CRISPR mutants were generated by using 4 sgRNAs targeting the FKS1dom1 and Glucan-synthase domain of the PMR4 protein in order to maximize editing efficiency.
In all, 87 tomato pmr4 transformants were obtained (T0 generation) of which 70 in ‘San Marzano’ and 17 in ‘Oxheart’. Twelve of ‘San Marzano’ mutants were tested and resulted positive for the presence of Cas9 gene. The Sanger analysis performed on target editing regions revealed 3 edited plants with large deletions (~2kb) and 9 showing a prevalence of 7bp deletions. In the next future, mutants will be test with PM and LB to quantify the level of resistance.

BIOp05

CRISPR/Cas9-mediated genome editing in *Solanum melongena* to reduce fruit flesh browning.

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Abstract
Eggplant (*Solanum melongena*) berry flesh turns brown after cutting and exposure to air and this affects fruit quality for both industrial applications and fresh consumption. This process is caused by the enzymatic oxidation of phenolic compounds catalysed by polyphenol oxidase enzymes (PPO). In eggplant, the PPO gene family is composed by 10 members (named ppo1-10). As highlighted by transcriptional analyses, ppo4, ppo5 and ppo6 were strongly up-regulated in the flesh after cutting. A CRISPR/Cas9 approach was applied to induce knock-out mutations on these three genes in the 'Black Beauty' variety, designing a single sgRNA targeting a conserved region. Following transformation with the gene editing construct, in vitro regenerated plantlets were obtained. Illumina deep sequencing of amplicons of the target sites confirmed the successful editing of ppo4, ppo5 and ppo6 with the insertion of a single nucleotide as the most frequent mutation.

Editing at target loci were stably inherited in the T1 and T2 progenies, while no off-target mutations were identified on the potential off-target loci. Upon cutting, edited T1 and T2 eggplant fruits showed a reduction of the typical brown coloration caused by phenolic oxidation. This study is the first example of CRISPR/Cas9 editing in eggplant, representing an alluring option for the introduction of specific traits through a targeted biotechnological approach.

BIOp06

Transcriptomic and phenotypic analysis of engineered tobacco (Nicotiana tabacum) editing the last steps of the alkaloid biosynthesis by CRISPR-Cas9.

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Abstract
The use of plant biofactories for the production of high-value-added compounds following application of biotechnological approaches is defined as Molecular Farming. Redirecting non-food crops into versatile biofactories is becoming an alternative for a sustainable bioeconomy. Its metabolic complexity and yield productivity position tobacco as an appropriate chassis for this purpose, but its elevated content in alkaloids may cause penalties in the production of desired compounds. Hence, engineering this trait could enhance the biofactory value of this crop. Here, we produced genome-edited tobacco lines targeting the final oxidation step in the biosynthesis of alkaloids, which is proposed to be catalysed by flavoproteins of the berberine bridge enzyme-like (BBL) family. We followed a CRISPR Cas9-based knockout strategy and identified a conserved target sequence present in all putative alkaloid-related BBL genes to enable the use of a single-guide RNA. Comparison of the transcriptomes of the resulting transformed control and bbl KO lines has revealed several differentially expressed genes, pointing to several perturbed cellular processes. Additionally, the bbl KO lines showed a clear reduction in the nicotine content, the major tobacco alkaloid, as well as in the amount of anabasine and anatabine. Notably, these lines also presented an unexpected concomitant increase in the concentration of nornicotine, suggesting the existence of some yet unknown biosynthetic steps in the alkaloid pathway. Taken together, the multiple knockout of the alkaloid BBL genes may be a promising approach to improve the chassis of the tobacco plant as production platform for plant-made added-value compounds.

BIOp07

Tomato, A symbol of food security for developing world

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Abstract
Tomato (*Solanum lycopersicum*) is a major horticultural crop worldwide and it has emerged as a symbol of food security for the developing world. Improved metabolic content signify the importance of the tomato fruit to overcome the malnutrition problems. The dynamics of metabolic changes during the tomato growth cycle and the regulatory networks that underlie these changes are worth to investigate. In this study, AsA biosynthesis pathways through Myo-inositol oxygenase (MIOX) enzyme was studies to improve the nutritive value of tomato fruit and enhance the plants tolerance to environmental stresses. MIOX proteins identification and MIOX transgenic lines characterization indicated significant involvement of Myo-inositol (MI) to improve the AsA biosynthesis in tomato fruit.

BIOp08

Evaluating biochemical and physiological effect of CRISPR/Cas9-mediated HQT gene editing in *S. lycopersicum*

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Abstract
Chlorogenic acid (CGA) and its isomers are the most abundant polyphenols in many plant species such as potato, tomato, eggplant, tobacco, coffee and apple. Due to their biological properties they are important compounds for plant protection against biotic and abiotic stresses. Their biosynthesis could occur by several different pathways, but considerable evidence suggests that the most active pathway is mediated by Hydroxycinnamoyl CoA Quinate Transferase (HQT). HQT converts caffeoyl-CoA and quinic acid to CGA and in some Solanaceous species its role has been demonstrated; in tomato the silencing of SlHQT resulted in a significant reduction of CGA and the overexpression of SlHQT led to an accumulation of CGA. To study the SlHQT contribution in CGA biosynthesis in tomato further, we designed a CRISPR/Cas9 construct to edit the SlHQT gene.
Here we present the characterization of hqt mutants and the evaluation of the effect of ko mutations on phenylpropanoid metabolism in normal conditions and under abiotic stress. In addition, the hqt mutants enabled us to study the histolocalization of caffeoylquinic acids (CQAs) in tomato leaf and to understand their involvement in the photoprotection against UV light.

BIOp09

Nicotiana benthamiana plants produced recombinant Hepatitis E virus ORF2 capsid protein suitable as a diagnostic reagent and vaccine

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Abstract
Nicotiana benthamiana has received a great deal of attention as an expression system of recombinant proteins. Varieties of therapeutic and diagnostic proteins have been produced in *N. benthamiana* and several of them are currently on the market. Plants have unique advantages over other expression systems such as rapid and affordable growth conditions; plants are free from pathogen; and post-translational modification is very similar to mammalian system. Several expression vectors have been developed to enable high levels of protein production in plants. In the current study, we describe the efficient transient expression of Hepatitis E open reading frame (ORF) 2 capsid protein in *N. benthamiana* using two expression vectors: pEAQ-HT, based on Cowpea Mosaic Virus (CPMV), and pEff, based on potato X virus (PVX). HEV ORF2 protein was purified from plant tissue by immobilized metal-anion chromatography and gradient centrifugation. The recombinant protein was used to develop an in-house ELISA for testing anti-HEV antibodies in both human and swine sera. Furthermore, the truncated HEV ORF2 protein consisting of aa residues 110 to 610 formed nanosized virus-like particles. The immunization of mice with plant-produced HEV 110-610 protein induced high levels of HEV-specific serum antibodies..

BIOp10

Edition of complex gene families in tobacco with GoldenBraid 4.0, a multipurpose web-based platform for plant genome engineering.

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Abstract
CRISPR/Cas ability to target several loci simultaneously (multiplexing) is a game-changer in plant breeding. Multiplexing not only accelerates trait pyramiding but also can unveil traits hidden by functional redundancy in polyploid crops. Furthermore, multiplexing enhances dCas-based programmable gene expression and enables cascade-like gene regulation. However, multiplex constructs comprising tandemly arrayed gRNAs are difficult to assemble, this hampering more widespread use. Here we present a comprehensive upgrade of the popular cloning platform GoldenBraid (GB), in which, on top of its classical multigene cloning software, we integrate new assembly tools for two-dimensions gRNA multiplexing with both Cas9 and Cas12a, using the gRNA-tRNA-spaced and the gRNA unspaced approaches, respectively. As functional validation, we show, among others, the assembly of up to 17 tandemly-arrayed gRNAs constructs against a subset of the Squamosa-Promoter Binding Protein-Like (SPL) and FT gene family in tobacco. With these constructs we generated a collection of Cas9-free SPL/FT mutants harboring up to 9 biallelic mutations in a single generation, unveiling their effects in flowering time, branching and juvenility. The functionality of GB-assembled dCas9 and dCas12a-based CRISPR activators and repressors using single and multiplexing gRNAs is also validated. With the incorporation of the new CRISPR tools and part´s collection, GB4.0 turns an unprecedentedly comprehensive open platform for genetic engineering in Solanaceae. .

Session 2: DIVERSITY AND EVOLUTION

Oral presentations

- **EVOop**: McDonnell & Martine. *Sexual fluidity among the bush tomatoes: Prickly solanums of the Australian Monsoon Tropics.*
- **EVOo01**: Gibson *et al. Reconstructing the history and biological consequences of a plant invasion on the Galápagos islands.*
- **EVOo02**: Tripodi et al. *Genebank genomics highlights novel centres of diversity and routes of migration in pepper (*Capsicum spp.*).*
- **EVOo03**: Ibañez *et al. Flower color evolution in the florally diverse genus Salpichroa (Solanaceae) seen through the eyes of its pollinators.*
- **EVOo04**: Kahlon *et al. Using wild tomato species to study diversity and evolution of biotic stress responses.*

Poster presentations

- **EVOp01**: Deanna *et al. A review of the seed fossil record for nightshades (Solanaceae)*.
- **EVOp02**: Doria. *Petal cell shape and flower-pollinator interaction in Nicotiana*
- **EVOp03**: Enciso-Rodríguez *et al. Population structure and genetic diversity of Cape gooseberry and related taxa using an optimized Genotyping by Sequencing SNP calling pipeline*.
- **EVOp04**: Forti *et al. Molecular dynamics of pre-germinative metabolism in primed eggplant (Solanum melongena L.) and seeds.*
- **EVOp05**: Gagnon *et al. Phylogenomic data reveals hard polytomies in the large genus Solanum (Solanaceae).*
- **EVOp06**: Gandini, Ibañez *et al. The phylogeny of the tribe Hyoscyameae based on complete plastomes and the evolution of the cox1 intron.*
- **EVOp07**: Jacobsen. *Growth rate and life history shape plant anti-herbivore resistance across* Physalis*.*
- **EVOp08**: Murúa Carrizo *et al. Recover of wild peppers* (Capsicum chacoense *Hunz.) in central valley of Catamarca, Argentina. Phenotypic characterization and selection by agronomical traits and fruit quality.*
- **EVOp09**: Nichodemus et al. *Morphological Characterization of Some Nigerian Solanum L. Species (Solanaceae)*.
- **EVOp10**: Palombo *et al. Exploring the origin and diversification of the locoto chile (Capsicum pubescens): multiple approaches using RAD-seq data*.
- **EVOp11**: Pezzi et al. *A misleading clue of hybridization between two* Petunia *species*.

- **EVOp12**: Ramírez-Ojeda et al. *Ecological Descriptors of Wild Tomato Species (Solanum Sect. Lycopersicon) and Close Related Species (Solanum Sect. Juglandifolia & Sect. Lycopersicoides) in Latinamerica*.
- **EVOp13**: Ranawaka *et al. The balance between pollinator attraction and anti-herbivory in Nicotiana benthamiana*.
- **EVOp14**: Rashid. *Collection and Evaluation of Genetic Diversity and Population Structure of Potato Landraces and Varieties in China.*
- **EVOp15**: Soares & Freitas. *Could a whole valley stop gene flow in* Petunia altiplana?

EVOop

Sexual fluidity among the bush tomatoes: Prickly solanums of the Australian Monsoon Tropics.

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Abstract
Just 1% of species in Solanaceae exhibit a dioecious breeding system, with the majority of the occurrences happening within the "spiny solanums" of the Australian Monsoon Tropics. In these species, morphologically hermaphrodite individuals produce inaperturate pollen that renders them functionally female. The "*S. dioicum* group", consisting of functionally dioecious taxa and a set of andromonoecious relatives has been a subject of systematic study for decades, yet the relationships among groups of species and, thus, the patterns in sexual system evolution are still poorly understood. We aim to illuminate the evolutionary history of the lineage using targeted enrichment data, evaluate areas and potential sources of phylogenetic conflict, reconstruct the evolution of diverse breeding systems, and revisit previous hypotheses regarding reproductive characters. We include 172 individuals representing 102 taxa and report on data obtained via the Angiosperms 353 probe set. Against a background of hermaphroditism, we detect one origin of andromonoecy, one or two origins of dioecy, and one possible reversal to the hermaphroditic state within a revised "*S. dioicum* group". Our study provides a framework of evolutionary relationships in Australian spiny Solanum; most inferred species relationships are well supported across multiple analyses while the detected discordance among gene trees highlights a complex history that includes rapid speciation, incomplete sorting of ancestral variation, and hybridization. We highlight the evolution of diverse reproductive traits and suggest that sexual system transitions in this group are not only more common than previously thought, but also underlie an ongoing radiation requiring further taxonomic effort.

EVOo01

Reconstructing the history and biological consequences of a plant invasion on the Galápagos islands

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Abstract
The introduction of non-native species into new habitats is one of the foremost risks to global biodiversity. Here, we evaluate a recent invasion of wild tomato (*Solanum pimpinellifolium*) onto the Galápagos islands from a population genomic perspective, using a large panel of novel collections from the archipelago as well as historical accessions from mainland Ecuador and Peru. We infer a recent invasion of *S. pimpinellifolium* on the islands, largely the result of a single event from central Ecuador which, despite its recency, has rapidly spread onto several islands in the Galápagos. By reconstructing patterns of local ancestry throughout the genomes of invasive plants, we uncover evidence for recent hybridization and introgression between *S. pimpinellifolium* and the closely related endemic species *Solanum cheesmaniae*. Two large introgressed regions overlap with known fruit color loci involved in carotenoid biosynthesis. Instead of red fruits, admixed individuals with endemic haplotypes at these loci have orange fruit colors that are typically characteristic of the endemic species. We therefore infer that introgression explains the observed trait convergence. Moreover, we infer roles for two independent loci in driving this pattern, and a likely history of selection favoring the repeated phenotypic transition from red to orange fruits. Together, our data reconstruct a complex history of invasion, expansion, and gene flow among wild tomatoes on the Galápagos islands. These findings provide critical data on the evolutionary importance of hybridization during colonization and its role in influencing conservation outcomes.

EVOo02

Genebank genomics highlights novel centres of diversity and routes of migration in pepper (*Capsicum spp.)*

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Abstract
Genebanks play a key role in collecting, maintaining, and distributing germplasm resources. A better understanding of the stored genetic resources is essential for their use in breeding programs, and genomics offers unique opportunities for their characterization and management. Here, we report the use of genome-wide genotyping-by-sequencing to characterize the genetic diversity and population structure of ~10,000 pepper accessions from major worldwide genebanks. Genome-scale data provide new insight into diversification and spread routes of pepper highlighting two novel centres of diversity in Southern Europe and in South Asia, the latter showing close genetic relatedness to the Mesoamerican primary centre of diversity, suggesting a direct migration to South Asia soon after domestication.

EVOo03

Flower color evolution in the florally diverse genus Salpichroa (Solanaceae) seen through the eyes of its pollinators.

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Abstract
Flower color is a key signal which pollinators use to find and distinguish resources, therefore it plays a relevant role in shaping plant-pollinator interactions. Studying floral color evolution can be challenging as it requires understanding how pollinators perceive flower signals, since animals see the world differently than humans. Flower color phenotype can be envisaged to shift through evolutionary change along visual spaces represented by the perceptive visual axes of the animals that pollinate them. We focused our study on Salpichroa (Solanaceae), a small Andean genus with a remarkable variation in floral phenotype to test whether interspecific and intrafloral (corolla tube vs. limb) variation in flower color is associated with changes in pollination modes along perceptive axes of moths and hummingbirds that act as primary pollinators. We used plant-phylogenetically informed and pollinator-visual modeling approaches to assess the evolution of color diversity taking into account the color perception capabilities of the primary pollinators acting as potential selective agents. Phylogenetic comparative analyses revealed significant association between perceptual color axes, nectar reward and transitions in the pollination mode (i.e. generalist, moth, hummingbird). Our results suggest that flower color evolution in Salpichroa is mainly concomitant with an adaptation to the perception of their current pollinators.

EVOo04

Using wild tomato species to study diversity and evolution of biotic stress responses.

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Abstract
Wild tomato species form an intriguing group of wild plant species. The relatively small number of wild tomatoes, each have their own specific habitats and corresponding ecological niches, though some overlap in their ranges does exist. Wild tomato species have been the source of pathogen resistance germplasm in tomato breeding. In a patchwork of studies several dozens of different pathogen resistance properties have been identified for a large number of pathogens. However, systematic analyses of such resistances and the underlying genetic variation within and between the wild tomato species are sparse.
We are especially interested in understanding such variation and evolution of pathogen resistance properties in a true demographic/ecological context. Our work predominantly focuses on the wild tomato species Solanum chilense. The species grows on the southern edges of the species range for wild tomato and its very specific demography, resulting from two different expansions into extreme environments make it the ideal species to study phenotypic and genetic diversity of biotic defences. In this talk, I will highlight several aspects of recent research projects. These range from genomics analyses that indicate clear resistance gene family evolution to phenotypic and biochemical studies that show tremendous variations in defence hormone responses between and within wild tomato populations.

EVOp01

A review of the seed fossil record for nightshades (Solanaceae).

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Abstract
The placement of extinct taxa on phylogenies relies on scoring informative morphological characters, which can be difficult given the fragmentary nature of the fossil record. Nonetheless, advances in imaging and visualization, such as X-ray micro-Computed Tomography (μ-CT), have made it possible to non-destructively score fine-scale structural variation in fossils. Although detailed studies of Solanaceae fossils remain few, the family exhibits wide variation in seed and fruit traits to use in estimating fossil placement from morphological data. Indeed, a recent application of μ-CT to Solanaceae fossils revealed that Cantisolanum daturoides, formerly considered to be the oldest seed fossil in the family, is instead a commelinid monocot. Therefore, we reviewed most of the previously published seed fossils of Solanaceae in addition to more than 20 findings currently not published. Carpological nightshade collections by Dorofeev, Mai, and Nikitin were studied at European and Russian museums. All fossilized seeds were analyzed using stereomicroscopy and 18 were μ-CT scanned to evaluate pyritization and infer internal preservation. A high-resolution Zeiss Versa 520 μ-CT system, which incorporates phase contrast imaging, was used for scanning. We scored 10 traits, including two continuous, and performed a cluster analysis to compare these fossil seeds to extant Solanaceae (sampling at least one species per genus). This preliminary analysis allowed us to determine which morphological traits are informative and to assign putative placements of the fossils into a phylogenetic tree. These results lay the foundation for a new total evidence dating analysis for the entire family.

EVOp02

Petal cell shape and flower-pollinator interaction in Nicotiana.

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Abstract
Petal epidermal cell shape has been shown to affect pollination success in flowering plants. Conical epidermal cells may increase grip for insect pollinators and enhance flower colouration compared to non-conical cells. Nicotiana presents a diverse range of petal cell shapes. Interestingly, sister species in at least two phylogenetically distinct clades of the genus have contrasting petal epidermal cell shapes (conical vs. non-conical). This provides a unique opportunity to explore the evolution of conical cells. Using a combination of molecular, morphological and behavioural ecology tools I studied the development, evolution and function of petal cell shape in Nicotiana. Differential expression of candidate regulatory genes rather than amino acid sequence differences in the proteins, might explain contrasting cell shapes between sister species. Flower choice experiments with bumblebees, using biomimetic replicates of petals, indicate that the bumblebees can discriminate flowers of contrasting texture using visual cues alone as well as tactile cues alone.

EVOp03

Population structure and genetic diversity of Cape gooseberry and related taxa using an optimized Genotyping by Sequencing SNP calling pipeline.

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Abstract
Cape gooseberry (*Physalis peruviana* L.) is a berry-bearing Solanaceae species, native to the Andean region with enormous potential for biomedical research and commercial purposes. Despite its importance, the species still lacks a more comprehensive platform for Single Nucleotide Polymorphisms (SNPs) discovery. Here we evaluated a total of 176 accessions representing wild, weedy, and commercial cultivars as well as related taxa from the Colombian germplasm bank using GBS. A robust Genotyping-By-Sequencing (GBS) pipeline platform was examined to provide accurate discovery of SNPs. A total of 7,425 SNPs, derived from P. peruviana common tags (unique 64 bp sequences shared between selected species), were identified using the GBS parameters mnLCov of 0.5 and a mnScov of 0.7. Within P. peruviana, five subpopulations with a high genetic diversity and allele fixation (HE: 0.35 to 0.36 and FIS: -0.11 to -0.01, respectively) were detected. Conversely, low genetic differentiation (FST: 0.01 to 0.05) was also observed, indicating a high gene flow among subpopulations. The results of this study provide a comprehensive insight into the genetic diversity and population structure of a relatively large cape gooseberry repository in Colombia.

EVOp04

Molecular dynamics of pre-germinative metabolism in primed eggplant (*Solanum melongena* L.) and seeds.

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Abstract
Eggplant (*Solanum melongena* L.) is a member of the large Solanaceae family domesticated in India and China and is cultivated worldwide for the high nutritional value of its berries that correlates with beneficial effects as disease prevention (Mennella et al., 2012; Gürbüz et al., 2018). Eggplant is difficult to manage in terms of seed quality. Dormancy, poor seed germination rate, and low uniformity have been documented in several accessions of S. melongena and its crop wild relatives (Demir et al., 2005; Taab et al., 2009; Ranil et al., 2015). Low uniformity and low germination percentage severely impact breeding programs, with a huge economic impact on seed industries that need to increase product performance while optimizing the use of economic resources.

Seed priming technology is used to enhance germination and provide faster emergence, uniform stands, and stress tolerant plants (Paparella et al. 2015). With seed priming, a low-cost and pre-sowing technique, imbibition is carried out under controlled conditions in order to delay water up-take and expand the pre-germinative metabolism, the crucial phase of seed germination, boosting antioxidant and DNA repair mechanisms (Paparella et al. 2015).

In the frame of WAKE-APT project, we explore the molecular dynamics of pre-germinative metabolism in hydro-primed eggplant seeds in order to assess the response to priming, select reliable molecular hallmarks (expression patterns of antioxidant/DNA repair genes and ROS profiles) useful to discriminate between high- and low- quality lots and define improved protocols to ameliorate seed quality.

EVOp05

Phylogenomic data reveals hard polytomies in the large genus *Solanum* (Solanaceae).

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Abstract
The increasing availability of phylogenomic data is revealing incongruent topologies in gene trees between and even within genomes. Some of these incongruences indicate hard polytomies that are due to underlying biological processes may remain impossible to resolve. Here we focus on the large and economically important genus Solanum which with 1,230 accepted species, is one of the ten largest flowering plant genera. To provide an evolutionary framework for the large research community working on the genus, we build a new supermatrix phylogeny comprising 60% of all accepted species (740 spp.), based on two nuclear (ITS and WAXY) and seven plastid markers. To assess whether the recovered topology is robust, we explore phylogenomic analyses of a full plastome alignment of 141 species and nuclear genome dataset, composed of a target-capture dataset of 39 species based on the Angiosperm353 probes and supplemented from data extracted from published genomes and transcriptomes. Both datasets contain species from all the major recognized lineages within the genus, and we explore how various taxon sampling, missing data, phylogenetic analyses, and data partitions influence the topology of the recovered species tree. A single strongly supported topology is recovered from the different plastome phylogenomic analyses, which is incongruent with the topology recovered from the supermatrix phylogeny. We quantify gene and site concordance factors to identify where the discordance occurs and discuss the biological significance of the various hypotheses. Our findings highlight how such topological uncertainty should be incorporated in downstream macro-evolutionary and ecological analyses for non-bifurcating evolution.

EVOp06

The phylogeny of the tribe Hyoscyameae based on complete plastomes and the evolution of the cox1 intron.

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Abstract
The tribe Hyoscyameae (Solanaceae) tribe comprises eight genera with two centers of diversity: the Mediterranean-Turanian region (Atropa and Archihyoscyamus) and the Tibetan Plateau area (Przewalskia, Anisodus, and Atropanthe). The genus Scopolia includes species with disjunct distribution in eastern Asia and in the Mediterranean basin. Previous studies based on morphological or molecular characters were not able to resolve the phylogenetic affiliations of the tribe. Here, we assembled the complete chloroplast genome of Scopolia carniolica, the second species of the genus to be described. Using publicly available chloroplast genomes we performed genomic comparisons and examined the phylogenetic relationships for seven of the eight genera of Hyoscyameae. Gene content was identical across the tribe with small differences in genome length. The phylogeny of the tribe was highly resolved, with strong support for relationships among genera. The major advancements included strongly-supported phylogenetic affiliations of Atropanthe, Anisodus, and Hyoscyamus. We also studied the Hyoscyameae phylogeny using a nuclear marker, the internal transcribed spacer 2 (ITS2). Interestingly, even though the ITS2 tree was poorly resolved in general; it recovered all genera as monophyletic, except for Scopolia, which was paraphyletic in respect to Physochlaina. Finally, we re-interpreted the mitochondrial cox1 intron evolution. Two independent, intrafamilial, horizontal acquisitions were inferred, one in the ancestor of Przewalskia, Physochlaina and S. japonica, and another in Hyoscyamus, with no intron losses.

EVOp07

Growth rate and life history shape plant anti-herbivore resistance across *Physalis*

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Abstract
The extensive trait variation across the *Physalis* genus is ideal to study how plant defensive strategies are shaped by a variety of factors, including herbivory, lifespan, and mating system. Using phylogenetic comparative methods, I examined the interacting influences of plant life history (annual/perennial), mating system (self-compatible/self-incompatible), and species growth rates on both constitutive and induced anti-herbivore resistance. Contrary to long-standing assumptions in the field of plant defense, I found no evidence for a trade-off between constitutive resistance and inducibility. Instead, species growth rates and life history traits interacted to determine plant resistance. These results indicate that constitutive resistance and inducibility are not alternative strategies in Physalis and therefore can be shaped by different selective pressures.

EVOp08

Recover of wild peppers (*Capsicum chacoense* Hunz.) in central valley of Catamarca, Argentina. Phenotypic characterization and selection by agronomical traits and fruit quality.

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Abstract
Capsicum chacoense is native to South America distributed in Bolivia, Argentina and Paraguay, and highly appreciated as food condiment by local communities in northwestern Argentina. Fruits of "ají del monte" or "uchuquita" are harvested in their natural habitats and commercialized regionally. Traditional harvesting consists in the extraction of productive branches or the whole plant, which is the main reason for the degradation and possible loss of this valuable plant genetic resource. This concern drives a more comprehensive study about the potential for use of this wild pepper species and its conservation status. In 2020 the recovery of germplasm began in 14 locations in the Central valley of Catamarca, where "uchuquita" forms small populations associated with trees, shrubs and cactaceous species of the Monte plant community (*Prosopis spp., Sarconphalus mistol, Celtis spp., Geoffroea decorticans, Parkinsonia praecox, Larrea spp., Pachycereus pringlei, Cereus forbesii*). In each population an ecological characterization was made and fruits of at least 10 plants were collected. Part of the recovered seeds are maintained in a germplasm bank, while others were selected to produce plants for cultivation in field trials. Preliminary results show a good adaptation of the plants to agronomical management. Phenotypic characterization includes 20 quantitative and qualitative variables comprising the seedling, vegetative and reproductive stages, as well as fruit pungency due to capsycinoid alkaloids, since preliminary studies have shown variability in populations. An integrative study of Capsicum chacoense, including cultural traditions, allows germplasm conservation strategies and promotes its use in horticultural production and breeding programs.

EVOp09

Morphological Characterization of Some Nigerian *Solanum L.* Species (Solanaceae)

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Abstract
The complexity within the genus *Solanum* has been of great taxonomic concern over the years. Resolving this problem has led to a detailed investigation into the morphological study of the genus as it is a primary line of evidence employed in plant taxonomy. Diagnostic qualitative and quantitative characters viz. fruit colour, level of hairiness, presence of appendages, flower colour, ratio of sepals to petals, leaf length/width, fruit length/diameter differentiated the species. Appendages were observed in *S. torvum*. The species have globous fruit shape except for *S. aethiopicum* and *S. melongena* with oval and oblong shapes respectively. High level of similarity exists across variants of *S. gilo* and *S. macrocarpon* but can be distinguished by their fruit colour while the number of stamen is diagnostic for *S. macrocarpon* variants. All the species have an erect growth form except for *S. americanum* which is decumbent. Corymb inflorescence was observed in *S. indicum*. Simple umbel inflorescence in *S. nigrum* and *S. americanum* with their fruit colour being dull black and shining black respectively. These valuable diagnostic characters were explored in this study and used to construct dendrogram and key illustrations which further aided the identification and delimitation of the species.

Keywords
Solanum, Morphology, Inflorescence, Appendages, Qualitative, Quantitative, Dendrogram

EVOp10

Exploring the origin and diversification of the locoto chile (*Capsicum pubescens*): multiple approaches using RAD-seq data.

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Abstract
Capsicum pubescens is a well-known hot chile from South American Andean highlands, nowadays cultivated from NW Argentina to Central America. The species is known only as a cultigen and not in wild form. The origin of *C. pubescens* has been puzzling while the knowledge of its evolutionary history and genetic diversity is scarce. A couple of wild Andean species have been proposed as its closest allies and/or putative ancestors, with which *C. pubescens* can interbreed. However, crossing experiments and DNA data analyses have produced some contradictory results, being *C. pubescens* resolved into an isolated clade. The RAD-sequencing approach was thus followed to analyze *C. pubescens* origin and affinities, diversification and genetic structure by using genome-wide data. The phylogenetic affinities of *C. pubescens* were strongly resolved, being a sister species to those considered its closest allies, but it is ascertained that none extant *Capsicum* species would be its wild ancestor. Within C. pubescens, two major genetic groups can be recognized: 1) individuals from Bolivia and Argentina and, 2) individuals from Peru, Ecuador and Central America, including Mexico. Based on phylogenetic reconstructions, *C. pubescens* area of origin could be located in the central-western Bolivian highlands. This would be in concordance with the wide morphological variation of the species in that region (i.e. flowers, fruits, pubescence, etc.). Overall, the current results allow deepening the knowledge of the affinities and distribution of the genetic diversity of the locoto chile, offering new ideas, supported by genome-wide data, about its origin and expansion.

EVOp11

A misleading clue of hybridization between two *Petunia* species

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Abstract
Recently divergent species challenge taxonomists since species may share genetic and morphological features. Delimiting species is further complicated if they hybridize. The *Petunia* genus hybridizes in natural and artificial conditions. *P. interior* and *P. inflata* are genetically and morphologically similar, occur in sympatry, and share pollinators. We tested if they hybridize in their contact zone or if the morphological and genetic sharing is due to their recent speciation. We used genome-wide polymorphisms to search for hybrids in Snapclust and we assessed population structure in FastStructure. A generalized linear mixed modeling tested whether distance, environment, or elevation better explained the genetic divergence between species. We did not find any evidence of hybridization. Population structure resulted in three clusters: one containing four *P. interior* collection sites; another with five collection sites of *P. inflata* and one misidentified *P. interior* population; and another with two collection sites of *P. inflata*. The model that best explained the genetic divergence among populations combined geographic distances, environment variables, and elevation. Even though they seem to have all prerequisites, these species do not hybridize, suggesting some reproductive barriers. These species inhabit a transitional area between two biomes, thus geographic distances, environmental variables, and elevation are somewhat correlated, and all play roles in species divergence. These species' ancestors lived at elevations lower than 500m, but current distribution includes sites up to 900m in elevation. Our results suggest that P. interior expanded its distribution to higher elevations, whereas P. inflata still occupies the ancestral area at lower elevations.

EVOp12

Ecological Descriptors of Wild Tomato Species (*Solanum* Sect. Lycopersicon) and Close Related Species (*Solanum* Sect. Juglandifolia & Sect. Lycopersicoides) in Latinamerica.

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Abstract
Natural habitat characterization of wild tomatoes and close related species along their distribution range, it is essential for conservation and sustainable use of species diversity. The objective of this research was to identify the edaphoclimatic characteristic of the original collection sites of 12 species of wild tomatoes (Solanum sect. Lycopersicon) and 4 species of phylogenetically related groups (Solanum sect. Juglandifolia and sect. Lycopersicoides), and determine ecological descriptors of representative specimens in Latin America. A similar approach was used in Solanum lycopersicum L, but considering the weedy nature and wide spread of variants of the cultivated tomato. Analysis of databases (Solanacea Source, TGRC, GBIF, and SNICS) allowed selecting 8,024 representative accessions. Using geographic information systems and 21 climatic variables (19 WorldClim bioclimatics, annual evapotranspiration and altitude) and 10 soil characteristics (pH, CEC, SB, Salinity, Sodicity, Percentage of lime, clay and sand, Bulk density and TEB), analyzed in raster format with spatial resolution of 900 m, were used to identified the ecological descriptors (average, maximum and minimum values). Subsequently, the importance and association of variables along the geographical distribution range of species was determined by Principal Component Analysis. Species similarity based on climatic and edaphic variables was established by Cluster Analysis. The results provided current information on the climatic conditions, environmental and ecological descriptors of natural habitats of 12 wild tomatoes and 4 phylogenetically related species as well as insights to understand the spread and distribution of Solanum lycopersicum populations in Latin America..

EVOp13

The balance between pollinator attraction and anti-herbivory in *Nicotiana benthamiana*.

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Abstract
Nicotiana benthamiana is an important research tool and a model plant, but its floral volatiles and protective insecticides have received little examination. While the originally desert-dwelling LAB isolate produces smaller flowers with structures favouring self-fertilisation, the wild QLD isolate, from a milder environment, produces flowers that favour insect pollination. Nicotiana plants produce secondary metabolites capable of attracting pollinators and repelling herbivores. Analysing the composition of floral headspace volatiles by SIFT-MS, we observed that QLD flowers emit high levels of the pollinator attractant benzyl alcohol during the night. However, the overnight emission of benzyl alcohol from LAB flowers is very low. Comparing the composition of flower and leaf tissues by LC-HESI-MS, identified differences in the production Hydroxygeranyllinallol Diterpenoid Glycosides and pyridine alkaloids, which are allelochemicals involved in plant defence and herbivory. Nicotianosides (III & IV) accumulated to higher levels in the flowers and leaves of LAB than in QLD and the reverse was found for two other diterpene glycoside forms. Most strikingly, nornicotine accumulated to levels ~50 and ~300-fold higher in QLD than in LAB flowers and leaves, respectively. RNA-seq confirmed that CYP82E4, responsible for the conversion of nicotine to nornicotine, is significantly higher in QLD. Analysis of CYP82E4 promoter identified a transcription factor (bZIP53) binding site in QLD which is mutated in LAB.
This suggest a scenario in which LAB, by not producing pollinator attractants, requires less protection against herbivorous insects whereas QLD by producing floral volatiles needs to produce a potent insecticide to protect itself from being eaten.

EVOp14

Collection and Evaluation of Genetic Diversity and Population Structure of Potato Landraces and Varieties in China.

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Abstract
China is the world's leading country for potato production but potato is not native to China. To gain insights into the genetic diversity of potato germplasm various studies have been performed but no study has been reported for potato landraces in China. To improve the available genepool for future potato breeding programs, a diverse population containing 292 genotypes (including foreign elite lines, local landraces and cultivars) was developed and genotyped using 30 SSR markers covering the entire potato genome. A total of 174 alleles were detected with an average of 5.5 alleles per locus. The model-based structure analysis discriminated the population into two main sub-groups, which can be further subdivided into seven groups based on collection sites. One sub-group (P1) revealed less genetic diversity than other (P2) and contained a higher number of commercial cultivars possibly indicating a slight reduction in diversity due to selection in breeding programs. The P2 sub-group showed a wider range of genetic diversity with more new and unique alleles attained from wild relatives. The potato landraces, clustered in sub-population P1 may be derived from historical population imported from ancient European and International Potato Center genotypes while sub-population P2 may be derived from modern populations from International Potato Center and European genotypes. It is proposed that in the first step, the potato genotypes were introduced from Europe to China, domesticated as landraces, and then hybridized for modern cultivars.

EVOp15

Could a whole valley stop gene flow in *Petunia altiplana*?.

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Abstract
The genus *Petunia* (Solanaceae) is endemic to southern South America with 15 wild species, which have diversified recently under ecological interactions and climate changes. *Petunia altiplana* grows in highland grasslands in southern Brazil, and the Pelotas river interrupts its distribution. A phylogeographic analysis involving this species showed that the riverbanks constitute reciprocal monophyletic groups, suggesting that the Pelotas river could be a phylogeographic barrier. The course of rivers explains the variability and genetic structure in different species of animals and plants, mainly in species from the Amazon Basin, but few studies address this topic in southern Brazil. Here, we used classic phylogeographic methods based on plastid intergenic spacers and microsatellites to investigate the Pelotas river's role as a barrier to gene flow among the *P. altiplana* populations and understand the species diversity and structure. The plastid and microsatellite results differed regarding the population structuring. The first dataset showed some differentiation between the north and south riversides, whereas the microsatellites showed low genetic structuring. Such results suggest the river acted as an ancient phylogeographic barrier, but this effect is no longer observed as contemporary gene flow was observed, even low.

Session 3: DEVELOPMENT

Oral Presentations

- **DEVop**: Soyk, Dissecting cryptic genetic variation with impact on tomato domestication and breeding.
- **DEVo01**: Philippe *et al. Elucidating the mechanisms of plant cuticle deposition and restructuring using tomato fruit development as a model*.
- **DEVo02***: Lira *et al. Light and ripening-regulated B-BOX protein-encoding genes in Solanum lycopersicum*
- **DEVo03**: Benoit *et al. Contribution of Transposons to Structural Variation and Phenotypic Diversity in Tomato.*
- **DEVo04***: Snouffer *et al. Regulation of cell division and cell shape by tomato OFPs and TRMs to control early ovary shape.*

Poster Presentations

Note: Oral presentations marked with a * will be presented also a poster. Their abstract will have a oral presentation ID (DEVo).

- **DEVo01**: Borovsky *et al. CaOFP20 underlies a major fruit shape QTL in pepper*.
- **DEVo02**: Forlani *et al. HEBE promotes leaf senescence in* Solanum lycopersicum.
- **DEVo03**: Huercano *et al. Stitching the gap: the case of SMP-containing proteins in Membrane Contact Sites*.
- **DEVo04**: Jiang *et al. FRUITFULL-like genes regulate flowering time and inflorescence architecture in tomato.*
- **DEVo05**: Kharshiing & Sinha. *A Role for Phytochrome A in Transitory Metabolism of Tomato*.
- **DEVo06**: Li *et al. Differential expression of SlKLUH controlling fruit and seed weight is associated with changes in lipid metabolism and photosynthesis related genes*.
- **DEVo07**: Namphengsone *et al. Investigating the Role of OFPs and TRMs in Tomato Organ Initiation and Shape Regulation in Tomato Tissue Culture*.
- **DEVo08**: Percio *et al. The fellowship of the membrane contact sites: a SMP domain to transfer lipids.*
- **DEVo09**: Quinteros *et al. Effect of grafting in yield and fruit quality of processing tomato crop in sub-optimum soils in Mendoza, Argentina*.
- **DEVo10**: Salazar-Sarasua *et al. Male sterility and the induction of seedless fruits in tomato*.
- **DEVo11**: Vazquez-Vilar *et al. Genome-wide identification and comparative analysis of the SQUAMOSA promoter binding-like genes in* N. benthamiana *and* N. tabacum.
- **DEVo12**: Zahn *et al. Unravelling the functions of SOC1-like genes in tomato*

DEVop

Dissecting cryptic genetic variation with impact on tomato domestication and breeding

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Abstract
A major goal in plant biology is to uncover the genes and variants that explain phenotypic diversity. However, it becomes clear that phenotypic variation often does not reflect the cumulative effect from individual gene mutations. This deviation is due to interactions between alleles, which is often unpredictable and quantitative in effect. In tomato, breeding with a mutation that improves fruit harvesting often results in excessive flowering and reduced fertility due to interaction with a cryptic variant in a homologous gene. We found that recently evolved copy number variants enabled breeders to neutralize this negative interaction. By dissecting the mechanisms by which these copy number variants restored normal flowering and fertility, we devised strategies that use genome editing to predictably improve harvesting. Using additional developmental pathways that were targets of selection during tomato domestication and breeding, we now investigate the impact of cryptic genetic variation on quantitative trait variation. Advancing our basic understanding of cryptic variation in crops can reveal new principles and approaches to engineer targeted improvements in agriculture.

DEVo01

Elucidating the mechanisms of plant cuticle deposition and restructuring using tomato fruit development as a model

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Abstract
The epidermis of the aerial organs of land plants is covered by a hydrophobic cuticle that plays many critical protective roles, most notably in preventing desiccation. This layer is structurally complex and highly dynamic, and must remain both flexible and intact, during organ growth and differentiation, but also retain its barrier properties. The mechanisms of assembly and remodeling of the cuticle are not well understood, but tomato fruit development provides an excellent model to study such processes. Members of the CUTIN SYNTHASE (CUS) gene family, which represent a subfamily of GDSL-motif lipases, have been shown in tomato (Solanum lycopersicum) to polymerize cutin, a lipidic polyester that form the major component of plant cuticles. However, a mechanism for cutin restructuring, involving localized degradation and reassembly, which would presumably be necessary to maintain cuticle integrity during epidermal expansion, has not yet been identified. We are testing the hypothesis that some GDSL-lipases contribute to such a process, including members of the CUTICLE DEFECTIVE (CDEF) gene family, since they are closely related to CUS genes and have been associated with cutinase activity. We have characterized the activities and biological functions of tomato CUS and CDEF gene candidates, with particular focus on phenotypes that affects the exceptionally thick cuticle of the fruit. Approaches included the generation and characterization of CRISPR/Cas9 lines, as well as in vivo and in vitro enzymatic studies. These investigations have led to a model of the mechanism of cutin deposition and restructuring in response to developmental or environmental demands.

DEVo02

Light and ripening-regulated B-BOX protein-encoding genes in *Solanum lycopersicum*

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Abstract
Light controls several aspects of plant development through a complex signalling cascade. Several B-BOX (BBX) proteins were identified as regulators of Arabidopsis thaliana seedling photomorphogenesis. However, the knowledge about the role of this protein family in other physiological processes and species remains scarce. To fill this gap, BBX protein encoding genes in tomato genome were characterised. A robust phylogenetic analysis revealed how the domain diversity in this protein family evolved in Viridiplantae and allowed the precise identification of 31 tomato SlBBX proteins. The mRNA profiling in different organs revealed that SlBBX genes are regulated by light and their transcripts accumulation is directly affected by the chloroplast maturation status in both vegetative and fruit tissues. As tomato fruits develop, three SlBBXs were found to be upregulated in the early stages, controlled by the proper chloroplast differentiation and by the PHYTOCHROME (PHY)-dependent light perception. Upon ripening, other three SlBBXs were transcriptionally induced by RIPENING INHIBITOR master transcriptional factor, as well as by PHY-mediated signalling and proper plastid biogenesis. Altogether, the results obtained revealed a conserved role of SlBBX gene family in the light signalling cascade and identified putative members affecting tomato fruit development and ripening.

DEVo03

Contribution of Transposons to Structural Variation and Phenotypic Diversity in Tomato

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Abstract
Structural variation has fueled phenotypic diversification and underlies important domestication and quantitative traits in crops plants. Nevertheless, the genetic drivers of plant structural variation at the population level remain poorly understood. We recently reported long-read sequencing of 100 diverse tomato genomes, which captured the extent and genomic features of structural variants. Most of this structural variation can be traced to transposable element (TE) activity. Annotation of TEs in 14 diverse accessions revealed their prevalence in tomato genomes, with a large fraction retaining transpositional potency, likely facilitating new structural variation. The Copia-like Rider family, which generated structural variants underlying several traits of agricultural interest in tomato, is over-represented within the TEs that maintain potential activity, but mechanisms regulating Rider activity remain unexplored. Through experimentally-controlled activation of the Rider family, we identified DNA methylation, phytohormones, and drought stress as molecular regulators of Rider activity in tomato. We further show differences in Rider distribution between Solanaceae species, suggesting contrasted evolutionary success of Rider and variable contribution to structural variation between species. Artificially promoting TE activity could generate agriculturally-relevant structural and epigenetic variation in tomato and related crops.

DEVo04

Regulation of cell division and cell shape by tomato OFPs and TRMs to control early ovary shape

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Abstract
Tomato fruits have a diverse range of shapes including round, pear shaped, and very elongated. Members of the Ovate Family Protein (OFPs) regulate organ shape in a number of plant species, and in tomato, mutations in ovate and ofp20 result in elongation of the proximal end of the ovary and pear-shaped fruits. OFPs interact with TON1 Recruiting Motif (TRM) proteins and mutations in these genes have also been found to regulate organ shape in tomato and other plants. However, the molecular mechanisms regulating shape remain unclear. OFPs and TRMs are expressed throughout tomato ovary and fruit development and have been implicated in cell division and cell shape. We found that the ovate mutant has reduced cell divisions in the floral meristem and during ovary initiation resulting in a narrower carpel early in development. Double mutants with ovate and ofp20 showed a further reduction in cell division resulting in an even narrower carpel. However, while the trm5 mutant did not alter cell division frequencies, trm5 did alter cell shape early in development resulting in smaller and flatter cells. Additionally, OFP-TRM interactions result in dynamic localization of these proteins between the cytosol and microtubules in N. benthamiana. We hypothesize that OFP and TRM protein families localize to microtubules to regulate cell expansion and division throughout floral meristem and ovary development and that members may have redundant functions to ensure robust organ shape throughout plant development.

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DEVp01

CaOFP20 underlies a major fruit shape QTL in pepper

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Abstract
Pepper (Capsicum spp.), exhibits a vast natural variation in fruit shape that is utilized for breeding of diverse fruit types. QTL mapping studies allowed the identification of several QTLs but to-date no genes underlying fruit shape QTLs have been conclusively identified and their function verified in pepper. In this study we mapped a major QTL in chromosome 10 in a cross of elongated and round-fruited parents. Combination of RNA seq, bulked segregant analysis (BSA) and fine mapping using fixed recombinant progenies allowed to define a 5 Mbp region that contains the QTL as well as CaOFP20, the ortholog of SlOFP20 that controls fruit shape in tomato. To prove the function of CaOFP20, we knocked down its activity by VIGS in the background of a round-fruited parent. Silenced plants exhibited elongated fruits and reduced expression of CaOFP20 in the ovary and in fruit pericarp and placenta, implicating the function of the gene in controlling fruit elongation. To further test whether the expression pattern of CaOFP20 is associated with natural variation in fruit shape, we selected 30 C. annuum accessions representing elongated and round fruits from the G2PSOL core collection. qRT-PCR of CaOFP20 indicated a strong negative correlation between the expression level of the gene and degree of fruit elongation. Histological analyses of ovary wall and fruit pericarp of QTL-NILs indicated that the QTL exerts its effect on fruit shape by modulating multiple cellular mechanisms including cell size, cell number and cell shape.

DEVp02

HEBE promotes leaf senescence in *Solanum lycopersicum*

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Abstract
Understanding the complex process of aging is one of the breeders' major goal to reach. Indeed, senescence timing and progression affects plant fitness, harvest time, product quality and post-harvest conservation. Senescence involves several cytological and biochemical changes that rely on numerous transcription factors, phytohormone-responsive elements and senescence-associated genes. All of them are interconnected and the processes they belong to are tightly regulated. As example, senescence in leaves is characterized by chlorophyll breakdown, nutrient reallocation and cell wall dismantling. Aging leaves are not supposed to perform photosynthesis anymore, so plastidial and cellular structures are disrupted, and, at the same time, macromolecules accumulated before are dismantled and brought to sink organs. Among all, a group of plant-specific transcription factors known to regulate these aspects is the NAC family (NAM No Apical Meristem, ATAF1/2 and CUC Cup-Shaped Cotyledon). They mediate reactions to biotic and abiotic stresses, they are involved in secondary cell-wall deposition and they regulate fruit ripening and leaf senescence. In this work we have identified a new tomato NAC transcription factor, called HEB, whose downregulation delays the onset of senescence, as demonstrated by the improved photosynthetic performance, the altered transcription of senescence-associated genes and the reduced chlorophyll dismantle. Plants where HEB has been silenced display a stay-green phenotype.

DEVp03

Stitching the gap: the case of SMP-containing proteins in Membrane Contact Sites

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Abstract
Membrane contact sites are (MCS) are microdomains in which two membranes are very close (~30 nm) but do not fuse. MCS are essential for non-vesicular transport of lipids which is mediated by several families of proteins containing lipid transport domains, like the synaptotagmin-like mitochondrial lipid-binding (SMP) domain.

The study of these proteins has increased due to their important role in plant-environment interactions. The most studied SMP containing protein in Arabidopsis SYT1 which is involved in tolerance to multiple abiotic stresses. However, little is known about the localization and function of other SMP proteins in plants. Arabidopsis SMP sequences were used to identify their orthologues in S. lycopersicum, allowing the identification of 16 genes encoding putative SMP domains (see poster Percio et al.). Interestingly, we have found that some SMP proteins are present exclusively in plants as they do not have orthologues in yeast and human. Here, we report the subcellular localization of these new identified proteins from S. lycopersicum and A. thaliana using transient expression in N. benthamiana, confocal microscopy and a set of organelle markers. Overall, we have found two proteins that localized in ER-Golgi, one protein localized in chloroplast-ER and several proteins being part of ER-PM MCS. We are now investigating the role of some of these proteins using biochemical, genetic and cell biology approaches.

This work is supported by grants from: Ministerio de Ciencia, Innovación y Universidades (grant PGC2018-098789-B-I00), Ministerio de Economía, Industria y Competitividad (grant RYC-2013-12699), UMA-FEDER (grant UMA18-FEDERJA-154) and Ministerio de Ciencia e Innovación BIO2017-82609-R.

DEVp04

FRUITFULL-like genes regulate flowering time and inflorescence architecture in tomato

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Abstract
The timing of flowering and inflorescence architecture are critical for the reproductive success of tomato, but the gene regulatory networks underlying these traits are still hardly explored. Here we show that the tomato FRUITFULL-like (FUL-like) genes FUL2 and MADS-BOX PROTEIN 20 (MBP20) induce flowering and repress inflorescence branching. FUL1 fulfils a less prominent role and appears to depend on FUL2 and MBP20 for its upregulation in the inflorescence meristem. Our results demonstrate that MBP10, the fourth tomato FUL-like gene, has probably lost its function. The tomato FUL-like proteins cannot homodimerize, but heterodimerize with JOINTLESS (J), SlMBP21 (J2), ENHANCER OF JOINTLESS (EJ2/MADS1) and the SOC1-homolog TOMATO MADS-box gene 3 (TM3), which are co-expressed during inflorescence meristem maturation. Transcriptome analysis revealed various interesting downstream targets, including five repressors of cytokinin signaling, which are all upregulated during the vegetative-to-reproductive transition in ful1/ful2/mbp10/mbp20 mutants. FUL2 and MBP20 can also bind in vitro to the upstream regions of these genes, thereby probably directly stimulating cell division in the meristem upon the transition to flowering. Our research reveals that the four tomato FUL-like genes have diverged functions, but together regulate the important developmental processes flowering time, inflorescence architecture and fruit development.

DEVp05

A Role for Phytochrome A in Transitory Metabolism of Tomato.

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Abstract

Starch is a storage carbohydrate synthesised by plants during photosynthesis and accounts for approximately 50% of the world's daily calorie intake. In addition to human consumption, starch is also extracted from crops for industrial applications and used as feedstock for first-generation bioethanol. In higher plants, starch is the major storage carbohydrate and accumulates in chloroplasts of leaves in light and is degraded/remobilised in the dark. Leaf or transitory starch is primarily synthesised in photosynthetic tissues during the day and undergo nocturnal breakdown, supplying the plant with sugars required for its metabolism. The synthesis and degradation of transitory starch in green leaves is therefore tightly linked to diurnal changes in the light environment. Previous studies have demonstrated that starch accumulation and degradation are finely controlled to synchronise with variations in growth conditions, including light.

Analyses of a phytochrome A mutant (phyA) of tomato altered in red-light responses show alterations in photosynthetic activity and leaf starch metabolism. In comparison to its isogenic wild type, phyA shows significant changes in photosynthetic activity under photosynthetically stimulating light conditions. Analyses of transitory starch content indicate lower levels of starch in light coupled with reduced starch degradation in dark in phyA. Concomitant decrease in plant growth and shoot biomass production is also observed for phyA compared to similarly aged wild type. The functional significance of phytochrome A in regulating these responses in tomato is highlighted.

DEVp06

Differential expression of SlKLUH controlling fruit and seed weight is associated with changes in lipid metabolism and photosynthesis related genes.

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Abstract
The size of plant organs such as fruit and seed are crucial yield components. Tomato KLUH underlies the QTL fw3.2 that is an important regulator of fruit and seed weight. However, the mechanism by which the expression levels of KLUH affects organ size is poorly understood. Here, we found that higher expression of SlKLUH increased cell proliferation in the pericarp within five days post anthesis (DPA) in tomato near-isogenic lines (NILs). Differential gene expression analyses showed that lower expression of SlKLUH was associated with increased expression of genes involved in lipid metabolism, especially genes involved in 'Cutin synthesis and transport' and 'Fatty acid elongation and wax biosynthesis'. Lipidomic analysis revealed that repression of SlKLUH mainly increased the contents of certain non-phosphorus glycerolipids and phospholipids and decreased four unknown lipids contents. Over-expression of a transcription factor that is known to influence lipids biosynthesis, SlSHN1, resulted in decreased fruit and seed weight, which supported the notion that changes in lipid metabolism may control organ size. Furthermore, co-expression network analyses revealed that lipid metabolism was possibly associated but not directly regulated by SlKLUH, and that this gene instead was regulating photosynthesis-related processes. In addition, many transcription factors (TFs) putatively involved in KLUH pathway were identified. Collectively, we show that SlKLUH regulates fruit and seed weight that is associated with altered lipid metabolism. The results from this study not only expand our understanding of fruit and seed weight regulation but also offer a valuable resource for functional studies of candidate genes putatively involved in the regulation of organ size in tomato and other crops.

DEVp07

Investigating the Role of OFPs and TRMs in Tomato Organ Initiation and Shape Regulation in Tomato Tissue Culture

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Abstract
Ovate Family Proteins (OFPs) interact with TONNEAU1-recruiting motif family of proteins (TRMs) at the M8 motif to control fruit shape and organ morphology in tomato and other plant species. We hypothesize that there are members of the OFP and TRM protein families that are part of a protein network that interacts with microtubules to coordinate multicellular growth and organ patterning in plants. We sought to investigate the role of OFPs and TRMs in organ initiation from tomato tissue culture given that the ubiquitous OFP-TRM interactions regulate organ morphology. This system allows us to study the cellular functions of these proteins in a system that is more amendable to manipulation than the developing flower or fruit, while still assessing protein function in living and dividing cells. The first organ initiation occurs as the callus transitions to producing shoots. This transition requires the activation of genes needed to coordinate cell division/expansion and may be regulated by certain OFPs and/or TRMs. We will 1) Investigate shooting morphogenesis in readily available mutants of OFPs and TRMs 2) Perform RNA-seq to compare the callus and shooting stages to confirm which OFPs and TRMs are active and required for organogenesis. To further investigate the functional role of the M8 motif in TRMs interaction with OFPs, we will characterize CRISPR generated in-frame mutations within the M8 domain of TRM17/20a, TRM26a, and TRM30/34a. Furthering our understanding of the cellular functions and interactions between OFPs and TRMs will broaden our understanding of plant organ morphogenesis and shape regulation.

DEVp08

The fellowship of the membrane contact sites: a SMP domain to transfer lipids

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Abstract
The non-vesicular transfer of lipids between different organelle membranes is essential for their proper functioning, and it relies on the formation of membrane-contact sites (MCS). These are discrete regions where two membranes are close but not fused (10-30 nm). One of the best described MCS is stablished between the endoplasmic reticulum and the plasma membrane (ER-PM), and is well known for stress tolerance, as well as other physiological processes. The formation of those MCS is dependent of proteins which promote the apposition of the membranes and mediate the lipid transport. There are more MCS in plants aside ER-PM, such as ER-Golgi or ER-chloroplast contact sites, but which proteins are involved as well as their role in tethering and lipid transport remains elusive.
The synaptotagmin-like mitochondrial-lipid-binding (SMP) domain, which is contained in proteins as SYT1 to SYT6, among others, is a domain involved in glycerolipid transport in the MCS. We have analysed the SMP-containing proteins in silico in Arabidopsis thaliana and Solanum lycopersicum, including their expression, protein domains, and phosphorylation sites. The amino acid sequence and domain analyses have allowed us to stablish groups among them. In this communication we describe the obtained results that led us to the identification of uncharacterized proteins containing SMP domains as a first step to identify their function in lipid transport.

This work is supported by grants from: Ministerio de Ciencia, Innovación y Universidades (grant PGC2018-098789-B-I00), Ministerio de Economía, Industria y Competitividad (grant RYC-2013-12699), UMA-FEDER (grant UMA18-FEDERJA-154) and Ministerio de Ciencia e Innovación BIO2017-82609-R..

DEVp09

Effect of grafting in yield and fruit quality of processing tomato crop in sub-optimum soils in Mendoza, Argentina.

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Abstract
In recent years, processing tomato crop requires an intensive use of resources in relationship to implementation of pressurized irrigation technologies that involves land rotation, an increase of pests and diseases incidence and a reduction of soil quality due to salinity and compaction. Coping with this problem, grafting can be a promising technology for alternative crop management in affected areas of Mendoza, the most important processing tomato producer province in Argentina. The effect of rootstocks on yield and fruit quality of tomato cultivars was evaluated in field parcels with different soil characteristics at the Experimental Agriculture Station La Consulta INTA, Mendoza. In 2018-2019 trials, the best combination of rootstocks and varieties (Protector/HM 1892) increased 43.4% of commercial yield (132.4 t.ha-1) while other combinations produced around 25% more than the controls. In the 2019-2020 assay, grafted plants could recovered their biomass and adequate production after an early destruction by hail. These results demonstrated that vigor imparted by rootstocks would favor processing tomato yield, although with a delay in fruit maturation of approximately one week. Fruit quality of grafted plants was not affected, and soluble solids content and pH were adequate for processing products. Grafting technologies are being studied in the Integrated Tomato Production Management Strategy (PITI) developed by the Tomato 2000 Association in Argentina, as an alternative to allow processing tomato crops in suboptimal soils through ecologically sustainable methods.

DEVp10

Male sterility and the induction of seedless fruits in tomato.

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Abstract
Male gametogenesis in plants occurs within the anther in a synchronized manner with the development of the anther itself. During this process, the tapetum that surrounds the developing reproductive cells has a central role acting as a nutritive tissue. Therefore, mutations in genes that affect this tissue result in male sterility. We have previously observed that male sterility triggers parthenocarpic fruit development in tomato plants (1, 2). Undoubtedly, seedless fruit production is an appealing trait for many fleshy fruit crops. To get insight into this process we generated male sterile tomato plants using CRISPR/Cas9 technology. We targeted candidate tomato genes based in protein homology to previously characterized Arabidopsis tapetum-specific genes. We have generated several loss-of-function mutations that showed male-sterile flowers and produced seedless fruits. Detailed characterization of these plants and the targeted genes is providing relevant information on the role of tapetum in pollen formation. Besides, they will help to decipher the molecular mechanisms that drive parthenocarpic fruit growth in male-sterile tomato plants, which remain largely unknown. This work was supported by Spanish grant: RTI2018-094280-B-100.

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DEVp11

Genome-wide identification and comparative analysis of the SQUAMOSA promoter binding-like genes in *N. benthamiana* and *N. tabacum*

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Abstract
SQUAMOSA promoter binding-like proteins are known to play key roles in growth and developmental processes, including leaf development, plant architecture and juvenile-to-adult and vegetative-to-reproductive phase transitions. In this study, we report the identification of 54 putative SPL genes in *Nicotiana tabaccum* cv. K326 and 40 candidate SPL genes in *N. benthamiana* LAB strain. The SPL genes of the two species were classified into 8 phylogenetic groups according to the SPL classification in Arabidopsis. The exon-intron gene structure and SBP domains were highly conserved between homeologues and ortologues. 32 of the 40 NbSPL genes and 28 of the NtSPL genes are targets of miR156. These results serve as basis for candidate gene selection for a knock-out experiment using CRISPR/Cas9 in *N. tabacum* that revealed some clues of the biological functions of SPL13 in branching and juvenility and of SPL9 and SPL15 in flowering time. All together our results present a comparison of the SPL gene family in two allotetraploid species, *N. benthamiana* and *N. tabacum*, that provide the basis for elucidation of the biological role of each SPL.

DEVp12

Unravelling the functions of SOC1-like genes in tomato

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Abstract
The moment at which a plant starts flowering is very important for its reproductive success and therefore tightly regulated by many genes. Few master regulators control this process by integrating internal and environmental signals. We focus on close homologs of the MADS-domain transcription factor SUPPRESSOR OF OVEREXPRESSION OF CONSTANS1 (SOC1) in tomato.

These homologs, SlSOC1, SlMBP18, TM3 and STM3, show different protein-protein interaction patterns and thus are likely to have subfunctionalized through evolution. STM3 is most highly expressed during floral transition. We identified two evolutionary conserved regions with putative transcription factor binding sites in its promoter that may be responsible for the high activity of STM3. We are developing in vitro approaches to identify upstream regulators of SOC1 homologs to further unravel the tomato flowering network.

Session 4: NETWORKS OF METABOLITES, GENES AND ORGANISMS

Oral presentations

- **NETop**: Aharoni et al. *The Bitter - Sweet Sides of Solanaceae-Specialized Metabolism.*
- **NETo01**: Bermúdez *et al. Deciphering the epigenetic variability in S. lycopersicum accessions and their influence on hybrid vigor*.
- **NETo02**: Pereira *et al. Natural genetic diversity in tomato flavor genes*
- **NETo03** Silva-Arias & Tellier. *Ecological genomics in wild tomatoes to reveal mechanisms of adaptation to living in the driest region of the world.*
- **NETo04**: Torres-Montilla *et al. A novel system for the artificial differentiation of chromoplasts from pre-existing chloroplasts in leaves*.

Poster Presentations

- **NETp01**: Bianchetti *et al. Phytochromes B1/B2 are Key Regulators of Epigenome Reprogramming during Tomato Fruit Development*.
- **NETp02**: Datir, Yousf *et al. Metabolomic profiling of potato (*Solanum tuberosum *L.) cultivars differing in their processing and non-processing characteristics.*
- **NETp03**: Dono *et al. Fruit biochemical characterization of four tomato mutant lines in the San Marzano background.*
- **NETp04**: Gramazio *et al. Genome editing of promoter region to improve GABA accumulation in tomato fruits by multiplex CRISPR/Cas9 system.*
- **NETp05**: Londoño-Giraldo *et al. Effect of 1-methylcyclopropene on volatilomic profile of ripening stages of cherry tomato fruits*.
- **NETp06**: Madlung *et al. Genomic network analysis reveals subfunctionalization of phytochrome B1 and B2 in tomato.*
- **NETp07**: Muñoz *et al. Comparative metabolomics of* Solanum lycopersicum *to elucidate anti-fungal defence mechanisms*.
- **NETp08**: Wheeler et al. *Phylotranscripomic analyses of the Petunieae clade of Solanaceae*

NETop

The Bitter - Sweet Sides of Solanaceae-Specialized Metabolism

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Abstract
The metabolomes of plant are notorious for their size and structural diversity. Secondary metabolites represent a large portion of this metabolic repertoire counting thousands in an individual plant. Generating such chemical complexity in secondary metabolism requires continues evolution of genes encoding proteins producing novel metabolites with selective advantage in a particular environmental niche. In the past years, we discovered a series of enzymes, regulatory and signalling proteins as well as transporters involved in steroidal glycoalkaloids (SGAs) metabolism, predominant secondary metabolites found in the genus Solanum. In the presentation, I will describe our recent efforts to complete the understanding of steroidal glycoalkaloids (SGAs) biosynthesis as well as production of unusual SGA structures in wild Sol species. We used several approaches mainly integrated 'omics' data and network analysis, deep phenotyping of tomato introgression lines and classical mapping combined with the analysis of hundreds re-sequenced tomato genomes. The results of these studies demonstrated how structural diversity of secondary metabolites is formed in the course of evolution. Moreover, it exemplifies how selected alleles involved in generating secondary metabolites having beneficial attributes to humankind where part of the domestication of Solanum crop plants (e.g. tomato and potato) cultivated today.

NETo01

Deciphering the epigenetic variability in *S. lycopersicum* accessions and their influence on hybrid vigor

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Abstract
Heterosis is a fundamental biological phenomenon defined by the superior performance of hybrids over its parents in many economically important traits. Even though heterosis has been extensively used in agriculture, both in plants and animals, the underlying molecular basis remains elusive. This lack of knowledge hampers the rational design of hybrids in order to obtain, in a faster and more efficient way, benefits resulting from heterotic effects. Evidence obtained from several species allows hypothesizing that alterations in the epigenetic state, mediated by changes in the DNA methylation pattern, play a role in determining hybrid vigor. Nevertheless, how parental alleles interact in their progeny to influence the epigenome is poorly understood. We analyzed DNA methylomes, siRNAomes and transcriptomes of three tomato hybrids, and their corresponding divergent parents. Interestingly, the parental methylation, siRNAs and transcriptome patterns did not correlate with the genetic distance between the genotypes and several genes involved in key metabolic categories showed to be epigenetically regulated. Evenmore, hybrids displayed non-additive DNA methylation levels throughout the genome. These results add to the growing evidences that point epigenetic mechanisms as key determinants of hybrid performance and make them able to future applications in breeding programs.

NETo02

Natural genetic diversity in tomato flavor genes

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Abstract
In many crops, domestication and continued selection have focused primarily on agronomic traits such as yield and disease resistance. For vegetables, this strong selection has come at the expense of traits that are less driven by grower demands such as flavor. Product flavor is complex and defines the quality of the vegetable in fresh market produce. Tomato fruit flavor is mainly determined by the balance of sugars, acids and secondary metabolites, including many volatile compounds. Several genes controlling the levels of these compounds have been cloned using crosses between cultivated tomato and the relatively distant green-fruited *Solanum pennellii*. The aim in this study is to provide insights into the genetic diversity of these cloned flavor genes in the red-fruited tomato clade. We used a combination of genomic, metabolomic and transcriptomic data and a unique germplasm including wild, semi-domesticated and early domesticated tomato accessions to explore the natural diversity at the genes causing major impact on fruit flavor. We identified GWAS signals at the known genes for sugars, malic acid and other diverse metabolites such as acetate esters and lipid-derived volatiles. Novel haplotypes carrying potential causative variants were associatiated with levels of specific metabolites, suggesting they may have had an impact in tomato flavor during domestication and improvement steps. In addition, we incorporated RNA-seq data from five stages of fruit development and ripening in nine phylogenetically diverse accessions. In some cases, the expression pattern of flavor genes differed depending on the haplotype at the locus. Our results provide new understanding about the alleles impacting fruit flavor that arose during domestication and early improvement and how its selection shaped the biochemical profile of cultivated tomato. Additional beneficial alleles from this germplasm could be incorporated into breeding programs and contribute to improving the flavor of modern tomatoes.

This research is funded by NSF IOS 1564366 and IOS-1732253 projects.

NETo03

Ecological genomics in wild tomatoes to reveal mechanisms of adaptation to living in the driest region of the world

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Abstract
The study of mechanisms that allow species to adapt to their local environment is a long-standing question that remains a central topic in evolutionary biology. Currently, the disentangling of genetic mechanisms involved in adaptation processes related to recent range expansions are receiving special attention. The wild tomato species *Solanum chilense* is an ideal model to study mechanisms of abiotic-stress resistance because is adapted to extremely stressful environments such as highland hyper-arid regions around the Atacama Desert. Using a fine-scale sampling scheme and a landscape genetics framework, we studied a recent expansion process in *S. chilense*. Using a high-throughput target sequencing, we genotyped 170 individuals from populations arranged in four Andean valleys that encompass strong altitudinal gradients. We sequenced 500 intergenic regions and ca. 1500 candidate abiotic-stress resistance genes previously identified in *S. chilense* or related species using gene expression analyses. Genetic structure analyses performed on the neutral markers showed strong latitudinal differentiation indicating higher similarity among populations from the same valley but with a clear isolation-by-distance signal. Besides, we found that the highland lineage that occupies the southern edge of the species distribution likely diverged from highland populations from a single valley. Using genetic populations statistics calculated from the most likely demographic scenario, we detected outlier genes related to the highland colonization process and resistance to abiotic stress.

NETo04

A novel system for the artificial differentiation of chromoplasts from pre-existing chloroplasts in leaves.

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Abstract
Chromoplasts are plastids specialized in the production and storage of carotenoids that can be found in carotenoid-accumulating non-photosynthetic organs of many plant species, such as tomato ripe fruits, carrot roots or marigold flowers. These chromoplasts can be differentiated from other plastid types, including proplastids, leucoplasts, and most frequently, chloroplasts. Even though chloroplast-to-chromoplast differentiation process, named chromoplastogenesis, has been intensively studied in ripening fruits, little is known about the underlying molecular and physiological mechanisms. This lack of knowledge chiefly stems from the fact that chromoplastogenesis in these natural systems is coupled to the developmental program of ripening. In this study, we present a novel artificial system to induce chromoplast biogenesis from pre-existing chloroplasts in leaves that uncouples the chromoplastogenesis from other associated developmental programs. This system is triggered from the expression of the gene crtB, that encodes a bacterial phytoene synthase, and depends on the supply of phytoene, the product of crtB and the first committed intermediate of the plant carotenoid pathway. We found morphological, physiological, and molecular evidence that plastids that differentiate from previously existing chloroplasts in crtB-expressing leaf tissue are indeed chromoplasts. We propose a model for this process, based in two sequential phases: the loss of chloroplast identity (I) and the activation of carotenoid biosynthesis (II). The enhanced production of carotenoids changes plastidial ultrastructure and results in the differentiation of chromoplasts through a genome-wide reprogramming of plastid-to-nucleus communication. Details of the underlying molecular changes will be presented.

NETp01

Phytochromes B1/B2 are Key Regulators of Epigenome Reprogramming during Tomato Fruit Development.

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Abstract
Phytochrome-mediated light and temperature perception has been shown to be a major regulator of fruit development. Furthermore, chromatin remodelling via DNA demethylation has been described as a crucial mechanism behind the fruit ripening process; however, the molecular basis underlying the triggering of this epigenetic modification remains largely unknown. Here, through integrative analyses of the methylome, siRNAome and transcriptome of tomato fruits from phyA and phyB1B2 null mutants, we report that PHYB1 and PHYB2 control genome-wide DNA methylation during fruit development. The experimental evidence indicates that PHYB1B2 signal transduction is mediated by the coordinated expression of DNA methylases/demethylases, histone-modifying enzymes and chromatin remodelling factors, resulting in the transcriptional regulation of photosynthetic and ripening-associated genes. This new level of understanding provides insights into the orchestration of epigenetic mechanisms in response to environmental cues affecting agronomical traits.

NETp02

Metabolomic profiling of potato (*Solanum tuberosum* L.) cultivars differing in their processing and non-processing characteristics.

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Abstract
Storage of potato tubers at low temperatures causes cold-induced sweetening (CIS) which is an important consideration in tuber quality. CIS leads to significant losses to the potato processing industry. Therefore, identification and selection of cultivars using biochemical information have become a priority in potato breeding programs. We have performed 1H NMR spectroscopy to identify metabolic perturbations from the tubers of processing (Atlantic and Frito Lay-1533) and non-processing (Kufri Jyoti, Kufri Pukhraj, and PU1) cultivars at harvest and after one month of cold storage (4°C). A total of thirty-nine water-soluble metabolites were detected wherein significantly affected metabolites after cold storage were categorized into sugars, sugar alcohols, amino acids, and organic acids. Variations observed in glucose, fructose, sucrose, asparagine, glutamine, citrate, malate, proline, 4-aminobutyarte, etc., across five cultivars especially after cold storage indicated that these candidate metabolites could be used to unravel the biological basis of CIS. The correlation between the amino acids, organic acids, and sugars suggests a close biochemical relationship as well as an interactive metabolic network between the amino acid metabolism, the tricarboxylic acid (TCA) cycle, and glycolysis in CIS. Low levels of glucose, fructose, and asparagine with high citrate levels in processing cultivar (FL-1533) and higher glucose, fructose, and malate levels in non-processing cultivars (Kufri Pukhraj and Kufri Jyoti) can be utilized for the prediction, selection, and development of potato cultivars for altered storage and processing attributes. These metabolites can be potentially utilized as metabolic biomarkers for the identification of CIS resistant and susceptible potato cultivars.

NETp03

Fruit biochemical characterization of four tomato mutant lines in the San Marzano background

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Abstract
This study describes the metabolomic effects of four tomato fruit mutations on the cv San Marzano (SM), a worldwide famous Italian traditional tomato variety. Three single mutant lines affecting the content of all pigments (hp-1, hp-2, pd) and a double mutant (Aft_atv), which presents a typically black skin for the accumulation of anthocyanins were obtained. A deep metabolomic analysis of non-polar (NP), polar (P) and volatile (VOC) metabolite fractions in fruits revealed the differences between the mutated lines and SM recurrent variety. Regarding the NP compounds, many carotenoids increased in the fruit of hp lines, as reported in previous studies, in addition to a higher content of β-carotene detected in the Aft_atv. Furthermore, pd resulted in enriched levels of two xanthophylls (All-trans-neoxanthin and Luteoxanthin) but, simultaneously, the levels of α-and β-/γ-tochopherols decreased. Looking at the metabolites in the P fraction, some sugars (Sorbitol and Sucrose) decreased in pd, as well as Fructose/Glucose in hp-1 and Aft_atv. Conversely, many organic acids increased specifically in the Aft_atv line. Most P changes occurred in the phenylpropanoid class, with considerable increases of many metabolites mainly in the case of Aft_atv, followed by pd and hp-2 lines. Finally, the flavour/aroma volatiles were positively modified in all the mutants which showed increased levels in many Benzenoids, Lipids and Phenylalanine derivative VOCs, which are associated to sweeter taste and better aroma. In conclusion, the identified differences in the mutated lines might become new specialities of the traditional SM variety, which could bring some novel desirable nutraceutical and organoleptic properties.

NETp04

Genome editing of promoter region to improve GABA accumulation in tomato fruits by multiplex CRISPR/Cas9 system.

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Abstract
Hypertension is a primary risk factor for cardiovascular disease, the latter causing 7.5 million deaths every year. The ɣ-aminobutyric acid (GABA) is a non-proteinogenic amino acid that has shown effective in lowering the blood pressure of hypertensive patients. Intake of GABA through the daily diet may help reduce their symptoms and might be an effective way to prevent hypertension.
Tomato is one of the most produced vegetables worldwide and daily consumed in a plethora of recipes and, a part of many beneficial compounds, it also contains high levels of GABA. However, GABA levels are higher in mature tomato green fruits and rapidly decrease in ripe fruits due to two main mechanisms in the GABA pathway. In fact, GABA is synthesized from glutamate by glutamate decarboxylase (GAD) and reversibly converted to succinic semialdehyde by GABA transaminase (GABA-T).

A high-GABA content Micro-Tom line was developed deleting the autoinhibitory domain of SlGAD gene by introducing a stop codon through the CRISPR/Cas9 approach (Nonaka et al., 2017). However, the same would not suitable to edit SlGABA-T gene since it would lead to severe dwarfism and affected vegetative and reproductive growth (Koike et al., 2013).

Our study aims at further increasing the GABA content in tomato applying an alternative CRISPR/Cas9 approach by targeting the promoter region of SlGABA-T. In that way, using multiple target gRNAs, we expect to produce novel cis-regulatory alleles that may provide a continuum of variation in SlGABA-T gene expression and consequently a better balance between GABA accumulation and plant development.

References
Nonaka et al. "Efficient increase of ɣ-aminobutyric acid (GABA) content in tomato fruits by targeted mutagenesis." Scientific reports 7.1 (2017): 1-14.

Koike et al. "Suppression of γ-aminobutyric acid (GABA) transaminases induces prominent GABA accumulation, dwarfism and infertility in the tomato (Solanum lycopersicum L.)." Plant and cell physiology 54.5 (2013): 793-807.

NETp05

Effect of 1-methylcyclopropene on volatilomic profile of ripening stages of cherry tomato fruits.

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Abstract
The biosynthesis of volatile organic compounds (VOCs) related to tomato aroma and flavor is an important quality criterion and has been related to ripening stages of the fruit. An effective inhibitor of the action of ethylene, 1-methylcyclopropene (1-MCP) was used to study the relationship between volatile biosynthesis and fruit ripening in cherry tomatoes. The fruit was treated with 1-MCP vapors at room temperature at stages E3 and E5 for 15 days after harvest. 1-MCP prevented the climacteric increase of volatile production and therefore avoided the production of ethylene and the increase in the respiration rate. Untreated fruits developed typical climacteric changes and characteristic VOCs production. Apocarotenoids were the VOCs most affected by the presence of 1-MCP at stage 5. The above demonstrates the inhibitory effect of 1-MCP on the action of ethylene irreversibly in ripening stages in cherry tomato fruits marketed in the country and it relates its strong potential to be used as a tool in the post-harvest handling of this climacteric fruit.

NETp06

Genomic network analysis reveals subfunctionalization of phytochrome B1 and B2 in tomato

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Abstract
Gene- or genome duplication are powerful mechanisms that can have profound evolutionary consequences. Subsequent to genetic duplication events, sub- or neofunctionalization can lead to a species' adaptation to new ecological niches or to the fine tuning of its physiological responses. Plants use phytochromes to sense light and temperature changes in their environment and to respond accordingly with adjustments to their development. In most higher plant species phytochromes exist as a small gene family. In solanaceous plants, such as tomato, five phytochrome genes are present, of which the red-light responsive PHYB gene most recently underwent gene duplication into PHYB1 and PHYB2. We used genome-wide transcriptional network analysis to probe the genomes of mutants of PHYB1 and PHYB2 and compared them to gene networks in the wild type. We found that both genes have subfunctionalized since duplication with PHYB1 acting as a major integrator of light and auxin responses, and PHYB1 and PHYB2 antagonistically regulating aspects of photosynthesis.

NETp07

Comparative metabolomics of *Solanum lycopersicum* to elucidate anti-fungal defence mechanisms.

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Abstract
Tomato crops are attacked by diverse pathogens resulting in enormous losses of agricultural yield. Upon sensing the pathogens, plants mount various defence responses. In addition to well-studied responses such as a Reactive Oxigen Species Burst and strong up-regulation of Ethylene, Salycilic Acid, Jasmonic Acid,and other phytohormones, the Secondary metabolites (SM), are expected to be involved in the quantitative resistance of different plants to certain pathogens.
Leaf blight caused by species of genus *Alternaria* is a devastating disease in tomatoes and only very few cultivars show strong resistance against it. A large number of studies exist, investigating the role of SM in tomato, and have their structures determined by mass spectrometry. However, these focus predominantly of fruit and flavour-related compounds, SM after infection with *Alternaria* remain unknown.
We applied metabolomics based on UPLC-QTOF mass spectrometry in combination with multivariate data analysis compare the metabolomic profiling in *Solanum lycopersicum* after treatments with *A. alternata*, *A. solani* and chitin (a general elicitor of anti-fungal plant defense responses) at two different time points, 3 and 24 hours post inoculation (hpi). Here we present out latest analyses: we find large overlaps between generic (chitin-triggered) anti-fungal defence responses and Alternaria-triggered responses, but also unique responses observed for each of the treatments and differences between the time points. We will discuss how these results might help resolve difference in quantitative resistance against closely related pathogen..

NETp08

Phylotranscripomic analyses of the Petunieae clade of Solanaceae

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Abstract
The Petunieae clade of Solanaceae is a culturally and economically important clade of plants with extensive floral diversity. Some of the genera, such as Petunia and Calibrachoa, are widely popular as ornamentals, due in part to their dramatic variation in floral coloration. Petunieae are native to Southern North America, Central America, South America, and the Caribbean where they grow in a diverse array of habitats including high and low deserts, tropical rain forests, coastal plains, tropical highlands, and sub-tropical wetlands. In addition to its floral diversity, the clade exhibits an assortment of other fascinating phenotypic shifts, such as transitions among life forms (trees, shrubs, herbs, and cushions). Currently, the internal relationships within Petunieae are poorly-resolved as is the placement of the clade relative to the rest of the Solanaceae. This poses a challenge to understanding biogeographic and phenotypic evolution in the clade. Here we present a phylotranscriptomic analysis spanning 70 of the approximately 145 extant species, representing one of the largest and most comprehensive studies of its kind. By characterizing phylogenetic relationships, gene duplication history, and gene-tree-species-tree conflict, we are laying the groundwork to study the phenotypic diversification and possible hybridization of Petunieae species over time and space.

Session 5: STRESS BIOLOGY (BIOTIC AND ABIOTIC)

Oral presentations

- **STRop**: Kahlon *et al. Population studies of the wild tomato species* Solanum chilense *reveal geographically structured major gene-mediated pathogen resistance*
- **STRo01**: Karlova *et al. Resilience to salinity in tomato – root transcriptome data analyses.*
- **STRo02**: Combest *et al. StPIP1, a predicted PAMP-induced peptide in potato, elicits plant defenses and is associated with disease symptom severity in a compatible interaction with potato virus Y.*
- **STRo03**: Mathur *et al. Decoding the regulatory networks of diverse coding and noncoding RNAs towards heat stress response in tolerant and sensitive tomato cultivars from Indian sub-continent.*
- **STRo04**: Ahammed et al. Nitric oxide is involved in the SlWRKY81 transcription factor-regulated stomatal movement and drought tolerance in *Solanum lycopersicum* L.

Poster Presentations

- **STRp01**: Aci *et al. Identification of different expressed genes in two contrasting NUE tomato genotypes under limiting N supply.*
- **STRp02**: Bansal *et al. MIR172-mediated regulation in combined heat and drought stress by engaging novel targets in tomato*.
- **STRp03**: Bashir *et al. Photosynthesis response under heat stress of wild potatoes (*Solanum commersonii*) from Embrapa Clima Temperado Potato Genebank.*
- **STRp04**: Borras *et al. Identification and Functional Characterization of two NACs Activated by Acute Water Stress in Sweet Pepper.*
- **STRp05**: Cavusoglu *et al. In Silico Genome-Wide Identification and Analysis of Na+/H+ Antiporter (NHX) Genes in* Solanum lycopersicum.
- **STRp06**: Francesca *et al. Increase tomato plant performances under combined abiotic stresses using a plant-based biostimulant.*
- **STRp07**: Garzon-Martinez *et al. Combining transcriptome analysis and GWAS for identification and validation of marker genes in the* Physalis peruviana-Fusarium oxysporum *pathosystem*
- **STRp08**: Gonzalo *et al. Genetic Control of Reproductive Traits in Tomato under High Temperature.*
- **STRp09**: Gryffroy *et al. Understanding the molecular mechanisms of interaction between tomato and rhizogenic agrobacteria through TurboID-mediated proximity labeling.*
- **STRp10**: Gupta *et al. Comparative miRNome analysis of contrasting tomato cultivars revealed their thermotolerance and tissue specific roles.*
- **STRp11**: Hadjieva *et al. Micro RNA expression changes are linked to a pepper cultivar-specific response to Potato Spindle Tuber Viroid infection.*

- **STRp12**: Hu *et al. High CO2- and pathogen-driven expression of the carbonic anhydrase βCA3 confers basal immunity in tomato*.
- **STRp13**: Jha *et al. Identification and characterization of heat-responsive microRNAs in inflorescence of tomato (*Solanum lycopersicum *L.).*
- **STRp14**: Karlova *et al. Resilience to salinity in tomato.*
- **STRp15**: Koseoglou *et al. Impairment of SlWAT1 leads to reduced susceptibility to different strains of* Clavibacter michiganensis.
- **STRp16**: Li *et al. How does the tomato development change in response to shade in different cultivars?*
- **STRp17**: Monino-Lopez *et al. Rpi-chc1.1 and Rpi-chc1.2, two Solanum chacoense allelic variants that evolved to recognise different members of the Phytophthora infestans PexRD12/31 effector superfamily*.
- **STRp18**: Mythri & Jayalekshmy. *Screening tomato germplasm for root-knot nematode resistance.*
- **STRp19**: Pereyra-Bistraín *et al. Identification of genes potentially related to resistance to Clavibacter michiganensis subsp. michiganensis: A transcriptomic approach*
- **STRp20**: Picarella *et al. Phenotypic analysis of tomato plants engineered for a proline transporter grown in contrasting thermal regimes*.
- **STRp21**: Rao *et al. An HSF:miR169:NF-YA module governing tomato and Arabidopsis heat stress tolerance.*
- **STRp22**: Romero-Rodriguez *et al. Integrated transcriptome, methylome and smallRNA profile analysis of tomato-geminivirus interaction*.
- **STRp23**: Rosa-Martinez *et al. Evaluation of 'de penjar' long shelf-life tomato under two N fertilization conditions.*
- **STRp24**: Rubina Das *et al. Unravelling a complex post-transcriptional regulation of SlHsf-18 in tomato during heat stress response.*
- **STRp25**: Sadder *et al. Physical mapping of salinity responsive biomarkers in tomato*
- **STRp26**: Santillán Martínez *et al. CRISPR/Cas9 targeted mutagenesis for functional studies in tomato- and Arabidopsis- powdery mildew interactions.*
- **STRp27**: Shohat *et al. Drought regulation of GA metabolism improves water-deficit responses in tomato*
- **STRp28**: Song *et al. Rootstock Variability and the Response of Tomato to Salinity*.
- **STRp29**: Szepesi *et al. Role of polyamine catabolism in tomato cultivars during salt stress*
- **STRp30**: Vainer *et al. Hormone profiling of tomato reproductive organs reveals the vital role of indole-acetic acid conjugation in flower development*
- **STRp31**: Zhou *et al. Postharvest handling induces changes in fruit DNA methylation status and is associated with alterations in fruit quality in tomato (*Solanum lycopersicum *L.)*

STRop

Population studies of the wild tomato species Solanum chilense reveal geographically structured major gene-mediated pathogen resistance

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Abstract
Natural plant populations encounter strong pathogen pressure and defense-associated genes are known to be under selection dependent on the pressure by the pathogens. We use populations of the wild tomato *Solanum chilense* to investigate natural resistance against *Cladosporium fulvum*, a well-known ascomycete pathogen of domesticated tomatoes. Host populations used in our studies are from distinct geographical origins and share a defined evolutionary history. We observed that distinct populations of *S. chilense* differ in resistance against the pathogen. Screening for major resistance gene mediated pathogen recognition throughout the whole species showed clear geographical differences between populations and complete loss of pathogen recognition in the south of the species range. In addition, we observed high complexity in a homologues of *Cladosporium* resistance (Hcr) locus, underlying the recognition of *C. fulvum*, in central and northern populations. Our findings show that major gene mediated recognition specificity is diverse in a natural plant-pathosystem. With this work we place major gene resistance in a geographical context that also defined the evolutionary history of the species. Our data suggest that the underlying loci are more complex than previously anticipated, with small-scale gene recombination being possibly responsible for maintaining balanced polymorphisms in the populations that experience pathogen pressure.

STRo01

Resilience to salinity in tomato – root transcriptome data analyses

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Abstract
Salinity is an increasing problem for the decreasing arable land surface. In coastal or irrigated areas, soil salinity is particularly increasing and can reach critical levels higher than tolerated by current cultivation. Novel cultivation practices including the use of resilient plant varieties and biostimulants might help to keep these areas accessible for food production. The salt stress response of above soil tissue is well documented, however, it is the root tissue which is exposed first to salt stress conditions either from the onset of its development or when increasing salt concentrations occur throughout cultivation.

Can changes in the root transcriptome be linked to the root metabolome and phenotype? Transcriptome data analysis from an RNAseq experiment with salt and biostimulant treated samples harvested at two timepoints already revealed interesting candidates. In brief, we used a principle component analysis (PCA) to reduce the dimensionality of the data. The PCA was combined with an over-representation analysis based on Mercator functional annotations (Mercator bins). This identified e.g. a transporter regulated upon salt stress. Interesting patterns of members from the same gene family were observed. Moreover, we found over-represented Mercator bins from secondary metabolism and two candidates from the same cellular process when differentiating samples treated with a biostimulant by the PCA.

These transcriptome analyses will serve as one building block for deriving gene and metabolite networks as well as mechanistic models to characterize resilient varieties and beneficial biostimulant treatment in order to allow cultivation at currently unfavourable conditions.

STRo02

StPIP1, a predicted PAMP-induced peptide in potato, elicits plant defenses and is associated with disease symptom severity in a compatible interaction with potato virus Y

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Abstract
The role of small secreted peptides in plant defense responses to viruses has been seldom investigated. Here, we report a role for potato (Solanum tuberosum) PIP1, a gene predicted to encode a member of the PAMP-induced peptide (PIP) family, in the response of potato to potato virus Y infection (PVY). We show that exogenous application of synthetic StPIP1 to potato leaves and nodes increased the production of reactive oxygen species and the expression of plant defense-related genes, suggesting that StPIP1 functions in defense signaling. In support of this hypothesis, transgenic potato plants that constitutively overexpress StPIP1 had higher levels of leaf callose deposition, and based on measurements of viral RNA titers, were less susceptible to infection by a compatible PVY strain. Interestingly, systemic infection of StPIP1-overexpressing lines with PVY resulted in clear rugose mosaic symptoms that were absent or very mild in infected non-transgenic plants. A transcriptomics analysis revealed that marker genes associated with both PTI and effector-triggered immunity (ETI) were induced in infected StPIP1-overexpressors but not in non-transgenic plants. Together, our results reveal a role for StPIP1 in eliciting plant defense responses and in regulating plant anti-viral immunity.

STRo03

Decoding the regulatory networks of diverse coding and noncoding RNAs towards heat stress response in tolerant and sensitive tomato cultivars from Indian sub-continent

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Abstract
The footprint of tomato cultivation, a cool region crop that exhibits heat stress (HS) sensitivity, is increasing in the tropics/sub-tropics. Knowledge of novel regulatory hot-spots from varieties growing in the Indian sub-continent climatic zones could be vital for developing HS-resilient crops. Thus, we identified a tolerant (CLN1621L) and sensitive (CA4) cultivar-pair, shortlisted from a pool of varieties exhibiting variable thermo-sensitivity using physiological, survival and yield-related traits. Further, we have utilized their comparative transcriptome (mRNA, long noncoding RNA and small RNA) to identify many novel heat stress regulators which have not been examined previously in thermotolerance. The antagonistically-expressing mRNA genes encode enzymes and proteins that have roles in plant defense and abiotic stresses. Functional characterization of three antagonistic genes by overexpression and silencing established Solyc09g014280 (Acylsugar acyltransferase) and Solyc07g056570 (Notabilis), that are up-regulated in tolerant cultivar, as positive regulators of HS-tolerance and Solyc03g020030 (Pin-II proteinase inhibitor), that is down-regulated in CLN1621L, as negative regulator of thermotolerance (Balyan et al., 2020). Transcriptional assessment of promoters of these genes by SNPs in stress-responsive cis-elements and promoter swapping experiments in opposite cultivar background showed inherent cultivar-specific orchestration of transcription factors in regulating transcription. Moreover, detailed regulation by heat stress transcription factors (Hsfs) on miRNA169-mediated thermotolerance in tomato (Rao et al., 2020) and regulation of Hsfs post-transcriptionally by miRNAs in a cultivar-specific manner has been discerned.

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STRo04

Nitric oxide is involved in the SlWRKY81 transcription factor-regulated stomatal movement and drought tolerance in *Solanum lycopersicum* L.

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Abstract
The WRKY transcription factors (TFs) play multifaceted roles in plant growth, development, and stress response. Previously, we found that SlWKRY81 negatively regulates tomato tolerance to drought; however, the mechanisms of stomatal regulation in response to drought remain largely unclear. Here, we showed that drought-induced upregulation in the SlWKRY81 transcripts induced photoinhibition and reduced the net photosynthetic rate in tomato leaves. However, silencing SlWKRY81 alleviated those inhibitions and minimized the drought-induced damage. A time-course of water loss showed that SlWKRY81 silencing significantly and consistently reduced leaf water loss, suggesting a role for SlWKRY81 in stomatal movement. Further analysis using light microscopy revealed that SlWKRY81 silencing significantly decreased stomatal aperture and increased the ratio of length to width of stomata under drought. Both biochemical assay and confocal laser scanning microscopy demonstrated that drought-induced upregulation in SlWKRY81 expression inhibited the nitric oxide (NO) accumulation in the guard cells, which was attributed to the simultaneous declines in the activity of NITRATE REDUCTASE (NR) and NR expression in tomato leaves. The inspection of 3-kb sequences upstream of the predicted translational start site of the NR identified three copies of the core W-box (TTGACC/T) sequence in the promoter region, indicating possible targets of SlWRKY81. Taken together, these data suggest that SlWRKY81 potentially represses NR transcription and thus reduces NO accumulation to attenuate stomatal closure and subsequent drought tolerance. These findings provide an improved understanding of the mechanisms of WRKY-induced regulation of stomatal closure, which can be exploited in the future to enhance drought tolerance in crops.

STRp01

Identification of different expressed genes in two contrasting NUE tomato genotypes under limiting N supply

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Abstract
Nitrogen Use Efficiency (NUE) improvement in high N demanding crops such as tomato (Solanum lycopersicum L.) has become a crucial approach for sustainable agriculture. Genotypic difference represents the basis for NUE improvement together with the understanding of both physiological and molecular mechanisms developed by genotypes differing in their NUE to cope low-NO3-. In the present study, two NUE contrasting tomato genotypes, Regina Ostuni (RO) and UC82, N-efficient and inefficient genotypes, respectively, were compared for differential expression patterns of some NO3- metabolism related genes (nitrate transport, assimilation, remobilization and storage/sequestration), in both roots and shoots, under limiting and non-limiting NO3-supply. Our results revealed no significant differences in nitrate and nitrite reductase expression levels (SlNR and SlNIR, respectively) between NO3- treatments in RO shoot, while they appeared significantly down-regulated in UC82 under limiting NO3- supply. However, SlNR transcript level was significantly higher in RO shoot compared to UC82 in NO3- limiting supply. In addition, the potential involvement of NO3- long-distance transporter genes in root (SlNRT1.5 and SlNRT1.8), remobilization and flux in shoot (SlNRT1.7 and SlNRT2.7) in RO efficiency was highlighted. Besides, the chloride channel protein (SlCLCa) expression, mediating NO3- storage in cell tonoplasts, revealed a higher NO3- storage/sequestration in both UC82 tissues. Taken together, our results suggested that the strategy of the efficient tomato genotype is mainly determined by plant ability to modulate long-distance N transport, assimilation, remobilization and sequestration genes (SlNRT1.5, SlNRT1.7, SlNRT2.7, SlNR and SlCLCa). Finally, transcriptome analyses are being performed to identify candidate genes to improve NUE in tomato.

STRp02

MIR172-mediated regulation in combined heat and drought stress by engaging novel targets in tomato

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Abstract
Combination of abiotic stresses has negative effect on the plant growth and productivity. Plant microRNAs control entangled gene regulatory networks and have been implicated in different stress responses. The core miRNome was identified in combined heat and drought stress in tomato leaf tissue. We identified miRNAs that showed up-regulation at both mature and precursor level in individual heat, dehydration and combined stress like miR172. MIR172 family is an evolutionarily conserved miRNA family, however in-depth analysis of MIR172 family in tomato is lacking. We validate four new loci of MIR172 in addition to the four loci reported at miRBase. We also did comparative study for identification of miRNA family members loci in the closest wild relative S. pimpinellifolium and in distant wild relative S. pennellii. Expression profiles of MIR172: target pair suggest MIR172 family as pervasive regulator of various abiotic stresses and developmental pathways. This regulation of miR172 was also shown by their promoter activity confirmed by promoter MIR172:GUS-reporter assays. With the degradome data, we identify Plastidic ATP/ADP-transporter, Beta-glucosidase 01, heat shock protein 90, Sec14p-like phosphatidylinositol transfer family protein as novel targets of miR172. We validate some of them using transient assays in Nicotiana benthamiana and chelation of miR172 by short-tandem-target-mimic construct. We show different processivity of miR172 precursors coding for same mature miRNA as well as also target cleavage efficiencies by miR172:AP2a pair. The present study will help in understanding the molecular studies on the miRNA172 involved in the regulatory networks involved in individual and combined stress response in tomato.

STRp03

Photosynthesis response under heat stress of wild potatoes (Solanum commersonii) from Embrapa Clima Temperado Potato Genebank

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Abstract
The chlorophyll fluorescence parameter Fv/Fm reflects the maximum quantum efficiency of photosystem II (PSII) and is widely used for early stress detection. We have evaluated three *S. commersonii* wild potato accessions (BGB003, BGB008, BGB027) from Embrapa Clima Temperado Potato Genebank to search for phenotypic expression of genetic variation for tolerance to high temperatures. Fv/Fm were measured after 16, 28 and 43 days. We investigated the performance (high and low Fv/Fm value) in terms of photosynthetic traits under control (C) and heat stress (HS) (14/27 OC and 24/34OC day/night temperature respectively in growth chambers). The highest Fv/Fm value was observed in BGB027 followed by BGB003 in stress conditions with high Fv/Fm value accompanied by higher stomatal conductance (gs). For BGB003, high Fv/Fm was accompanied by higher total chlorophyll (CC), net photosynthetic rate (PN) and transpiration rate (E). Stomatal conductance (gs) in stress environment and photochemical quantum yield of photosystem II (Yll) in control environment was positively correlated to Fv/Fm. Genotype and environment interaction was found nonsignificant but the genotypic effect was significant which shows variation is genotypic. BGB027 with high Fv/Fm maintained significantly higher total photochemical quantum yield of photosystem II (Yll), than BGB003 accompanied by higher Stomatal conductance (gs) net photosynthetic rate (Pn), and transpiration rate (E). The evaluated genotypes may serve as sources for further studies to understand the physiological mechanisms underlying the genetic variability in heat sensitivity of photosynthesis in *S. commersonii*.

STRp04

Identification and Functional Characterization of two NACs Activated by Acute Water Stress in Sweet Pepper.

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Abstract
Capsicum annuum L. is one of the most cultivated Solanaceae globally, and in open field water stresses affect its fruit setting, size and quality.
Following RNA-seq transcriptome analyses of a breeding line (CCu07) subjected to acute water stress followed by recovery (rewatering), at three stages of plant development, we identified stage-specific and common core sets of differentially expressed genes (DEGs). Among them, 2 NAC transcription factors (TF): CaNAC072 and CaNAC104 were always up regulated after water stress and down regulated after recovery. Following their transient expression in Nicotiana benthamiana leaves, the two TFs were localized in the nucleus.
The expression of the two NACs was otherwise induced by NaCl, PEG and ABA treatments, highlighting that CaNAC072 is an early, while CaNAC104 a late abiotic stress responsive gene.
The interactions between NAC proteins and the cis-acting elements of target genes vary in relation to the plant species or under different environmental conditions. NACs participate in regulating water stress responses, either as suppressors or activators, depending on the family member and the nature of the stress. The Virus induced gene silencing (VIGS) of CaNAC072 in CCu07 plantlets improved water stress tolerance, suggesting that it acts as a suppressor of drought tolerance. On the other hand, VIGS of CaNAC104 did not affect drought tolerance.
Taken together our results emphasize the complex role of NACs as transcriptional switches in the response of sweet pepper to water stress.

STRp05

In Silico Genome-Wide Identification and Analysis of Na+/H+ Antiporter (NHX) Genes in *Solanum lycopersicum*

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Abstract
Salinity which is spreading throughout the world is one of the most important abiotic stress factors limiting the agricultural productivity worldwide. The Na+/H+ antiporter (NHX) genes play a considerable role during plant growth and development in tolerance to salt stress. The objective of this study is to identify NHX genes using version SL4.0 and version ITAG4.0 of tomato genome. Seven putative NHX genes distributed on chromosome 1, 4, 6, and 10 were identified. While SlNHX1, -2, -3, -4 and -6 genes were localized on Vacuole, SlNHX7 and SlNHX8 were localized on plasma membrane and Plasma Membrane-Vacuole, respectively. SlNHX1, -2, 3-, -4, -6 proteins have amiloride-binding site [FFIYLLPPI] which is located in transmembrane helix domain-3 and is known an inhibitor of Na+/H+ exchanger activity and characteristic feature of Vacuole class NHX proteins. SlNHX4 and SlNHX7 hypothetically interact with CBL-interacting protein kinases (CIPK) based on Protein-protein interaction (PPI) prediction analysis. The High-throughput gene expression data analysis which was retrieved from TomExpress database and SolGenomics project. Whereas SlNHX3 gene only expressed in unopened flower, SlNHX2, -4 and SlNHX1, -6 genes showed the highest expression levels in root and mature green fruit stage, respectively. The tissue specific gene expression levels treated with salt shock stress at different salt concentrations will be performed using qRT-PCR after plants reach at targeted development stage.

Keywords
Tomato, Salt stress, Abiotic stress, NHX, Bioinformatic

STRp06

Increase tomato plant performances under combined abiotic stresses using a plant-based biostimulant

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Abstract
Drought and heat stress are reported to be major abiotic stresses limiting crop yield worldwide. In particular, tomato (Solanum lycopersicum), is regarded as a heat sensitive crop, although this sensitivity varies among genotypes. We investigated physiological responses of two tomato genotypes ('E42' and 'LA3120') that were cultivated in greenhouses under control, heat, drought and combined stress and treated or not with a plant-based biostimulant named CycoFlow (Agriges). The application of the biostimulant stimulated tomato growth under combined stress (plants up to 11.86% taller and number of leaf up to 29.89%). In 'E42', plants treated with the biostimulant under drought showed the same net photosynthetic rate (PN) level as the non-treated and non-stressed plants. Moreover, PN levels in 'LA3120' treated with the biostimulant under drought were higher compared to non-treated plants. The Fv/Fm values in the two genotypes were affected by drought, but a higher value was observed in the biostimulant-treated plants of 'E42' compared to non-treated plants. Also, biostimulant-treated plants under heat stress showed a higher stomatal conductance and transpiration rate compared to non-treated plants. Interestingly, a higher content of chlorophylls was also detected in both genotypes treated with the biostimulant compared to the non-treated plants under combined stress. Altogether, the effect of the biostimulant depended on the stress applied. The outcomes of this work will be important for the selection of genotypes tolerant to abiotic stresses and will help select the management practise to be used to improve plant performances and final yields.

STRp07

Combining transcriptome analysis and GWAS for identification and validation of marker genes in the *Physalis peruviana-Fusarium oxysporum* pathosystem

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Abstract
Cape gooseberry (*Physalis peruviana* L.) is a valuable fruit-bearing species from the Solanaceae family, recognized as a source of pharmacological compounds with anti-inflammatory, antibacterial and antitumor activities. This fruit is economically important in countries such as Colombia where stands out as the second most important export fruit. However, one of the major constraints for cape gooseberry production in Colombia is the vascular wilt caused by the fungal pathogen Fusarium oxysporum f. sp physali (Foph). In this study, we validated key genes underlying Foph recognition and cape gooseberry defense responses. Candidate genes were identified and selected from 1,653 differentially expressed genes (DEGs) derived from RNA-Seq analysis and from a previous genome wide association study (GWAS) of this plant-pathogen interaction. The RT-qPCR validation showed candidate genes highly expressed earlier during infection in a susceptible genotype, while three others were overexpressed later, mostly in the tolerant genotype. These genes are mainly involved in pathogen recognition and a subsequent signaling pathways mediated by hormones such as ethylene and salicylic acid. This study provided the first insight to uncover and understand the molecular mechanisms from the P. peruviana - Foph pathosystem. The candidate genes validated allow a better understanding of the defense response in this orphan crop at the molecular level, and can be applied for the development of molecular markers that could facilitate the identification of tolerant/susceptible genotypes for use in breeding schemes.

STRp08

Genetic Control of Reproductive Traits in Tomato under High Temperature

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Abstract
Global climate change is increasing the temperatures that crops face during their life cycle, having negative effects in yield. Understanding the genetic control of plant responses to heat is a prerequisite for developing cultivars with increased resilience. The current work reports the identification of Quantitative Trait Loci (QTL) involved in reproductive traits (flower (FLN) and fruit number (FRN) per truss, percentage of fruit set (FRS) and pollen viability (PV)) under heat stress in 168 Recombinant Inbred Line (RIL) and 52 Introgression Line (IL) populations derived from the *Solanum lycopersicum* var. "MoneyMaker" and S. pimpinellifolium accession TO-937 cross. Plants were cultivated under increased temperature regimen conditions: T1 (25_C day/21_C night), T2 (30_C day/25_C night) and T3 (35_C day/30_C night). The effects of the heat stress was important at T3 for FLN, whereas the effects were evident already at T2 for FRN and FRS. A total of 20 QTLs involved in reproductive traits at different temperatures were identified by multi-environmental QTL analysis. Furthermore, two ILs with introgression at chromosomes 1 and 12 showed consistent heat tolerance in replicated trials. These results represent a catalogue of QTLs and pre-breeding materials that could be used as starting point to decipher the genetic control of the genetic response of reproductive traits at different temperatures and pave the road to develop new cultivars adapted to climate change.

STRp09

Understanding the molecular mechanisms of interaction between tomato and rhizogenic agrobacteria through TurboID-mediated proximity labeling

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Abstract
Cultivation of hydroponically grown Solanaceae and Cucurbitaceae crops is currently facing problems due to the occurrence of a root disorder called 'hairy roots'. This disease is characterized by an extensively expanded root system, suppressed water-uptake, defective fruit development and eventually withering of the plant. The causal agents of this disease are gram-negative rhizogenic Agrobacterium biovar 1 strains harbouring a root-inducing (Ri) plasmid. To date, the molecular mechanisms behind the development of hairy roots on infected plants remain largely unknown. Protein-protein interactions are essential in the communication between a plant and a microbe and eventually determine successful mounting of the plant's defense response or emergence of the disease. In our research, we are using an innovative, high-throughput interactomics approach to map the key events in the development of hairy root disease. More specifically, we make use of TurboID-mediated proximity labeling coupled to LC-MS/MS, which enables the identification of direct and indirect protein interactors in planta. The rationale for our interest in this topic is that hairy root cultures are proven attractive and cost-effective options for the mass production of high-value plant metabolites and can be grown in contained conditions. Hence, besides filling longstanding gaps in our fundamental understanding of this plant-pathogen interaction, we anticipate that this research line will also yield novel insights into the regulation of plant metabolism and means to increase its exploitation. Eventually, this project may also generate novel targets for tomato pest resistance engineering and breeding.

STRp10

Comparative miRNome analysis of contrasting tomato cultivars revealed their thermotolerance and tissue specific roles

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Abstract
Plant genomes encode for hundreds of miRNAs which are involved in a variety of functions like growth, metabolism, development and adaptive response to biotic and abiotic stresses. In the present study, 78 small RNA datasets from a pair of tomato cultivars exhibiting contrasting response to heat stress (HS) have been analysed to identify miRNAs which are differentially expressed in different tissues and under heat stress conditions. This led to the identification of 923 unique and 1153 precursor miRNAs whose hairpin structures fulfil all defined criteria. Comparative expression analysis between HS tolerant and sensitive cultivar under varied HS regimens showed conserved to cultivar-specific HS response. In the sensitive cultivar, 108 miRNAs were downregulated in heat stress and 97 were upregulated, while in the tolerant cultivar, 55 miRNAs were downregulated and 182 were upregulated. This indicates important roles for miRNAs in heat stress tolerance in tomato. Further, the targets of all miRNAs were identified using the degradome analysis of 10 previously published degadome datasets of tomato. Based on current miRNA annotation guidelines, 15 putative novel miRNAs were selected and their precursors were confirmed by cloning followed by sequencing. Tissue-specific expression analysis revealed that two of these miRNAs were inflorescence-specific, seven were highly expressed in tomato fruits while others were leaf-specific. This data will serve as an important resource for the identification of key miRNAs and their target genes which may be involved in fruit formation or ripening pathways, flower development and tolerance to heat stress.

STRp11

Micro RNA expression changes are linked to a pepper cultivar-specific response to Potato Spindle Tuber Viroid infection

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Abstract
Potato Spindle Tuber Viroid (PSTVd) is the smallest pathogenic RNA that infects various plants species. PSTVd pathogenicity is a complex phenomenon mediated by the specific features of the viroid molecule, host species- specific genomic traits and viroid-host interactions in a dynamic environment. Two major classes of small non-coding RNAs (21-24 nt), namely micro RNAs (miRNA) and small interfering RNAs (siRNA) have been identified to mediate post-transcriptional RNA silencing as an anti-viroid defense mechanism.
Viroid- responsive miRNAs, and their potential role as regulatory determinants in viroid pathogenicity, were studied in two Bulgarian pepper cultivars: Djulunska shipka (DS) and Kurtovska kapia (KK). The viroid infection was performed with PSTVd KF 440-2 and small RNA populations were analyzed at 28 days post-inoculation. Several conserved miRNAs (miR408, miR397, miR398, miR482) display cultivar-specific expression in response to PSTVd infection, as shown by sRNA sequencing and validated by RT-qPCR. The expression dynamics of miR397a-5p and its target Laccase-like 4, evaluated by RT-qPCR at 14, 28, and 43 dpi, revealed a cultivar- specific response.

Acknowledgments
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STRp12

High CO2- and pathogen-driven expression of the carbonic anhydrase βCA3 confers basal immunity in tomato

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Abstract
Atmospheric CO2 levels exert a strong influence on the susceptibility of plants to pathogens. However, the mechanisms involved in the CO2-dependent regulation of pathogen resistance are largely unknown.
Here we show that the expression of tomato (Solanum lycopersicum) β-CARBONIC ANHYDRASE 3 (βCA3) is induced by the virulent pathogen Pseudomonas syringae pv. tomato DC3000. The role of βCA3 in the high CO2–mediated response in tomato and two other Solanaceae crops is distinct from that in Arabidopsis thaliana. Using βCA3 knock-out and overexpression plants, we demonstrate that βCA3 plays a positive role in the activation of basal immunity, particularly under high CO2.
βCA3 is transcriptionally activated by the transcription factor NAC43 and is also post-translationally regulated by the receptor-like kinase GRACE1. The βCA3 pathway of basal immunity is independent on stomatal- and salicylic-acid-dependent regulation. Global transcriptome analysis and cell wall metabolite measurement implicate cell wall metabolism/integrity in βCA3-mediated basal immunity under both CO2 conditions.
This study not only highlight the importance of βCA3 in plant basal immunity under high CO2 in a well-studied susceptible crop-pathogen system, but they also point to new targets for disease management strategies in a changing climate.

STRp13

Identification and characterization of heat-responsive microRNAs in inflorescence of tomato (*Solanum lycopersicum* L.)

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Abstract
On account of changing climatic conditions, heat stress has instigated reduction in total yield by 50% of major cereal and vegetable crops at worldwide scenario. It is imperative to understand the plant developmental modulation occurring at heat sensitive reproductive stages to combat the environmental perturbations and simultaneously respond fast to adapt and survive. The study attempts to unveil the molecular mechanism of miRNA-mediated regulation in heat sensitive critical stages of flower development using contrasting tomato cultivars in response to heat stress (HS). To achieve this feat, evaluation of different tomato cultivars with known HS tolerance/sensitivity was performed using various physiological, biochemical and yield related parameters that identified CLN1621L (CLN) and CA4 as most heat-tolerant and sensitive cultivars, respectively. To account the HS sensitivity at inflorescence stage, a comparative analysis of the pollen viability and germination at different bud lengths was performed. The microtome sections highlighted the male meiotic stages as highly HS sensitive in both cultivars. The sensitive cultivar exhibited poor pollen germination in all post-meiotic stages of bud development as well. The cumulative analysis of in-house generated heat-responsive inflorescence miRNome and literature search highlighted the 21 known differentially expressing miRNAs between the two contrasting cultivars. The expression profiling of miR319 and miR169 showed differential expression at mature and precursor level and were inversely related to their targets under HS in inflorescence tissues. Transgenic tomato plants and Arabidopsis plants overexpressing miR169 showed better performance with more number of flower and fruit retention in overexpression lines than wild type in HS.

STRp14

Resilience to salinity in tomato

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Abstract
Agriculture will have to feed an increasing world population, using a decreasing arable land surface. Salinity is an increasing problem, in particular in coastal or irrigated areas. Due to climate change, these traditionally fertile areas are suffering from increased soil salinity, which has reached concentrations higher than tolerated by current cultivation practices. In the near future these areas will no longer be suitable for cultivating food unless we adopt novel production practices, including the use of novel resilient plant varieties. For plants to be resilient to abiotic stresses such as salinity and drought, the root system is of vital importance. Roots are the primary organs that adapt their architecture and physiology to drought and salt stress. Their performance is key to the ability of the whole plant to take up nutrients and water. However, we have limited knowledge of how the root functions and this translates into a limited capability to control plant resilience to abiotic stress. Novel developments in biostimulants show that it is possible to affect root functioning and resilience towards abiotic stress such as high-salinity. However, despite their potential for agriculture, there is very limited knowledge on the mechanisms through which biostimulants act. In this study we use genome-wide association mapping and CRISPR/Cas9-mediated forward genetics to understand the mechanism by which biostimulants contribute to tomato resilience under salinity stress conditions. The link between changes in root architecture and salt stress resilience will be discussed together with its importance in understanding salt tolerance in tomato.

STRp15

Impairment of SlWAT1 leads to reduced susceptibility to different strains of *Clavibacter michiganensis*

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Abstract
Bacterial canker of tomato caused by the vascular pathogen *Clavibacter michiganensis* (Cm), is considered to be one of the most important bacterial diseases of cultivated tomato. Due to the lack of effective control measures against it, Cm is regulated as a quarantine or regulated non quarantine pest in multiple countries. No resistance (R) genes against the pathogen have been identified. Furthermore, a limited number of QTLs from wild accessions, with a complex genetic background have been shown to be involved in tolerance to Cm. As a result, there are no Cm resistant tomato cultivars. We decided to investigate the potential of using impaired susceptibility (S) genes as an alternative. Arabidopsis Wall Are Thin 1 (WAT1) encodes for a plant-specific protein that is involved in auxin transportation and secondary cell wall biosynthesis. Studies have shown that mutation of WAT1 is linked to enhanced resistance of Arabidopsis to a broad range of vascular pathogens. In our study, we identified and impaired the tomato ortholog of Arabidopsis WAT1. SlWAT1 silenced transgenic tomato lines were challenged with four genetically diverse Cm strains with different aggressiveness. SlWAT1 silenced plants showed reduced susceptibility to all tested strains, without severe adverse pleiotropic effects observed. To further study the effect of a full knock-out, a mutant slwat1 line was generated through CRISPR/Cas9. Full knock-out of the gene led to loss-of-susceptibility to Cm, accompanied with severe pleiotropic defects. To our knowledge, this is the first time that impairment of a single gene has resulted in reduced susceptibility to Cm.

STRp16

How does the tomato development change in response to shade in different cultivars?

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Abstract
Food shortage is a global issue and becoming more and more severe, especially combined with the population increase. In order to get higher yield, farmers will sow more crops on limited area, leading to plants fighting over limited resources. One of the most important one is light. Plants often need to compete their neighbors for light. Many species respond by growing taller to get enough light and avoid further shading. This adaptation is called shade avoidance response.

Big amount of commercial tomatoes are produced every year and the Netherlands are a large producer of tomatoes. The shade avoidance systems vary from cultivar to cultivar. In this research, we use two tomato cultivars: field-grown M82 and greenhouse model Moneymaker. To answer the question-how is tomato cellular anatomy regulated in shade, we started with measuring tomato architecture and cellular traits in shade and in normal light environment. We found out what is the biggest responses are in stem elongation, where we then used microscopy to quantify all cell types.

Research questions: What are the phenotypic changes in response to far-red treatment? How does cellular anatomy of tomatoes respond to far-red treatment? What are the genes that regulate these far-red responses?

Methods: 1- Plant architecture phenotypic screen; 2- Histology of selected tissue; 3- Data analysis to identify most responsive cell/tissue type; 4- qPCR for time point selection; 5- RNA-seq analysis of time series and specific tissues; 6- Validation by e.g. overexpression and knockout line construction

Results: Stems elongate significantly, internode 1 elongates the most drastically. Pith cell features are the most significantly changed among all cell types. qPCR results show that pith cell and the whole internode FR responses differ, more details will be found by RNA-seq

Conclusions: We have currently found out that the pith cell is the most drastically elongating and increasing in cell layer number in response to far-red light. Pith qPCR showed a different gene expression pattern compared with the whole internode for selected FR response genes.

STRp17

Rpi-chc1.1 and Rpi-chc1.2, two Solanum chacoense allelic variants that evolved to recognise different members of the *Phytophthora infestans* PexRD12/31 effector superfamily

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Abstract
Phytophthora infestans is a pathogenic oomycete that causes late blight, the most devastating and costly potato disease. Breeders rely on the availability of resistance (R) genes to P. infestans (Rpi) to develop new resistant varieties. Such Rpi receptors trigger the plant defence response upon the recognition of cognate avirulence (Avr) effector proteins of the RXLR family. In this study, we characterised two allelic variants (Rpi-chc1.1 and Rpi-chc1.2) of the late blight Rpi-chc1 gene, from the resistant wild potato relative S. chacoense. Both alleles encode a Coiled-Coil (CC) – Nucleotide-Binding (NB) – Leucine-Rich Repeat (LRR) proteins, being the first functional representatives of the CNL16 family. An allele mining approach led to the identification of 15 Rpi-chc1-like homologs, classified into four main clades. These alleles have distinct patterns of RXLR effector recognition. While Rpi-chc1.1 and other alleles from clade A recognise PexRD12 (Avr-chc1.1), Rpi-chc1.2 and other members from clade B recognise PexRD31 (Avr-chc1.2), both belonging to the PexRD12/31 effector superfamily. We hypothesise that Rpi-chc1.2 is an ancient R gene that has been overcome in the recent past by reduction of PexRD31 expression. Rpi-chc1.1 may have evolved more recently since it is still active and provides resistance to a broad spectrum of *P. infestans* isolates. Additionally, we identified the LRR subdomain of both Rpi-chc1.1 and Rpi-chc1.2 to be responsible for the difference in effector recognition. With this study, we expand the knowledge on the molecular plant-pathogen interaction contributing to a better R gene exploitation and consequently to a better control of the late blight disease.

STRp18

Screening tomato germplasm for root-knot nematode resistance

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Abstract
Tomato is a well-known solanaceous vegetable crop grown worldwide. Root-knot nematodes are one of the major pests that cause severe damage to tomato leading to potential yield losses up to 70%. The use of resistant varieties controls these pests effectively over other methods. Thirty-seven genotypes were collected and evaluated for resistance through artificial inoculation. Fifteen days after transplanting the healthy seedlings, hatched egg masses were injected @ 2000 juveniles/plant. Observations were recorded for the number of larvae in 5 g root, root-knot count in 5 g root, number of females in 5 g root, number of egg masses in 5 g root, the average number of eggs in egg mass, and nematode population in 200 cc soil. The reproductive potential was assessed by calculating the reproduction factor. Analysis of variance was found to be significant for all the parameters observed. Root-knot indexing was done using the method suggested by Heald. Vellayani Vijai was found to be moderately susceptible with a root-knot index of 3 and EC – 160855 was susceptible with a root-knot index value of 4, while all other genotypes in the study; including resistant checks were highly susceptible. The study highlights the urgent need for new potential resistance sources.

STRp19

Identification of genes potentially related to resistance to *Clavibacter michiganensis* subsp. michiganensis: A transcriptomic approach

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Abstract
Bacterial canker of tomato is one of the most important bacterial diseases of this crop causing important economic losses worldwide. The disease is caused by the actinomycete *Clavibacter michiganensis* subsp. michiganensis (Cmm). There are no effective control strategies and only few preventive methods work efficiently. Currently, some wild tomato species such as *Solanum arcanum* and *Solanum habrochaites* are tolerant to Cmm. The study of these wild species represents an important approach for identifying a natural resistance source that can be used in commercial cultivars for controlling bacterial canker. In order to gain insight related to potentially tolerance genes, we contrasted the transcriptomes of the resistant wild tomato species *S. arcanum* LA2157 and the susceptible species *S. lycopersicum* cv. Ailsa Craig. We accomplished three different strategies: mapping to the reference genome SL3.0, Semi de novo transcriptome assembly, and de novo transcriptome assembly. Our results suggest that both tomato species exhibit a high amount of differentially expressed genes from 0 hours to 24 hours after the Cmm challenge, and the more contrasting results were obtained at 8h, particularly in the wild species *S. arcanum* LA2157, in which several functional groups related to defense response were enriched. Global transcriptional changes seem to be conserved between both species, suggesting that resistance in S. arcanum is associated with an upstream regulatory mechanism that probably diverged during the domestication process. The future work relies on the functional validation of the potentially tolerance-related genes to in order to overexpress the candidate genes in commercial cultivars of tomato.

STRp20

Phenotypic analysis of tomato plants engineered for a proline transporter grown in contrasting thermal regimes

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Abstract
Temperature affects plant growth and productivity, influencing both the vegetative and reproductive phase. The negative effect of high temperature is a major problem because of predicted increase of earth surface in the coming years. The level of proline in anthers plays important roles in acquiring heat tolerance in tomato, although proline transport may seriously be impaired by heat stress. Here, we engineered tomato cv Microtom (MT) plants with the endogenous LePROT1 proline transporter gene under the control of the conditional HSP18.2 promoter from Arabidopsis. MT plants and two T3 progenies were grown in optimal conditions; half of the plants were subjected to repeated heat stress (38°C, 3 h/d for 2 weeks). An in vitro experiment was also carried out to subject seedlings to an acute heat treatment. Whereas MT plants under chronic heat stress showed a decrease in anther proline content, T3 plants had significantly more proline than either the stressed control and the unstressed transformants. This pattern was paralleled by estimation of viable pollen. At phenotypic level, transformed plants under stress performed better than controls for inflorescence length, number of flowers, fruit set and Brix value. In vitro grown T3 seedlings after heat shock showed better root growth than the controls. In the epigeal part of seedling, the proline level was higher in trasformed plants than in controls irrespectively of the treatment. Total expression levels of LePROT1 were higher in trasformed plants at 48 h after heat shock. In conclusion, our data show that proline transport engineering represents a promising tool to endow tomato plants with thermotolerance.

STRp21

An HSF:miR169:NF-YA module governing tomato and Arabidopsis heat stress tolerance

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Abstract
MIR169 family is an evolutionarily conserved miRNA family in plants known to target Nuclear Factor-YA (NF-YA) transcripts. A systematic in-depth analysis of MIR169 family in tomato (*Solanum lycopersicum*) by us annotated eighteen MIR169 precursors, these include new loci for MIR169a, b and d, as well as three novel mature isoforms namely, MIR169f/g/h (Rao et al., 2020). This family has expanded by both tandem- and segmental-duplication events during evolution. A tandem-pair MIR169b/b-1 and MIR169b-2/h is bicistronic in nature coding for three MIR169b isoforms and a new variant miR169h that is evidently absent in the wild relatives *S. pennellii* and *S. pimpinellifolium*. Seven novel miR169 targets picked from degradome data were confirmed by efficient target cleavage in presence of specific MIR169 precursors as well as increased target abundance upon miR169 chelation by short-tandem-target-mimic (STTM) construct in transient assays. Expression analysis of various MIR169s under different abiotic stresses showed significant increase in response to heat stress. Yeast-one-hybrid screens and co-expression in transient assays showed that seven tomato HSFs recognize five MIR169 promoters whereas, silencing HSFs using virus induced gene silencing (VIGS) reduced miR169 expression. Functional analysis using Sly-NF-YA-VIGS tomato plants and Arabidopsis plants overexpressing At-MIR169 or At-nf-ya mutants showed a link with increased heat tolerance in both plants. In contrast, Arabidopsis plants overexpressing At-NF-YA, or those expressing a non-cleavable At-NF-YA form as well as plants inhibited for At-miRNA169 regulation are more sensitive to HS, highlighting NF-YA acts as a negative regulator of heat tolerance. We propose a retroactive control of HSFs by the miR169:NF-YA node.

STRp22

Integrated transcriptome, methylome and smallRNA profile analysis of tomato-geminivirus interaction

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Abstract
Geminiviruses constitute the largest family of plant-infecting viruses with small, single-stranded DNA genomes that replicate through double-stranded DNA intermediates. Because of their limited coding capacity, geminiviruses use plant nuclear machinery to amplify their genomes, which are packaged into nucleosomes forming chromatin as multiple circular minichromosomes. Thus, viral minichromosomes must encounter the nuclear pathways that regulate host gene expression and chromatin states. DNA methylation and post-transcriptional gene silencing play critical roles in controlling infection of geminiviruses and this pathogen can counteract these host defense mechanisms and promote its infectivity.
Tomato Yellow Leaf Curl Virus (TYLCV) belongs to the Begomovirus genus and is transmitted by the whitefly Bemisia tabaci. With only six viral proteins, this geminivirus must create a proper environment for viral replication, transcription and propagation. Behind the apparent simplicity of geminiviruses lies a complex network of molecular interactions with their host and their natural vector, which induces a wide variety of transcriptional, post-transcriptional and chromatin changes in the host. To better understand this virus-host interaction at a genetic and epigenetic level we have analysed the transcriptome, sRNA profile and methylome of tomato plants (Moneymaker) infected with the geminivirus, TYLCV (Tomato yellow leaf curl virus). Total RNA and DNA was extracted from tomato–infected plants (three biological replicates) and analysed at 2, 7, 14 and 21-day post-infection (dpi). Analysis of the changes in host transcription during the infection and its correlation with changes in sRNA profiles and DNA methylation will be presented and examined.

STRp23

Evaluation of ‘de penjar’ long shelf-life tomato under two N fertilization conditions

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Abstract
The ‘de penjar’ tomato (*Solanum lycopersicum*) is a group of local varieties from the Spanish Mediterranean region carrying the alc mutation, which provides long shelf-life. Their evolution under low input management practices has led to the selection of resilient genotypes to adverse conditions. Here we present the first evaluation of agronomic performance and nutritional fruit composition of a collection of 44 varieties of ‘de penjar’ tomato under two N levels, provided by doses of manure equivalent to 162 kg N/ha in the control and 49 kg N/ha in the low N treatment. Traits analysed included yield, fruit weight, N, fructose, glucose, citric and malic acid contents, and sugars:acids ratio. Main tomato bioactive compounds, vitamin C, lycopene and β-carotene, were also evaluated. No significant effect of N supply was found for yield and most fruit compounds, except for fructose and glucose contents, which on average were reduced by 11.5% and 15.8%, respectively, under low N conditions. Significant genotype effect was observed for all the traits studied, revealing the wide variability in the collection. Fruit weight and lycopene content showed the highest relative range of variation (more than 4-fold) under both N treatments. In addition, lycopene and β-carotene presented a strongly significant interaction genotype × N input. These results revealed the potential of ‘de penjar’ varieties as a genetic resource in breeding for low N inputs and improving the organoleptic and nutritional tomato fruit quality.

STRp24

Unravelling a complex post-transcriptional regulation of SlHsf-18 in tomato during heat stress response

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Abstract
Plant cells undergo extensive reprogramming of molecular events to combat stress conditions like heat stress (HS). One such adaptive strategy is post-transcriptional regulation by alternative-splicing (AS), which can tremendously increase the transcriptome and proteome. Experimental validation heat stress transcription factor (Hsf) AS-forms in tomato highlighted that AS-variants express either differentially or specifically under different stress condition or developmental stage. In-depth analysis of Hsf18 identified five splice variants (Hsf18-V3, Hsf18-V6, Hsf18-V7, Hsf18-V17 and Hsf18-V23) of which only Hsf18-V3, Hsf18-V6 and Hsf18-V7 have coding potential which was confirmed by Western blotting using an Hsf18 genomic context:GFP construct and GFP antibody. These variants have an intact DNA binding domain and like the full length Hsf18 are nuclear localized indicating their probable role as transcription factors (TF). Interestingly, Hsf18 is also regulated post-transcriptionally by microRNA (miR-sm-1) under HS while the variants lack the target site and thus bypass target cleavage. Furthermore, a HS responsive long non-coding RNA (lncRNA) is transcribed from the complementary strand of Hsf18 locus. Yeast one-hybrid assays confirmed that Hsf18 and variants bind to the lncRNA promoter. Further experiments confirmed that Hsf18 negatively regulates lncRNA while variants regulate its expression positively. Moreover, the expression of full-length Hsf18, its variants and the lncRNA was either non-differential or not detected in other abiotic stresses like cold, salt and drought suggesting that this module is regulating thermotolerance in tomato. The precise mechanistic regulation in this complex module involving miRNA, TF and lncRNA and role of AS in Hsfs in HS adaptation is being investigated.

STRp25

Physical mapping of salinity responsive biomarkers in tomato

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Abstract
Salinity stress is becoming a major challenge for modern agriculture. Development of robust breeding lines adapted to salinity stress is urgently needed cope with future land and water quality limitation. The expression of salinity responsive biomarkers (SRB) was profiled using Affymetrix 9k tomato microarray. Three advanced tomato breeding lines (salinity susceptible genotype L46, salinity tolerant genotype L56, and salinity intermediate genotype L66) along with check tolerant line (BL 1076). Salinity treatments started 5 days after transplantation until the end of growth period (three months). The irrigation water was applied three times a day at a target rate of 100% ETc. High level expressing SRBs were assembled for all four genotypes. Advanced tomato breeding lines L56 showed the majority of unique over-expressed SRBs even when compared with the check. SRBs were mapped to current tomato reference genome. Expression levels ranged between 3-125 folds. Most SRBs were localized towards chromosome telomeres. However, several biomarkers were clustered in major hotspots including q arms of chromosomes 2, 3, 6 and 8. The constructed map is an invaluable additive for tomato breeders for future biomarker assisted selection (BAS)-based breeding programs.

STRp26

CRISPR/Cas9 targeted mutagenesis for functional studies in tomato- and Arabidopsis- powdery mildew interactions.

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Abstract
The tomato- and Arabidopsis-powdery mildew interactions have become well-characterized plant systems to study the interactions between plants and obligate biotrophs. Nevertheless, many questions still remain to be answered. Previously, knock-down-based methods, such as RNAi or Virus-induced gene silencing (VIGS) have been used to identify and characterize resistance and susceptibility genes. However, residual expression of the genes targeted through these methods may affect their clear characterization. This becomes particularly problematic when studying susceptibility (S) and resistance (R) genes conferring incomplete or partial resistance. The development of CRISPR/Cas9 has allowed precise and efficient targeted mutagenesis to identify and functionally characterize the resistance genes that plants use to defend themselves against powdery mildews. We have made use of this technology to verify a few R and S genes for their contribution to (in)complete resistance and susceptibility to PMs, respectively. This technology has provided us with a better resolution for our studies, allowing us to further understand the interaction between tomato or Arabidopsis and powdery mildews.

STRp27

Drought regulation of GA metabolism improves water-deficit responses in tomato

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Abstract
Plants avoid water-deficit stress by stomatal closure and inhibition of shoot growth, both leading to reduce transpiration. While abscisic acid (ABA) has a central role in drought avoidance, we demonstrate in tomato that gibberellin (GA) is also involved. Drought-induced growth suppression was partially inhibited in the DELLA loss-of-function mutant procera (pro) with a constitutive GA response. We found that drought reduced the levels of bioactive GAs in leaves, by inhibiting the expression of the GA biosynthesis genes GA20 oxidase1 (GA20ox1) and GA20ox2, via ABA-independent and dependent pathways, respectively. Leaves of ga20ox1 and ga20ox2 CRISPER-derived mutants are smaller and exhibited reduced water loss. Our previous study shows that inhibition of GA activity in leaves, or specifically in guard cell promotes stomatal closure. We found strong upregulation of the GA deactivating gene GA2ox7 under water-deficit conditions specifically in guard cells. ga2ox7 mutant had normal leaves, but exhibited faster water loss under water-deficit conditions. Taken together, our results show that water deficiency reduces GA levels in leaves and guard cells, leading to reduce canopy expansion and faster stomatal closure. We suggest that reduced GA activity under water-deficit conditions contributes to plant adaptation to drought.

STRp28

Rootstock Variability and the Response of Tomato to Salinity

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Abstract
Among the strategies developed to overcome abiotic and biotic stresses, grafting was demonstrated to significantly enhance plant tolorance. Nevertheless, gaps of knowledge exist in our understanding of the mechanisms by which rootstocks mediate scion-response to, e.g., salinity and consequently in developing enhanced graft-combinations. We explored the natural variation existing in rootstock mediated response to salinity in tomato. Tomato (Solanum lycopersicum) cv M82 grafted onto 254 different tomato rootstocks, including wild and commercial races. was grown in a nethouse in semi-randomized block design and treated with saline water to a final concentration of 200 mM NaCl. Following a 34 d period, leaf tissue was collected for GC-MS based metabolite profiling and oxidative stress (MDA) estimation. In addition, morphological traits were measured at harvest. Results showed that grafting resulted in phenotypic diversification of M82. When compared with self-grafted M82 under saline condition, highest CV was measured for MDA content and lowest CV for fruit weight to biomass ratio. Metabolite profiling based PCA separated between “best” and “worst” combinations (determined from fruit weight and MDA analysis). Highly responsive metabolites included malate, citrate, Leu and Asp and shikimate. Fruit weight-related traits associated with changes in a number of metabolites, such as glycerol-3-phosphate, threonate, shikimate, and erythronate.

STRp29

Role of polyamine catabolism in tomato cultivars during salt stress

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Abstract
Salt stress is an abiotic stress factor threatening agriculture causing severe economic and yield loss of some crop. Plant cultivars show different salt sensitivity and application of the salt tolerant genotypes could be an effective method for sustainable agriculture. Tomato is one of the most important vegetable crops worldwide providing many different cultivars. During salt stress, polyamines (PAs), as 'hub' molecules connect important signal pathways eg. ethylene, nitric oxide or proline helping plants contributing an enhanced salt tolerance. Hydrogen peroxide can also synthesize during catabolism of polyamines. We compared the polyamine catabolism of some tomato cultivars differing growth type or fruit color in order to investigate how polyamine degradation can contribute to improved salt tolerance in these cultivars. We found that level of PA catabolism was cultivar dependent, in the indeterminate cv. Romus with yellow fruit color had higher levels of free polyamines than the determinate cv. Rio Fuego (red fruit) or cv. Manó (red fruit), while diamine- and polyamine oxidase enzymes also showed highest activities in cv. Romus. L-aminoguanidine (AG) was used for pharmacological inhibition of diamine oxidase in order to clarify the role of this enzyme in the salt stress induced PA catabolism.

STRp30

Hormone profiling of tomato reproductive organs reveals the vital role of indole-acetic acid conjugation in flower development

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Abstract
Phytohormones play a crucial regulatory role in the majority of developmental processes in plants. We performed a hormone metabolome analysis along with transcriptome and proteome profiling for the identification of components of the hormonal system that are involved in natural processes of tomato reproductive organs development. These measurements were conducted at different stages during flower and early fruit development and covered the following flower organs (sepals, petals, stamen, pollen, carpels) and fruit organs (ovary, peel and pericarp, jelly, placenta, seeds) organs. UPLC-ESI-MS/MS analysis revealed the gradual decrease in active auxin's concentration together with the accumulation of oxidized and conjugated forms towards anthesis, especially in the stamen. Co-expression analysis revealed tomato Grethen-Hagen 3 (GH3) genes, namely SlGH3-2, SlGH3-7, SlGH3-15, putatively participating in these inactivation processes. In vitro analysis of recombinant enzyme activity and the transient over-expression of GH3 genes in N. Benthamiana leaves confirmed their ability to bind indole-3-acetic Acid (IAA) and indole-3-butyric acid (IBA) to several amino acids. Slgh3-2 and Slgh3-15 CRISPR mutant lines displayed increased free IAA levels in mature stamen, while the levels of IAA-Asp conjugate were higher in Slgh3-2. Proteomic analysis of mutant stamen tissues revealed the enrichment of the proteins, putatively involved in stress resistance. Moreover, the pollen of Slgh3-2 and Slgh3-7 plants was more viable after long-term heat stress..

STRp31

Postharvest handling induces changes in fruit DNA methylation status and is associated with alterations in fruit quality in tomato (*Solanum lycopersicum* L.)

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Abstract
Tomato is one of the most economically important crops with significant global appeal. Improving tomato fruit quality and prolonging shelf-life would reduce postharvest loss and waste, improve sustainability, and increase consumption of this healthful commodity. Many postharvest practices, specifically low-temperature storage and early harvest are sometimes used to extend tomato shelf life, but often reduce fruit quality. It has been reported that DNA methylation is important for regulating fruit ripening through gene silencing. However, the influence of postharvest handling on DNA methylation and how it relates to fruit quality is still unclear. This work aimed to clarify these issues by analyzing DNA methylation using methyl-sensitive amplification polymorphism (MSAP) and semi-quantitative transcriptional analysis of marker genes, and, assessing fruit quality biomarkers. Preliminary data shown that DNA methylation was influenced more by postharvest handling than ripening stage, however, fruit quality was influenced mainly by ripening. Ongoing work examining fruit using whole genome bisulfite sequencing (WGBS), and transcriptional analysis (RNA-Seq), aims to connect transcriptome and methylome changes due to postharvest practices. Incorporating these data is expected to broaden our finding and advance the interpretation of tomato fruit ripening regulatory mechanisms.

Session 6: BREEDING (TECHNOLOGIES AND TRAITS)

Oral presentations

- **BREop**: Rochsar *et al. 'Exotic Genetic Libraries' map resistance to Tomato Brown Rugose Fruit Virus (ToBRFV) to the Tobacco Mosaic Virus locus, TM1*.
- **BREo01**: Fenstemaker & Francis. *Using* Solanum galapagense *to achieve tolerance to water deficit through introgression breeding and grafting*.
- **BREo02**: Tikunov *et al. The genetic and functional analysis of flavor in commercial tomato: a novel FLORAL4 gene underlies a QTL for floral aroma volatiles in tomato fruit*.
- **BREo03***: Arrones *et al. Towards the development of the first eggplant MAGIC population and QTL analysis of selected morphological traits.*
- **BREo04**: Eggers *et al. The S-Locus Inhibitor gene encodes an F-box protein with a Lectin domain and crucially enables hybrid potato breeding.*
- **BREo05**: Kaiser *et al. Assessing the contribution of Sli to self-compatibility in North American diploid potato germplasm using KASP markers*.

Poster Presentations

Note: Oral presentations marked with a * will be presented also a poster. Their abstract will have a oral presentation ID (BREo).

- **BREp01**: Achakkagari *et al. Understanding potato genetic resources through plastome analyses.*
- **BREp02**: Asprelli *et al. Inheritance of Morphometric and Quality Fruit Traits, and Selection of Transgressive Segregants Derived from Crosses of Contrasting Tomato Accessions*.
- **BREp03**: Cachiarelli *et al. Transcriptome analyses of Solanum pimpinellifolium LA0722 at three ripening stages.*
- **BREp04**: Cappetta *et al. Genomic Selection for Heat Stress Tolerance in Tomato*.
- **BREp05**: Cerruti *et al. DNA methylation and transcriptomic analyses in hetero-grafted eggplants (*Solanum melongena *L.).*
- **BREp06**: Duduit *et al. Coordinated Transcriptional Regulation of the Carotenoid Biosynthesis Pathway Genes Contributes to Fruit Lycopene Content in High-Lycopene Tomato Cultigens.*
- **BREp07**: Feng *et al. Mapping Novel Tomato Fruit Weight and Volatile QTLs Using QTL-seq*.
- **BREp08**: Fortuny *et al. Heterosis and Reciprocal Effects of Agronomic Traits and Metabolites in Tomato Fruits.*
- **BREp09**: Granell representing the HARNESSTOM Consortium. *HARNESSTOM: harnessing the value of tomato genetics resources for now and the future*.
- **BREp10**: Heiden *et al. Genetic resources and pre-breeding of wild potatoes from Brazil: unlocking the treasure chest.*
- **BREp11**: Kneib *et al. Advances in screening potato germplasm for heat tolerance*.

- **BREp12**: Kyriakidou *et al. Copy Number Variation in Solanum species as a potential biomarker for potato breeding*.
- **BREp13**: Mangino *et al. Analysis of fruit shape in a collection of eggplant introgression lines with Solanum incanum as a donor*.
- **BREp14**: Martina *et al. The genetic basis of tomato aroma I : QTL regions involved in lipid VOCs accumulation.*
- **BREp15**: Martina *et al. The genetic basis of tomato aroma II : QTL regions involved in amino acid volatiles metabolism*.
- **BREp16**: Nicolao *et al. Tuber dry matter content in Solanum malmeanum accessions from Embrapa Clima Temperado Potato Genebank*.
- **BREp17**: Sapkota *et al. Identification of novel loci underlying fruit weight in tomato.*
- **BREp18**: Silvar & García-González. *Biochemical characterization of pepper (Capsicum spp.) landraces from Ecuador and analysis of relationships to fruit morphology*.
- **BREp19**: Soares et al. *CRISPR/Cas9-mediated mutagenesis of SlGRAS10: role during tomato fruit development and ripening*.
- **BREp20**: Sulli *et al. Metabolic QTLs for fruit nutritional quality in a recombinant inbred eggplant population*.
- **BREp21**: Tavares Flores *et al. De novo domestication of Solanum cheesmaniae via CRISPR/Cas9 gene editing: A proof-of-concept study to alleviate water demands of tomato cropping*.
- **BREp22**: Topcu *et al. The Molecular and Genetic Basis of Blossom End Rot in Tomato.*
- **BREp23**: Wu *et al. Genetic analysis of flavonoids regulation in pepper fruits*.
- **BREp24**: Xiao *et al. Breeding Pepper for Fruit Size and Sunscald Tolerance in Organic Environments*.
- **BREp25**: Yu *et al. Engineering high fiber-like starch potatoes through a transient Cas9 expression system.*
- **BREp26**: Zhang *et al. Mining novel fruit weight genes in semi-domesticated tomato population.*

BREop

‘Exotic Genetic Libraries’ map resistance to Tomato Brown Rugose Fruit Virus (ToBRFV) to the Tobacco Mosaic Virus locus, TM1.

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Abstract
Exotic genetic libraries constitute a strategy of dealing with the unexpected in agricultural fields such as new pathogens, the need to improve yield stability, etc. Our research is driven by the knowledge that wild tomato species contribute beneficial traits to improve tomato production. Our lab continues to develop interspecific populations; the latest library is of 2000 Back-Cross Inbred Lines (BILs_BC2S6) and is derived from a LOST Accession of S. pennellii (LA5240). This highly self-compatible inbred accession and its F1 hybrids were both resistant to a most threatening viral disease of tomato today (ToBRFV). The BILs were phenotyped for virus symptoms in apical shoot, side-shoots, fruits and by Eliza tests. This Disease data was compared to the genotypes of the BILs generated with 10,000 markers. The many recombinants in the BILs allowed us to place a major resistance locus on Chromosome 2 in a 0.5 Mb window that includes Tomato Mossaic-1 (TM1). The original TM1 was derived from S. habrochites (PI126445) and was introgressed on a ~ 1.5 MB segment that encodes an inhibitor of viral RNA replication that overlaps to both species’ introgressions. Seed of different TM1 lines from the Tomato Genetics Resource Center at Davis, had a similar level of ToBRFV resistance as the corresponding LOST-BILs. Further research indicates that TM1 alleles are not a ‘silver bullet’ that protects all tomatoes from the Tobamovirus. As always breeders need to select for the genetic backgrounds that will maximize TM1 protection in tomato varieties with yield and quality.

BREo01

Using *Solanum galapagense* to achieve tolerance to water deficit through introgression breeding and grafting.

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Abstract
The wild tomato relative *S. galapagense* accession LA1141 exhibits tolerance to water deficit. We hypothesize that this tolerance can improve cultivated tomato through breeding or grafting. The objectives of this study were 1) to determine the genetic basis of water deficit tolerance in LA1141, 2) select progeny with tolerance to deficit irrigation, and 3) measure the ability of rootstocks to reduce plant stress under water deficit. Greenhouse studies were conducted to quantify the water stress response in inbred backcross lines (IBLs) developed from the cross between accession LA1141 and OH8245. Plants were phenotyped using a wilt index, and leaf temperature, which was measured with an infrared thermometer and thermal images. IBLs were genotyped with single nucleotide polymorphisms and analyzed using composite interval mapping to reveal genetic loci associated with maximum temperature, maximum wilt, and area under temperature (AUTPC) and wilt (AUWPC) progression curves. Few major quantitative trait loci (QTL) were identified. LA1141 contributed positive alleles, but they had a marginal effect. A reproducible QTL was detected on chromosome 5 for AUWPC (LOD=3.5), explained 5% of the phenotypic variation, and decreased wilt by 8% compared to the trial average. The small effect of allele substitutions suggested that grafting may be a better method of trait delivery. When used as a rootstock, the IBL selection SG18-197 and LA1141 significantly slowed scion wilting compared to un-grafted controls. In these experiments, grafting shows more promise than introgression breeding in mitigating plant stress in arid environments.

BREo02

The genetic and functional analysis of flavor in commercial tomato: a novel FLORAL4 gene underlies a QTL for floral aroma volatiles in tomato fruit.

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Abstract
Tomato (*Solanum lycopersicum* L.) has become a popular model for genetic studies of fruit flavour in the last two decades. Here we present a study of tomato fruit flavor, including an analysis of the genetic, metabolic and sensorial variation of a representative collection of contemporary commercial greenhouse tomato cultivars, followed by a validation of the associations found by Quantitative Trait Loci (QTL) analysis of representative biparental segregating populations. This led to the identification of the major sensorial and chemical components determining the fruit flavour variation and detection of the underlying QTLs. A high representation of the QTL haplotypes in breeder's germplasm suggested a high potential applicability of these QTLs in current breeding programs aimed at improving tomato flavour. A QTL locus on chromosome 4 was found to affect the content of the phenylalanine derived volatiles (PHEV) 2-phenylethanol, phenylacetaldehyde and 1-nitro-2-phenylethane, which are all characterized floral odors. Although this locus has been reported in several different QTL studies, however, the underlying gene was never identified. Fruits of Nearly Isogenic Lines contrasting for this locus and the content of PHEV showed a significant difference in the perception of fruity and rose-hip like aroma by a trained sensory panel. The PHEV locus was fine mapped, which, along with gene expression analysis and protein annotation, allowed to identify FLORAL4 as a candidate gene for PHEV regulation. Using a gene editing based (CRISPR-CAS9) reverse genetic approach FLORAL4 was demonstrated to be the key factor in this QTL locus affecting PHEV accumulation in tomato fruit.

BREo03

Towards the development of the first eggplant MAGIC population and QTL analysis of selected morphological traits

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Abstract
Several years ago we started the development of a MAGIC population in eggplant using an 8-way funnel scheme of crossings. Parents of the MAGIC population include seven cultivated eggplant (Solanum melongena) accessions, selected for representing a wide phenotypic and genetic diversity as well as different origins, plus an accession of the cross-compatible wild relative S. incanum. After obtaining the 2-way, 4-way and 8-way hybrid generations, a single seed descend process has been followed for several generations with the aim of reaching the S5 generation. Over 400 individual plants of the S3 generation were phenotyped for several selected qualitative morphological traits and genotyped with the eggplant Single Primer Enrichment Technology (SPET) platform. A wide morphological diversity was observed in the S3 generation, with new recombinant phenotypes. Over 6,500 SPET markers were polymorphic and association analysis was performed to identify potential causative SNPs for the traits assessed. The GWAS analysis allowed the detection of clear associations for most of the traits. In addition, for almost all traits, such as anthocyanin pigmentation, presence of prickles, flower colour and fruit shape, associations co-localized with previously described QTLs in other populations of eggplant or of other Solanaceae, while others pointed at new genomic regions. The results obtained reveal that this first MAGIC population of eggplant, once finished, will be a powerful tool for the dissection of traits of interest in eggplant and for the selection of élite recombinant material.

BREo04

The S-Locus Inhibitor gene encodes an F-box protein with a Lectin domain and crucially enables hybrid potato breeding

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Abstract
In recent years, several groups have been working on converting potato to a diploid inbred-line based hybrid crop. However, most diploid potato have an active S-RNase based self-incompatibility system that prevents inbreeding. One way to generate self-compatible diploid potato is by crossing with an Sli gene donor line. The Sli gene is a dominant gene that inhibits the self-incompatibility system in potato. To improve the breeding process, we set out to clone the Sli gene. First, we mapped the Sli gene to an 628 kb interval on the distal end of chromosome 12 in a segregating F1 population. We then used a recombinant screening approach to reduce this interval to 12.6 kb. One of the two candidate genes present in this interval, PGSC0003DMG400016861, encoding an F-box protein PP2-B10, contains variation that is exclusively present in self-compatible haplotypes and is highly expressed in pollen from self-compatible genotypes. We designed an expression vector containing the SC allele of PGSC0003DMG400016861 under control of its native promoter and terminator and used this vector to transform self-incompatible diploid potato genotypes. The resulting transgenic lines are highly self-compatible, proving that PGSC0003DMG400016861 is the Sli gene. These results enable more efficient generation of potato inbred lines and will improve our understanding of S-RNase based self-incompatibility systems..

BREo05

Assessing the contribution of Sli to self-compatibility in North American diploid potato germplasm using KASP markers

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Abstract
Diploid hybrid potato variety development requires the introduction of reliably transmitted self-compatibility (SC) to largely self-incompatible (SI) elite diploid germplasm. The diploid Solanum chacoense line M6 has been widely used to introgress SC into North American potato diploid breeding programs. We determined that M6 is homozygous for six DNA Kompetitive Allele Specific PCR (KASP)TM markers spanning a 224kb region, linked to Sli in Dutch germplasm. The SC S. tuberosum lines US-W4 and RH were found to be heterozygous at these six marker loci. We appraised the transmission of Sli in a diploid recurrent selection and a diploid backcross population, each designed to introgress S. chacoense-mediated SC while improving agronomic traits. The frequency of the homozygous M6 genotype at the six marker loci increased nearly to fixation over the course of five cycles of recurrent selection and the M6 genotype at these loci was significantly associated with proportion of fruit set upon selfing. Self-compatibility was transmitted at a low frequency in the backcross population, where a diverse panel of S. tuberosum dihaploids were used as recurrent parents, and the M6 Sli allele was largely maintained in the heterozygous condition at the six marker loci. We delimited a 80.8kb region on chromosome 12 (58,960,090-59,040,898bp) associated with SC in the recurrent selection population and found that a marker located at 58,962,561bp on chromosome 12 was the best predictor of SC. The presence of the homozygous haplotype alternate to M6 in SC lines 1S1 and DRH-89 suggest another genetic component underlaying SC.

BREp01

Understanding potato genetic resources through plastome analyses

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Abstract
Plastid phylogeny along with nuclear phylogeny is proven useful in studying hybridization and introgression in potato. In addition, different potato plastome types have been demonstrated to affect agronomic traits. This study reveals that while a panel of thirteen assembled and annotated potato plastomes from different potato taxa are highly similar in gene order and content, a great number of SNPs and InDels exist between them. Five different potato plastomes types (C, S, A, W, W2) were identified in the thirteen plastomes. It is interesting to observe that the two accessions of *S. tuberosum* ssp. andigena, ADG1 and ADG2, have different plastome types as do two accessions of *S. bukasovii* (BUK1 and BUK2). A conserved 48 bp deletion is observed only in the S-type plastome, which can be used as a marker for identifying S-type plastomes. The phylogenetic analysis shows that they cluster according to their plastome types. Comparing plastome phylogeny with the nuclear phylogeny of the panel reveals some congruency, with considerable differences, suggesting introgression and hybridization between potato species. The *S. bukasovii* (BUK1, but not BUK2), a wild potato species, and *S. curtilobum* (CUR) grouped with the diploid landraces. This was not observed in the nuclear phylogeny, and marks the importance of plastome analyses for a more complete understanding of potato genetic resources.

References
Achakkagari et al., 2020 Complete plastome assemblies from a panel of 13 divers potato taxa PLoS ONE 15(10): e0240124.

BREp02

Inheritance of Morphometric and Quality Fruit Traits, and Selection of Transgressive Segregants Derived from Crosses of Contrasting Tomato Accessions.

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Abstract
Two half-sibs were developed crossing tomato accessions of contrasting fruit colour, size and shape, from La Consulta INTA Germplasm Bank, Mendoza, Argentina. Parentals, F1 and F2 generations were evaluated through 13 morphometrical and quality fruit traits, and 18 carotenoid and chlorophyll pigments content. Segregant frequencies for pericarp colour suggest three genes with complementation and epistatic effects. Red fruits shows higher licopene and carotenes contents, and chlorophylls and pheophytins for brown fruits. Allele contributions and dominance ratios shows partial, complete and overdominance effects for different traits, and also differential correlations between them. A total of 77 transgressive F2 individuals were selected for its fruit attributes, and families were derived by selffing until F5 under a genealogical selection scheme focussed on round fruits, thick pericarp and high soluble solids content. F5 individuals were pooled by their fruit colour in red, pink, orange, dark and light yellow, brown, purple, and green groups. Fruit selection was stabilized at around 25 g weight, height-width ratio of 1.0, soluble solids rise up from 5.6-6.5 ºBrix in F1 to 8.8 ºBrix in F5, and pericarp width increased up to 27%. Broad sense heritability values of F5 colour-groups rise down with respect to F2 for size, shape and color. Each F5 colour-group shows different patterns of heritability reduction, retaining considerable variability for pigments, soluble solids content and pericarp thickness. A better understanding of the genetic components of tomato fruit attributes, and associations between agronomic traits and quality, allowed selecting individuals of outstanding characteristics for differential and gourmet markets..

BREp03

Transcriptome analyses of *Solanum pimpinellifolium* LA0722 at three ripening stages

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Abstract
In a previous report, transcriptome of *S. pimpinellifolium* LA0722 was aligned as *S. lycopersicum* cv. Heinz 1706 as a reference. In this report, we have realigned LA0722 transcriptome using as a reference the S, pimpinellifolium LA4791 genome, recently available to the scientific community. The objective was to compare results of both transcriptome analyses, one made on a same species reference genome and the other, on a related species genome. In both cases, the green mature transcriptome was used to normalize the data. Differences in the number of over-expressed genes and under-expressed genes were detected when comparing both analyses, the smallest values corresponding to alignment of LA0722 transcriptome against the same species LA4701 genome (7024 and 6676 differentially expressed genes in LA0722 between breaker and green mature stages and between red ripe and green matures stages, respectively, vs. 7313 and 6929 in the same conditions when using cv. Heinz 1706 as the reference genome). Our results pointed out the importance of using an appropriate reference for alignment of new transcriptomes.

BREp04

Genomic Selection for Heat Stress Tolerance in Tomato

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Abstract
Tomato crop production is seriously limited by extreme high temperatures during summer time. Developing tomato genotypes tolerant to high temperature may be a valuable strategy to cope with climate changes. However, heat stress tolerance (HT) it a very complex trait to dissect. In this work, a tomato genome selection (GS) model was build up to increase the rate of genetic gain for yield under heat stress conditions. To reach our goal, a F4 segregating population, deriving from a tomato variety, previously selected for yield performance under heat stress, has been characterized for nine phenotypic traits (e.g. yield, fruit number, SSC). A PCA analysis based on phenotyping scoring allowed us to select the best and worst performers. One-hundred F4 individual have been genotyped by sequencing (GBS) to build up a prediction model. Several statistical methodologies were tested to predict the breeding value (GEBV) of candidates for the next round of selection. A robust and accurate rrBLUP regression method was developed and adopted for further analysis. After fitting the prediction model in a training population, we measured its accuracy using a test sample for which the phenotype was available. For complex trait such yield (controlled by many genes with small effect) we found a correspondence between predicted and real values up to 70 %. The model has been also applied on genotypic data of F5 individuals and validated on F6 phenotyped lines. A new breeding paradigm for optimizing tomato improvement procedures is beginning to emerge.

BREp05

DNA methylation and transcriptomic analyses in hetero-grafted eggplants (*Solanum melongena* L.).

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Abstract
Grafting is a vegetative propagation method widely applied in horticulture to join the top part of a plant (scion) onto the base of the stem and roots of another plant (rootstock), in order to combine positive traits from the two different plants. However, the molecular mechanisms implicated in the rootstock-scion interaction remains largely unknown.
Epigenetic mechanisms play a relevant role in plant distance signalling, thus we studied the genome-wide changes induced by DNA methylation in eggplant (*Solanum melongena*), one of the most commonly grafted Solanaceous crops. Plants of an eggplant double haploid line (DH) derived from the commercial hybrid 'Ecavi' were hetero-grafted onto two commercial rootstocks: (i) *Solanum torvum*, which provides resistance to bacterial, Fusarium and Verticillium wilts and to root-knot nematodes, and (ii) 'Emperador RZ', a tomato hybrid resistant to Verticillium. Self-grafted 'Ecavi' plants were used as control.
Hetero-grafted plants showed a significant increase in vigour compared to the self-grafted plants. We generated the first eggplant methylome (coverage 10X), which displayed 90% methylation in CG, 83% in CHG and 16% in CHH contexts, and found out that their vigour was associated with a genome-wide hypomethylation in CHH context. Following RNA-seq analyses, we also investigated the effect of DNA methylation on transcriptional activity of genes and transposable elements (TEs) in hetero-grafted and self-grafted plants. A down-regulation of younger and potentially more active LTR retrotransposons (LTR-TEs) correlated with CHH hypomethylation, suggesting that graft-induced epigenetic modifications are associated with both physiological and molecular phenotypes in grafted plants.

BREp06

Coordinated Transcriptional Regulation of the Carotenoid Biosynthesis Pathway Genes Contributes to Fruit Lycopene Content in High-Lycopene Tomato Cultigens

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Abstract
Lycopene content in tomato fruit is largely under genetic control and varies greatly among genotypes. Little is known about the molecular mechanisms regulating fruit lycopene content in high-lycopene tomatoes. In the present study, 42 potential high-lycopene tomato cultigens with different genetic backgrounds were collected worldwide. High performance liquid chromatography (HPLC) analysis was used to quantify fruit carotenoid (lycopene, phytofluene, prolycopene, and beta-carotene) contents at four fruit developmental stages (i.e., breaker, orange, pink, and ripe) of each cultigen. Real-time RT-PCR was used to quantify the relative expression levels of all the 25 pathway genes individually at the breaker and ripe stages. In these cultigens, we found i) a general trend of strong expression of upstream genes prior to lycopene biosynthesis and weak expression of most downstream genes at both stages; ii) significant higher expression in 7 upstream genes at the breaker or both stages than in the negative control Moneymaker, resulting in significantly higher fruit lycopene content; and iii) significant higher expression in 8 downstream genes at the breaker or both stages than in the positive control the wild tomato, leading to significantly lower fruit lycopene content . This was the first systematic investigation of the role of the complete carotenoid biosynthesis pathway genes in fruit lycopene content across many high-lycopene cultigens, which will enable tomato breeding and gene editing for improved fruit lycopene content..

BREp07

Mapping Novel Tomato Fruit Weight and Volatile QTLs Using QTL-seq

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Abstract

Fruit weight has been one of the most agronomically important traits in tomatoes (*Solanum lycopersicum*). Volatiles, on the other hand, is an emerging trait of interest that substantially affects tomato flavor and consumer preference. The highly quantitative nature of fruit weight and the complex volatile networks make the genetic characterization of these traits challenging for plant breeders. Bulk segregant analysis (BSA) coupled with next-generation sequencing technology has become a powerful tool for quick identification of quantitative trait locus (QTL). The goal of this study is to utilize this QTL-seq method and to discover novel fruit weight and volatile QTLs by mining the allele diversity from our germplasm collection. Several F2 populations were created by crossing plants among wild, semi-domesticated and domesticated tomatoes. Current F2 bulks pooled from the phenotypic extremes for fruit weight, locule number (indirectly affect fruit weight and size) and volatiles (isovaleronitrile, 3-pentanone and benzaldehyde) can reveal QTL candidate regions after sequencing. Progeny testing and fine mapping with future selfing generations will allow us to narrow the locus to a selection of gene candidates. Gene editing tools such as CRISPR/Cas system will help us validate the causal factor. Similar pipeline will be applied to more F2 populations with segregating fruit weight and volatile profiles. Overall, this study can provide us more insights into the genetics behind tomato fruit traits and facilitate tomato breeding.

BREp08

Heterosis and Reciprocal Effects of Agronomic Traits and Metabolites in Tomato Fruits.

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Abstract
The hybrids in tomato (*Solanum lycopersicum* L.) are mostly cultivated due to their disease resistance, productivity, and fruit quality. The existence of heterosis has been studied in tomato for many years. However, the influence of the parental order in the cross over the hybrid's performance, i.e. the reciprocal effect, has not been explored. This work aimed to detect heterosis and reciprocal effects in agronomic traits and metabolites. The plant material included 20 hybrids obtained by crossing two American heirlooms: Purple Pear and Green Zebra, and three RILs obtained from the Tomato Breeding Program at Facultad de Cs. Agrarias, UNR: Querubín, Gema, and ToUNR17 following a full diallelic mating design. We measured 12 agronomic traits and 28 metabolites. A PCA analysis, including the means of all traits and genotypes, showed that the hybrid's performance was enlarged compared to the phenotypic variation of parental genotypes. Heterosis and reciprocal effect were confirmed for each cross and trait using ANOVA. There was heterosis when the hybrid had a better performance than the best parental genotype ($P<0.05$). The reciprocal effect occurred when, changing the parental order in the cross, the reciprocal hybrids were phenotypically different ($P<0.05$). We detected 12.4% of heterosis and 21% of reciprocal effect for all possible cases. Both phenomena were more frequent in metabolites. These findings highlight how important is the male and female parental genotype election in a hybrid cross. The possibility of exploiting heterosis, mainly for metabolites, in the generation of new hybrids is a remarkable result as well..

BREp09

HARNESSTOM: harnessing the value of tomato genetics resources for now and the future

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Abstract
Tomato is a paradigmatic case of crop domestication: a widely cultivated and consumed vegetable but with reduced genetic diversity and therefore highly vulnerable to emerging diseases and climate change. Fortunately tomato is rich in genetic resources and information to overcome those difficulties, and a coalition of those scientists and breeding experts who have generated a large amount of this information has been organized under an effective management structure of HARNESSTOM to overcome those threats. By capitalizing on the large effort done recently in several EU-funded projects to connecting phenotypes/genotypes in a large number of accessions from different germplasm banks and academia HARNESSTOM will first collect, centralize and normalize this wealth of information in a way that is easily searchable and displayed in a user-friendly manner adapted to different type of users. Second, HARNESSTOM will develop four pre-breeding programs addressing the major challenges of the field: 1) introducing DRG against the major emerging diseases, 2) improving tomato tolerance to climate change, 3) improving quality, and 4) increasing resilience in traditional European tomato by participatory breeding. An additional goal is to increase speed and efficiency in pre-breeding, which is needed to be able to respond to the emerging challenges in a timely and effective manner. Joint leadership of both academia and industry in each of the work packages and the participation of two NGOs representing different stakeholders guarantees the results of the project will have an impact in industry and society innovation.

BREp10

Genetic resources and pre-breeding of wild potatoes from Brazil: unlocking the treasure chest

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Abstract
When people think about potato and its wild relatives (*Solanum* sect. Petota), Brazil is certainly not the first place which comes to mind. Most cultivated and wild potatoes available worldwide in genebanks have their roots in Andean highland tropical or temperate adjacent lowland areas. The Brazilian biota has a distinct evolutionary and biogeographic history and lies under diverse environmental conditions in eastern and central South America. Thus, the Brazilian germplasm is a distinct set of genetic resources to search for novel traits in potato breeding to face a constantly changing and challenging world. The potato breeding program at Embrapa Clima Temperado started in 1946. Since 1986, wild potatoes were sampled and are currently deposited in the Herbarium ECT and the Potato Genebank. These facilities are the most representative collections of exsiccates and accessions of wild potatoes from Brazil, representing around three hundred records of *S. chacoense*, *S. commersonii*, and *S. malmeanum*. Accessions are continuously documented, characterized morphologically and genetically, evaluated agronomically, and phenotyped under stress conditions. Currently, six registered cultivars developed by Embrapa have at least one wild progenitor in their genealogies. Despite the efforts, we still believe our germplasm is a neglected treasure chest. To unlock the vast potential of Brazilian wild potatoes, we are increasing our efforts and collaborations within Brazil and neighbouring countries to boost sampling, characterization, and evaluation under stress conditions. The most promising genotypes are being evaluated for crossability and introgression to move them into pre-breeding initiatives and enhance their future incorporation into breeding pipelines.

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BREp11

Advances in screening potato germplasm for heat tolerance

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Abstract
Heat stress is considered the main uncontrollable factor affecting potato yield. This study was conducted aiming to evaluate the response of potato genotypes to high temperature. The potato genotypes were cultivated in growth chambers, in a 12-hour photoperiod, under two temperature conditions: control (14-27°C) and supra-optimal temperature (24-34°C). Initially, a study of the effect of supra-optimal temperature was carried out in the early stages of tuberization. Later, physiological and morpho-agronomic analyses were used to carry out non-invasive selection of potato genotypes tolerant to exposure to supra-optimal temperatures. Finally, 18 potato genotypes were characterized for heat tolerance based on these physiological and morpho-agronomic characters. As a result, it was observed that temperature did not influence induction to the tuber initiation phase. However, it prolonged the period of plant emergence, reduced the number of plants that reached the emergence stage, as well as reduced yield and quality of the tubers. Changes in the parameters of gas exchange and chlorophyll fluorescence allowed to distinguish genotypes with different levels of heat tolerance. In this way, a methodology for a fast and non-destructive selection of heat tolerant potato germplasm was established. The supra-optimal temperature caused changes in morpho-agronomic and physiological traits. The genotypes with the best responses in the supra-optimal condition were the same ones identified as superior in the control condition. The results obtained in this work will contribute to the definition of future studies to develop a potato germplasm more tolerant to the adverse effects of global warming.

BREp12

Copy Number Variation in *Solanum* species as a potential biomarker for potato breeding.

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Abstract
While complete polyploid plant genome assembly is still a challenge (Kyriakidou et al., 2018; Kyriakidou, Anglin, et al., 2020), much can be learned from copy number variants (CNVs) in genome data. CNVs are believed to be the reason for many complex phenotypic variations in plants. In this project, the genomes of six diploid (*S. stenotomum subsp. stenotomum, S. phureja, S. xajanhuiri, S. bukasovii, S. stenotomum subsp. goniocalyx*), two triploid (*S. juzepczukii, S. chauca*), three tetraploid (*S. tuberosum subsp. andigena; S. tuberosum subsp. tuberosum*) and a pentaploid (*S. curtilobum*) potato landraces were sequenced, and together with two wild, diploid, publicly available genomes (*S. commersonii* and *S. chacoense*) were used to explore structural variation compared to two potato reference genomes; the cultivated DM1-3 and the wild *S. chacoense* M6. The results shows CNV clusters containing genes involved in metabolic processes, disease resistance and stress tolerance that can be used as potential biomarkers for potato breeding in order to overcome the susceptibility of the modern European cultivars to biotic and abiotic stresses (Kyriakidou et al., 2020b).

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BREp13

Analysis of fruit shape in a collection of eggplant introgression lines with *Solanum incanum* as a donor

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Abstract
Eggplant fruit shape is an important quantitative agronomic and economic trait and using suitable mapping population like a set of introgression lines (ILs) could contribute to elucidate its complex genetic. To achieve this challenging objective, a set of 16 eggplant ILs, each harboring a single marker-defined chromosomal segment from the wild eggplant relative S. incanum in the genetic background of S. melongena, was assessed for fruit shape in two environments (open field and screenhouse). Fruits of the two parents, their interspecific hybrid and ILs were phenotyped using the phenomics tool Tomato Analyzer. Many morphological differences were found among parents and the hybrid for many fruit shape traits. Significant differences were also found between ILs and the recipient parent, suggesting the existence of a relevant effect of the introgressions, even in presence of small wild donor fragments. A total of 41 stable QTLs spread over ten chromosomes were detected. Of these, twenty QTLs co-localized with other previously reported in intraspecific and interspecific eggplant populations, while twenty-one QTLs, including Blockiness, Homogeneity, Asymmetry and Internal Eccentricity traits, were novel. In addition, variations associated to genes belonging to SUN, OVATE and YABBY families described in tomato were reported in the ILs potentially underlying genes for the QTLs identified. Eleven SUN and YABBY genes were proposed as potential candidate controlling fruit shape variations in eggplant. Our results provide novel and highly relevant insights on the genetic of fruit shape in eggplant.

BREp14

The genetic basis of tomato aroma I : QTL regions involved in lipid VOCs accumulation

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Abstract
Tomato aroma is determined by the interaction of volatile compounds (VOCs) released by the fruit with nose receptors. These compounds are both derived from primary metabolites (fatty acids and branched-chain amino acids) and secondary metabolites (phenylalanine-derived compounds and carotenoids). Aim of our researches is to collect, compare, integrate and summarize the available literature, selecting 17 scientific papers and supplemental data focused on QTLs associated with tomato aroma. Here we report our finding regarding fatty acids-derived compounds.

BREp15

The genetic basis of tomato aroma II : QTL regions involved in amino acid volatiles metabolism

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Abstract
Tomato aroma is determined by the interaction of volatile compounds (VOCs) released by the fruit with nose receptors. These compounds are both derived from primary metabolites (fatty acids and branched-chain amino acids) and secondary metabolites (phenylalanine-derived compounds and carotenoids). Aim of our researches is to collect, compare, integrate and summarize the available literature, selecting 16 scientific papers and supplemental data focused on QTLs associated with tomato aroma. Here we report our finding regarding amino acids-derived compounds

Two classes of amino acids-derived compounds can be identified, according to their origin: i) BCAA VOCs; ii) phenylalanine-derived VOCs. BCAAs derived compounds are highly volatile compounds with a low molecular weight, some of which are considered important in the development of tomato aroma. Data collection identified a total of 129 QTLs over 29 QTLs Genomic Regions (QGRs), defined by different authors. 112 QTLS were within a 5Mb window and were merged into 16 QGRs. The impact of phenylalanine-derived VOCs on tomato flavor appears not so easy to predict, since some studies show positive while others show negative effects of these compounds on consumer perception. Data collection identified a total of 81 QTLs over 35 QTLs Genomic Regions (QGRs), defined by different authors. 46 QTLS were within a 5Mb window and are merged into 11 QGRs.

Our findings provide a tool that can make it possible to (i) select donors for specific traits, (ii) narrow down QTL regions by combining information from different populations, and (iii) pinpoint potential candidate genes.

BREp16

Tuber dry matter content in *Solanum malmeanum* accessions from Embrapa Clima Temperado Potato Genebank

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Abstract
Solanum malmeanum is a wild potato from Argentina, Brazil, Paraguay, and Uruguay. Crop wild relatives are unique reservoirs of potential traits for plant breeding. High tuber dry matter content (TDMC) confers better culinary quality, longer storage and shelf life, being an index of commercial tuber quality for potato breeders. The objective of this study was to evaluate TDMC of 11 S. malmeanum accessions (BGB015, BGB017, BGB021, BGB080, BGB081, BGB084, BGB443, BGB446, BGB447, BGB448, BGB471) compared to two clones of S. tuberosum (BRSANA, C1750-15-95) from the Embrapa Clima Temperado Potato Genebank, Pelotas, Brazil. Plants were cultivated at greenhouse in Spring 2020. Tubers were oven dried until reach constant weight at a temperature of 60ºC. TDMC [%TDMC = (dry weight/fresh weight) X 100] was calculated and the means of triplicate samples were analyzed in RStudio (v. 1.3.1093) and grouped in clusters using Scott-Knott multiple comparison ($p<0.05$). TDMC ranged from 21.36% to 51.74% (CV = 14.99%) and accessions were arranged in three groups. Group A comprised S. malmeanum accessions with higher TDMC: BGB021 (51.74%), BGB017 (50.48%) and BGB015 (45.45%). Group B comprised S. malmeanum accessions with lower TDMC: BGB471 (42.46%), BGB446 (40.45%), BGB443 (40.33%), BGB080 (38%), BGB084 (37.9%), BGB447 (37.46%), BGB448 (36.91%) and BGB081 (33.93%). Group C comprised the two clones of S. tuberosum, C1750-15-95 (23.20%) and BRSANA (21.36%) which bear standard TDMC for potato cultivars. S. malmeanum accessions contains much higher TDMC than minimum recommended levels (>20%) and are promising sources for this trait for potato breeding.

BREp17

Identification of novel loci underlying fruit weight in tomato

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Abstract
Tomato fruit weight is a quantitative trait resulting from selections that are governed by multiple loci or QTL. Few QTLs have been cloned and confirmed in addition to other candidate loci that have been mapped. Among the cloned QTL are fw2.2, fw3.2 and fw11.3 underlying CNR, SlKLUH and CSR respectively. To identify new QTL controlling fruit weight, an F2 population developed from a cross between PI406890 with smaller fruit and BGV008041 with larger fruit was evaluated. Both accessions are fixed for known fruit weight alleles. The QTL-seq BSA approach was applied to map the loci associated with fruit weight. We identified two QTLs affecting fruit weight on the bottom of chromosomes 3 and 8. The fw3.3 QTL was confirmed in an F3 population through progeny testing of 8 F2 families to a region of 3.7Mb. This QTL was further mapped using a population of 157 recombinant plants and Inclusive Composite Interval Mapping to 1.7Mb. An additional 270 recombinants plants led to the fine mapping of the locus to a 614.5 kb region. Similarly, 145 recombinant plants confirmed the fw8.1 QTL to a 4.2 Mb region. We aim to further fine map the loci on ch3 and ch8 to a few candidate genes and investigate the effect of these genes on fruit weight in tomato.

Funding
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BREp18

Biochemical characterization of pepper (*Capsicum spp*.) landraces from Ecuador and analysis of relationships to fruit morphology.

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Abstract
The impact of fruit morphology on pepper composition for health-promoting compounds was investigated. For that purpose, a collection of pepper (*Capsicum* spp.) accessions from Ecuador, one of the hotspots in Capsicum's origin, was analyzed for ascorbic acid, polyphenols, capsaicinoids, and prevention of cholesterol oxidation. Plant and fruit phenomics were assessed with conventional descriptors and the Tomato Analyzer digital tool. Significant differences among accessions and species revealed a large diversity within the collection. The conventional descriptors related to the magnitude of plants and fruits, as well as digital attributes under the categories of size, shape index, and latitudinal section, mostly explained the variance among *Capsicum* groups. On the other hand, *C. frutescens* displayed the highest levels of capsaicinoids, whereas the polyphenols shortly varied among the five domesticated species. C. pubescens exhibited the lowest content of ascorbic acid. Correlation test revealed that phytochemical components were negatively correlated with the morphometric fruit attributes, suggesting that huge fruits contained lower amounts of nutraceutical compounds. Multivariate analysis showed that parameters related to fruit size, shape, and nutraceutical composition primarily contribute to the arrangement of pepper accessions, suggesting that those traits have been subjected to higher selection pressures imposed by humans.

BREp19

CRISPR/Cas9-mediated mutagenesis of *SlGRAS*10: role during tomato fruit development and ripening

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Abstract

The GRAS genes are plant-specific transcriptional factors that play critical roles in processes of plant growth and development. However, their role in fruit ripening is not fully understood. Recent genome-wide analysis of the GRAS family showed that several genes were differentially expressed during fruit development, ripening, or biotic and abiotic stress conditions. Gene expression data of tomato (Solanum lycopersicum) suggested that the gene *SlGRAS*10 might be involved in fruit ripening.

In this study, constructs using CRISPR/Cas9 technology were generated for tomato targeted mutations. Plants were transformed and T_1 progeny was obtained. All T_1 plants were screened for the absence (due to genetic segregation) of both Cas9 and NptII (kanamycin resistance) transgenes and 33% of the plants were T-DNA free. Sequence analysis revealed different mutant alleles, from 1 bp deletions to 5 bp deletions or 1 bp insertion. Moreover, no off-targets was detected in the transformed plants.

Ripening processes did not seem to be influenced by the mutation of *SlGRAS*10; however, seeds´ number was affected in some mutated lines. Expression of the gene is increased during flower anthesis in the wild type and the knockout of this gene may be interfering with flower fertilization and seed formation. However, further analysis is necessary to elucidate the role of the *SlGRAS*10 in these processes. For that, T_2 of the lines with a reduced number of seeds are being generated and seed number and fruit development parameters will be evaluated.

BREp20

Metabolic QTLs for fruit nutritional quality in a recombinant inbred eggplant population

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Abstract
With a global production of ~50 Mt, eggplant (*Solanum melongena* L.) represents the third most important crop of the Solanaceae family after potato and tomato, and is an important component of our daily diet. A population of 164 F6 Recombinant Inbred Lines (RILs), derived from two eggplant lines differing with respect to several key agronomic traits, '305E40' and '67/3', was grown to the commercial maturation stage. The fruits were harvested, separated into peel and flesh, and subjected to untargeted LC-MS analysis. A number of metabolites belonging to the glycoalkaloid, anthocyanin and polyamine classes, showed a differential accumulation in the two parental lines and F1 hybrid. Following the metabolic profiling of the RILs and by using a recently developed high-resolution map constituted of 7,249 SNPs, we identified several metabolomic quantitative trait loci (mQTLs) associated to the accumulation of metabolites. Each of the metabolic traits proved to be controlled from one to three QTLs, and for most of the traits one major mQTL (PVE≥10%) was spotted. Data on mQTL mappig and sequence analysis as well as dominance-recessivity relationships of measured compounds in the parental lines and F1 hybrid suggest the possible molecular nature of the mutations underlying the mQTLs..

BREp21

De novo domestication of *Solanum cheesmaniae* via CRISPR/Cas9 gene editing: A proof-of-concept study to alleviate water demands of tomato cropping

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Abstract
Agriculture is the economic sector that utilizes most of the freshwater resources available globally. Salinization of arable lands is a major concern due to the increasing limitations of water supply and the substantial use of continuous irrigation systems worldwide. Salinity stress has a significant impact on crop development and yield, which limits cultivation in marginal lands and agricultural use of saline water. A glycophyte crop, such as the cultivated tomato (*Solanum lycopersicum*), requires high amounts of water while being highly sensitive to soil salinity. Introgression of salinity resistance into tomato cultivars via conventional breeding remains challenging due to the highly polygenic nature behind abiotic traits. We aimed to domesticate tomato de novo as a high-salinity resistant crop by harnessing the feature of its wild relative, *S. cheesmaniae*. Based on published data, the accession LA0421 was chosen as the genetic baseline for editing genes involved in domestication traits (plant architecture, flowering, yield, fruit size, and nutritional value) due to its lower yield penalty when exposed to saline conditions. We are using a multiplex CRISPR/Cas9 strategy to produce mutated alleles for the domestication-related genes BIF, cycB, J2, EJ2, MULTI, SP, SP5G, and FW11.3 in order to create a novel, halophyte tomato harboring an inherent high-salinity resistance along with desirable cultivation traits. This proof-of-concept research aims to engineer crops using a speedy reverse breeding approach that could potentially use (at least partially) seawater hydroponics or saline soils for food production.

BREp22

The Molecular and Genetic Basis of Blossom End Rot in Tomato

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Abstract
Blossom end rot (BER) is one of the most devastating physiological disorders in tomato and other vegetables resulting in significant crop losses as high as 70%. Due to changes in weather patterns of excessive rain alternating with prolonged droughts, the disorder is becoming more widespread. To decipher the genetic basis of BER, an F2 population derived from a cross between BER-resistant accession BGV007900 and BER-susceptible accession BGV007936 as well as a BC1F1 population using BGV007936 as a recurrent parent were evaluated. The QTL-seq approach was employed to map the loci associated with BER. We identified two QTLs for BER at the bottom of chromosomes 3 and 11. Association of identified QTL(s) with the trait was confirmed in 17S28 F2 and 18S243 BC1F1 populations using KASP markers. Confirmation and further fine-mapping were done using progeny tests of selected F2 recombinant plants and F3:4 plants. QTL interval on ch03 was narrowed down from 11.2 Mbp to 1.28 Mbp at 95% confidence intervals. Moreover, QTL interval on ch11 was narrowed down from 1.98 Mbp to 792 kbp at 95% confidence intervals. To further fine-map the QTL on ch11, 192 recombinant plants will be selected by screening 1728 F4:5. Similarly, 4032 F5:6 seedlings will be screened to select 192 recombinants for fine-mapping on ch03. Ultimately, BER loci on ch03 and ch11 will be further fine-mapped and subsequent expression analysis will be implemented to identify genes that will hopefully yield molecular and developmental insights into the causes of BER.

Funding
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BREp23

Genetic analysis of flavonoids regulation in pepper fruits

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Abstract
Pepper is a good source of health-related metabolites such as flavonoids. A segregating F2 population was derived from a cross between high level flavonoids *C.annuum* Long Sweet and *C.annuum* AC2212 with low flavonoids level. QTL analysis of F2 population helped to identify a candidate gene, CaMYB12-like with high homology with SlMYB12 known to regulate flavonoids in tomatoes. To characterize the function of CaMYB12-like gene, virus-induced gene silencing of CaMYB12-like gene resulted in a significant decrease in the accumulation of flavonols, flavones and chalcones achieving by regulating flavonoids structural genes. Besides, CaMYB12-like-overexpressing transgenic tomato plants were generated and significant increases in flavonols and chalcones were identified. Our results suggests the CaMYB12-like transcription factor plays an essential role in flavonoids biosynthesis in pepper fruits.

BREp24

Breeding Pepper for Fruit Size and Sunscald Tolerance in Organic Environments

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Abstract
As part of the UC Davis Student Collaborative Organic Plant Breeding Education (SCOPE) project, a student-led pepper breeding program specific for California organic growth environments has been conducted since 2016. Graduate and undergraduate students are trained to develop goals, select parents, evaluate and select progeny to varietal release. Thus far 6 graduate and 15 undergraduate students have been trained. After consultation with the organic industry, the following breeding goals were developed: 1) enlarged cavity (Jalapeño Popper) for jalapeño pepper, and 2) sunscald tolerance for bell pepper. Collaborating with local organic growers, open pollinated/inbred selection was done in organic environments through multiple years across different locations. A few elite lines show better performance than controls on targeted traits and yield. A significant correlation between sunscald and marketable yield is observed. In addition to field selection, outreach activities (field day, taste test, chef interview, etc.) also provide meaningful information. The results of the program will be presented.

BREp25

Engineering high fiber-like starch potatoes through a transient Cas9 expression system.

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Abstract
Starch is the major component of potato tubers, providing calories for 1B people worldwide. However, potato starch has a high glycemic index, which is problematic for diabetics. Further, during cold-storage, potato starch is degraded to sugars, and when they are fried or baked, acrylamide is produced. Making potato starch more resistant to digestion may provide a solution to these problems. Starch branching enzymes (SBEs) catalyze the branch structure of starch, and high branch frequency enhances starch digestibility. This project aims to use CRISPR/Cas9 gene editing to reduce SBE activity, thus creating starch that is resistant to digestion in two US commercial cultivars. Edited lines that are 'transgene-free' and have high resistant starch will be selected by developing efficient screening tools. Constructs with Cas9 and multiple sgRNAs targeting the functional domains of the SBEs were delivered into potato stems using Agrobacterium-mediated transformation and optimized regeneration protocols. First, red-fluorescent protein (DsRed) was used as a visual marker to select regenerants that only transiently expressed the constructs, and were thus 'transgene-free'. Second, iodine-staining of DsRed-negative lines was used to visually select plantlets with an altered starch phenotype. PCR-amplified DNA from the prescreened plantlets were sequenced, and the nature of the Cas9-induced allelic variants were determined. Our initial results suggest that (1) the double-screening method used is robust, and may have broader applications for gene-editing of other starch-related traits, and (2) allelic variants of SBEs were identified that have altered starch. Precise assessments of starch composition and tuber postharvest traits will be performed.

BREp26

Mining novel fruit weight genes in semi-domesticated tomato population

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Abstract
During tomato domestication, the fruit size increased from the blueberry-sized wild tomato (SP) to cherry-sized semi-domesticated tomato (SLC) which gave rise to the large modern cultivated tomato (SLL). To date, only five fruit weight genes have been identified and the alleles leading to higher fruit weight were identified in modern tomatoes. We focus on the germplasm of SP and SLC for novel fruit weight gene discoveries and potential crop improvement.
Two SLC accessions (BGV006768 and BGV007931) carry wild-type alleles of all the known fruit weight genes; yet their fruit weight differs 10-fold. We aim to identify the genetic causes of such fruit weight difference using F2 population developed from these accessions. A major fruit weight QTL (fw2.3) at the bottom of chromosome 2 was identified by bulk-segregant analysis and fine-mapped to an interval of about 100 kb near the known fruit weight gene FW2.2. Phylogeny based on SNP information at fw2.3 interval among 167 diverse tomato accessions suggests fw2.3 is not present in modern tomatoes, because the fw2.3 alleles in both BGV006768 and BGV007931 are distinct from the cultivated allele of FW2.2. Differential expression of two candidate genes between F3 progenies carrying contrasting fw2.3 genotypes narrowed down the search for candidate genes further. In addition, the fruit weight data from multiple bi-parental F2 populations derived from SLC x SLC or SLC x SP crosses were utilized to narrow down the causal variants and hopefully will lead to the identification of the causal variant in the time scale of tomato domestication.

LIST OF ATTENDANTS

Last Name	First Name	Affiliation	Country	Type
Abales	Raquel	East West Seed Company	Philippines	Attendant
Achakkagari	Sai Reddy	McGill University	Canada	Poster Presenter (BREp01)
Aci	Meriem Miyassa	Università degli Studi Mediterranea di Reggio Calabria	Italy	Poster Presenter (STRp01)
Acquadro	Alberto	University of Turin	Italy	Attendant
Adil	Muhammad	NA	NA	Attendant
Admon-Edri	Tzadok	Nirit Seeds Ltd.	NA	Attendant
Ahamed	Farruk	NA	NA	Attendant
Ahammed	Golam Jalal	Henan University of Science and Technology	China	Oral Presenter (STRo04)
Aharoni	Asaph	Weizmann Institute of Science	Israel	Oral Presenter (NETop)
Ak	Dhanya	NA	NA	Attendant
Akler	Tamar	NA	NA	Attendant
Akler	Tamar	NA	Israel	Attendant
Alagoz	Gamze	The Mediterranean Agronomic Institute of Zaragoza (IAMZ)	Spain	Attendant
Alamu	Olabisi	National Centre for Genetic Resources and Biotechnology	Nigeria	Attendant
Albuquerque Silva	Fredy	Federal University of Vicosa	Brazil	Attendant
Alekhya	Dindu	UoH	NA	Attendant
Alexander	Agnieszka	The Sainsbury Laboratory, Norwich	UK	Attendant
Allie	Farhahna	University of Johannesburg	South Africa	Attendant
Almasia	Natalia	INTA- CONICET	Argentina	Attendant
Almiron	Ruben	Michigan State University	USA	Attendant
Alonge	Michael	Johns Hopkins University	USA	Poster Presenter (BIOp01)
Alonso Martín	David	Universitat Politècnica de València	Spain	Attendant
Althiab-Almasaud	Rasha	GBF Toulouse INP	France	Attendant
Amano	Masashi	Saitama Gensyu Ikuseikai Co.,Ltd	Japan	Attendant
Anglin	Noelle	International Potato Center (CIP)	Peru	Attendant
Anjali	Miss	Mody University	India	Attendant
Aprea	Giuseppe	ENEA	Italy	Attendant
Arabikothanuru Muniyappa	Anithakumari	BASF Vegetable Seeds	NA	Attendant
Aravena-Calvo	Javiera	University of Copenhagen	Denmark	Attendant
Arazi	Tzahi	Agricultural Research Organization (ARO) Volcani Center	Israel	Attendant
Argerich	Cosme	INTA- CONICET	Argentina	Attendant
Ariizumi	Tohru	University of Tsukuba	Japan	Attendant
Arroyo	Patricio	Universidad de Chile	Chile	Attendant
Arruabarrena	Ana	Instituto Nacional de Investigaciones Agropecuarias (INIA)	Uruguay	Poster Presenter (BIOp02)
Artur	Mariana	Utrecht University	Netherlands	Attendant
Aruhuanca Aguilar	Marie	NA	NA	Attendant
Asano	Satoshi	Kagome co.,LTD	Japan	Attendant
Ashihara	Sayaka	Takii Seed	Japan	Attendant
Ashkenazi	Varda	Hazera Seeds Ltd.	Israel	Attendant

Asiag-Tabatznik	Amit	MIGAL - Galilee Research Institute, Israel	Israel	Attendant
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Atarashi	Hiroki	Kikkoman Corp.	Japan	Attendant
Augelletti	Floriana	Council for Agricultural Research and Economics (CREA)	Italy	Attendant
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Awais	Muhammad	IPK Gatersleben	Germany	Attendant
Baars	Joost	Rijk Zwaan Breeding B.V.	Netherlands	Attendant
Bach	Linh	Leibniz-Institute of Vegetable and Ornamental Crops	Germany	Attendant
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Bachiri	Samia	Goethe University Frankfurt	Germany	Attendant
Balatero	Conrado	East West Seed Company	Philippines	Attendant
Balazadeh	Salma	Leiden University	Netherlands	Attendant
Banakar	Chetankumar	NA	NA	Attendant
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Barrero	Luz Stella	Colombian Corporation for Agricultural Research - Agrosavia	Colombia	Attendant
Barry	Cornelius	Michigan State University	USA	Attendant
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Berny	Jorge	University of California, Davis	USA	Attendant
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Billaud	William	INRAE	France	Attendant
Bineau	Estelle	INRAE	France	Attendant

Bitton	Frederique	INRAE	France	Attendant
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Bombarely	Aureliano	University of Milan	Italy	Chair (NET)
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Boualem	Adnane	INRAE	France	Attendant
Bough	Raven	Colorado State University	USA	Attendant
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Boyaci	Filiz	Bati Akdeniz Agricultural Research Institute	Turkey	Attendant
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Brulé	Franco	NA	NA	Attendant
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Bryan	Glenn	James Hutton Institute	UK	Chair (STR)
Buchwalder	Anne	NA	NA	Attendant
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Bulot	Blandine	Université Laval	Canada	Attendant
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Cai	Jianghua	NA	NA	Attendant
Cambiaso	Vladimir	IICAR-CONICET-UNR	Argentina	Attendant
Camerini	Lorenzo	University of Milan	Italy	Attendant
Camoni	Lorenzo	University of Rome Tor Vergata	Italy	Attendant
Campobenedetto	Cristina	Green Has Italia S.p.A.	Italy	Attendant
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Cano	David	Enza Zaden	Spain	Attendant
Cantet	Melissa	Bayer Vegetable Seeds	USA	Attendant
Cara	Nicolas	Universidad Nacional de Cuyo	Argentina	Attendant
Carannante	Giuseppe	Vilmorin	Italy	Attendant
Cardenas	Pablo	University of Copenhagen	Denmark	Attendant
Caromel	Bernard	INRAE	France	Attendant
Carreño-Quintero	Natalia	Keygene	Netherlands	Attendant
Carreño-Quintero	Natalia	Keygene	Netherlands	Attendant
Carriero	Filomena	ALSIA	Italy	Attendant
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Cebeci	Esra	Bati Akdeniz Agricultural Research Institute	Turkey	Attendant
Cebrailoglu	Nicat	Gebze Technical University	Turkey	Attendant
Celis García	Laura Daniela	Universidad Nacional de Colombia	Colombia	Attendant
Cernadas	Andres	Universidad Nacional de Hurlingham	Argentina	Attendant
Chalivendra	Subbaiah	Lousiana State University	USA	Attendant
Chaluvadi	Srinivasa	USDA	USA	Attendant
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Chaouch	Sejir	Limagrain Vegetable Seeds	France	Attendant
Chen	Bixuan	United Genetics Seeds Co.	USA	Attendant
Chen	Rong	Huazhong Agricultural University	China	Attendant
Chen	Xiuling	Northeast Agricultural University	China	Attendant
Chen	Yi	Ningbo University	China	Attendant
Cheng	Yuan	Zhejiang Academy of Agricultural Sciences	China	Attendant
Chervin	Christian	GBF lab, Toulouse INP	France	Attendant
Chetelat	Roger	University of California, Davis	USA	Attendant
Choi	Jihyeon	The Sainsbury Laboratory, Norwich	UK	Attendant
Choi	Ms	Nuri arg. Inc. , paa	South Korea	Attendant
Choi	Seul	Axia Vegetable Seeds	Netherlands	Attendant
Chomdej	Ornubol	Kasetsart University	Thailand	Attendant
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Cooperstone	Jessica	The Ohio State University	USA	Attendant
Costanzo	Manuela	ENEA	Italy	Attendant
Crucitti	Antonino	Wageningen University & Research	Netherlands	Attendant
Cruz Oró	Eduard	Bayer Crop Science	Spain	Attendant
Cui	Lei	Wageningen University & Research	Netherlands	Attendant
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Da Ponte	Lorena	Rijk Zwaan Breeding B.V.	Netherlands	Attendant
Dahan	Inbal	Top Seeds International LTD	Israel	Attendant
Dale	Savanah	Cornell University	USA	Attendant
Dambrosio	Caterina	ALSIA	Italy	Attendant
Darnige	Eden	INP Toulouse/GBF	France	Attendant
Daron	Rodelyn	East West Seed Company	Philippines	Attendant

Das	Ayan	Presidency University, Kolkata	India	Attendant
Das	Jaishri Rubina	National Institute of Plant Genome Research, New Delhi, India	India	Poster Presenter (STRp024)
Datir	Sagar	Savitribai Phule Pune University	Canada	Poster Presenter (NETp03)
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Davila Olivas	Nelson	BASF Vegetable Seeds	Netherlands	Attendant
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De Maagd	Ruud	Wageningen University & Research	Netherlands	Attendant
De Paola	Carmine	Instituto de Biologia Molecular y Celular de Plantas (IBMCP)	Spain	Attendant
De Paola	Larissa	University of Laussane (UNIL)	Italy	Attendant
De Siqueira Pinto	Maísa	Universidade de São Paulo	Brazil	Attendant
De Vos	Martin	KWS Vegetables	Netherlands	Attendant
De Vries	Jeroen	Bayer Crop Science	Netherlands	Attendant
De Vries	Michiel	Solynta	Netherlands	Attendant
Dean	Jeffrey	Mississippi State University	USA	Attendant
Deanna	Rocio	University Of Colorado Boulder	USA	Poster Presenter (EVOp01)
Dechkrong	Punyavee	Kasetsart University	Thailand	Attendant
Dehmer	Klaus J	IPK Gatersleben	Germany	Attendant
Deng	Lei	Institute of Genetics and Developmental Biology Chinese Academy of Sciences	China	Attendant
Devi	Micha Gracianna	Leibniz Institute of Plant Biochemistry	Germany	Attendant
Di Giacomo	Melisa	CONICET Argentina	Argentina	Attendant
Di Matteo	Antonio	University of Naples Federico II	Italy	Attendant
Díaz Valenzuela	Erik	LANGEBIO CINVESTAV	Mexico	Attendant
Didierlaurent	Laure	LVS	France	Attendant
Diez	Maria Jose	Universidad Politécnica de Valencia	Spain	Attendant
Diggle	Pamela	University of Connecticut	USA	Attendant
Ding	Pingtao	The Sainsbury Laboratory, Norwich	UK	Attendant
Doganguzel	Ergun	NA	France	Attendant
Dolaptchiev	Yordan	The Sainsbury Laboratory, Norwich	UK	Attendant
Dono	Gabriella	Council for Agricultural Research and Economics (CREA)	Italy	Poster Presenter (NETp03)
Doria	Gabriela	University of Cambridge	UK	Poster Presenter (EVOp02)
Douches	David	Michigan State University	USA	Attendant
Du	Minmin	University of Minnesota	USA	Attendant
Du	Minmin	University of Minnesota	USA	Attendant
Du	Miru	Inner Mongolia University	China	Attendant
Duduit	James	North Carolina State University	USA	Poster Presenter (BREp06)
Egea-Cortines	Marcos	Universidad Politécnica de Cartagena	Spain	Attendant
Eggers	Ernst-Jan	Wageningen University & Research	Netherlands	Oral Presenter (BREo04)
Ehrhard	Lucie	INRAE	France	Attendant
Ein Gedy	Shachaf	NA	Israel	Attendant
El-Shaieny	Abdel-Haleem	South Valley University	Egypt	Attendant
Elbelt	Sonia	INRAE	France	Attendant
Enciso-Rodríguez	Felix	Colombian Corporation for Agricultural Research - Agrosavia	Colombia	Poster Presenter (EVOp03)
Endo	Makoto	Takii Seed	Japan	Attendant
Ercolano	Maria	University of Naples Federico II	Italy	Poster Presenter (BREp04)
Eybishitz	Assaf	Tomatech	Israel	Attendant
Ezquerro	Miguel	Centre for Research in Agricultural Genomics (CRAG)	Spain	Attendant
Ezura	Kentaro	National Institute of Advanced Industrial Science and Technology	Japan	Attendant

Fait	Aaron	The Jacob Blaustein Institutes for Desert Research, Sede Boqer Campus, Ben Gurion University of the Negev, Israel	Israel	Poster Presenter (STRp28)
Fal	Soufiane	Mohamed V University of Rabat	Morocco	Attendant
Farcuh	Macarena	University of Maryland	USA	Attendant
Farooq	Muhammad Awais	University of Agriculture, Faisalabad	Pakistan	Attendant
Fartyal	Dhirendra	Agricultural Research Organization (ARO) Volcani Center	Israel	Attendant
Feder	Ari	Technion	Israel	Attendant
Feldman	Max	USDA	USA	Attendant
Felici	Barbara	Council for Agricultural Research and Economics (CREA)	Italy	Attendant
Feng	Mingfang	NA	China	Attendant
Feng	Qian	The University of Georgia	USA	Poster Presenter (BREp07)
Fenstemaker	Sean	The Ohio State University	USA	Oral Presenter (BREo01)
Fernandez-Lochu	Lucie	INRAE	France	Attendant
Fernández-Muñoz	Rafael	Instituto de Hortofruticultura Subtropical y Mediterránea, (IHSM)	Spain	Attendant
Fernandez-Northcote	Enrique N.	Universidad Nacional Agraria La Molina	Peru	Attendant
Ferrante	Paola	ENEA	Italy	Attendant
Finkers	Richard	Wageningen University & Research	Netherlands	Attendant
Fiorentino	Luigi	Wageningen University & Research	Netherlands	Attendant
Fiorillo	Anna	Università di Roma Tor Vergata	Italy	Attendant
Fisher	Josef	IFF	NA	Attendant
Flandez - Galvez	Hayde	University of the Philippines Los Banos	Philippines	Attendant
Fleury	Delphine	University of Adelaide	Australia	Attendant
Florez Rueda	Ana Marcela	University of Zürich	Switzerland	Attendant
Florez-Sarasa	Igor	Centre for Research in Agricultural Genomics (CRAG)	Spain	Attendant
Florio	Francesco Elia	Council for Agricultural Research and Economics (CREA)	Italy	Attendant
Fontanet	Lilian	HM-Clause	France	Attendant
Forlani	Sara	University of Milan	Italy	Poster Presenter (DEVp02)
Forte	Valentina	Council for Agricultural Research and Economics (CREA)	Italy	Attendant
Fortes	Ana Margarida	Universidade de Lisboa	Portugal	Attendant
Forti	Chiara	Council for Agricultural Research and Economics (CREA)	Italy	Poster Presenter (EVOp04)
Fortuny	Agustina	CONICET Argentina	Argentina	Poster Presenter (BREp08)
Fragkostefanakis	Sotirios	Goethe University Frankfurt	Germany	Attendant
Francis	David	Ohio State University	USA	Attendant
Frederick	Curtis	Aardevo BV	Netherlands	Attendant
Freiman	Aviad	Top Seeds International LTD	Israel	Attendant
Frick	Elizabeth	University of Florida	USA	Attendant
Friel	James	University of Milan	Italy	Attendant
Fukudome	Chiaki	Kyoto University	Japan	Attendant
Gabriels	Suzan	Wageningen University & Research	Netherlands	Attendant
Gaddikeri	Guruprasad	HM-Clause	India	Attendant
Gagnon	Edeline	Royal Botanic Garden of Edinburgh	UK	Poster Presenter (EVOp05)
Gagnon	Samuel	Université Laval	Canada	Attendant
Gaiero	Paola	Universidad de la Republica	Uruguay	Attendant
Galili	Shmeul	Agricultural Research Organization (ARO) Volcani Center	Israel	Attendant
Galland	Marc	University of Amsterdam	Netherlands	Attendant
Gamrasni	Dan	MIGAL - Galilee Research Institute, Israel	Israel	Attendant
Gandini	Carolina	IBAM-CONICET	Argentina	Poster Presenter (EVOp06)
Gapper	Nigel	Fruinomics	USA	Attendant

García	Elena	Instituto de Biologia Molecular y Celular de Plantas (IBMCP)	Spain	Attendant
Garzon	Gina	Colombian Corporation for Agricultural Research - Agrosavia	Colombia	Poster Presenter (STRp07)
Gayosso Rosales	Luis Yobani	NA	NA	Attendant
Geijsberts	Joost	Enza Zaden	Netherlands	Attendant
Ghani	Muhammad Awais	University of Agriculture, Faisalabad	Pakistan	Attendant
Gharat	Sachin	Weizmann Institute of Science	Israel	Attendant
Ghazi Soltani	Giti	University of Laussane (UNIL)	Switzerland	Attendant
Gibson	Matthew	Indiana University	USA	Oral Presenter (EVOo01)
Gilan	Irit	Philoseed	Israel	Attendant
Ginzberg	Idit	Agricultural Research Organization (ARO) Volcani Center	Israel	Attendant
Giorio	Giovanni	Metapontum Agrobios - ALSIA	Italy	Attendant
Giovannoni	James	Cornell University	USA	Attendant
Giovenali	Gloria	Università degli Studi della Tuscia	Italy	Attendant
Giuliano	Giovanni	ENEA	Italy	Chair (BIO)
Godoy	Federico	NA	NA	Attendant
Goldberg	Yael	NewBreed seeds	Israel	Attendant
Goldshmidt	Alexander	Agricultural Research Organization (ARO) Volcani Center	Israel	Attendant
Goldway	Martin	MIGAL - Galilee Research Institute, Israel	Israel	Attendant
Gomez	Michelle	Heinz Seed	USA	Attendant
Gomez Roldan	Maria Victoria	CNRS	France	Attendant
Gómez-Mena	Concha	Instituto de Biologia Molecular y Celular de Plantas (IBMCP)	Spain	Attendant
Gonçalves Pereira	Aléxia	Universidade Federal do Rio Grande do Sul (UFRGS)	Brazil	Attendant
Gonzales Llontop	María Julia	INAIGEM	Peru	Attendant
González Doblas	Verónica	Instituto de Hortofruticultura Subtropical y Mediterránea, (IHSM)	Spain	Attendant
González Gaarslev	Natalia	University of Laussane (UNIL)	Switzerland	Attendant
Gonzalo	María Jose	Instituto de Biologia Molecular y Celular de Plantas (IBMCP)	Spain	Poster Presenter (STRp08)
Goossens	Alain	VIB-Ghent University	Belgium	Attendant
Gossens	Alain	VIB-Ghent University	Belgium	Oral Presenter (BIOop)
Gotch	Amber	UW Madison-Hancock Agricultural Research Station	USA	Attendant
Goto	Yukihisa	RIKEN Center for Sustainable Resource Science	Japan	Attendant
Goulet	Charles	Université Laval	Canada	Attendant
Goulet	Marie-Claire	Université Laval	Canada	Attendant
Goyer	Aymeric	Oregon State University	USA	Oral Presenter (STRo02)
Gramazio	Pietro	University of Tsukuba	Japan	Poster Presenter (NETp04)
Gramma	Vladislav	Max Planck Institute of Molecular Plant Physiology (MPIPZ)	Germany	Attendant
Grandgeorge	Lila	The Sainsbury Laboratory, Norwich	UK	Attendant
Granell	Antonio	Instituto de Biologia Molecular y Celular de Plantas (IBMCP)	Spain	Poster Presenter (BREp09)
Gruber	Jonathan	Bayer Crop Science	USA	Attendant
Gryffroy	Lore	VIB-Ghent University	Belgium	Poster Presenter (STRp09)
Guardia Velarde	Lorena	Swedish University of Agriculture Sciences	Sweden	Attendant
Guillaume	Maxime	Gautier Semences	France	Attendant
Guixiang	Wang	CAS Center for Excellence in Molecular Plant Sciences	China	Attendant
Gupta	Apoorva	National Institute of Plant Genome Research, New Delhi, India	India	Poster Presenter (STRp10)
Gupta	Neha	University of Hyderabad	India	Attendant
Gupta	Prateek	The Hebrew University of Jerusalem	Israel	Attendant
Gupta	Suresh Kumar	Agricultural Research Organization (ARO) Volcani Center	Israel	Attendant

Gutierrez	Diego	National Agrarian University – La Molina	Peru	Attendant
Hadjieva	Nikol	University of Plovdiv	Bulgaria	Poster Presenter (STRp11)
Haj Ahmad	Fatima	Al-Balqa Applied University	Jordan	Attendant
Hancock	Angela	Max Planck Institute of Molecular Plant Physiology (MPIPZ)	Germany	Attendant
Handa	Avtar	Purdue University	USA	Attendant
Hartman	Jordan	Ohio State University	USA	Attendant
Hasman	Roni	Agricultural Research Organization (ARO) Volcani Center	Israel	Attendant
Hatinoğlu	Gül	Wageningen University & Research	Netherlands	Attendant
Hause	Bettina	Leibniz Institute of Plant Biochemistry	Germany	Attendant
He	Jia	Cold Spring Harbor Laboratory (CSHL)	USA	Attendant
Heiden	Gustavo	EMBRAPA - The Brazilian Agricultural Research Corporation	Brazil	Poster Presenter (BREp10)
Hernández Ciro	Natalí	Universidad de Antioquia	Colombia	Attendant
Hilfiker	Aurore	Philip Morris International R&D (PMI)	Switzerland	Attendant
Hirschberg	Joseph	The Hebrew University of Jerusalem	Israel	Attendant
Hofstede	René	Keygene	Netherlands	Attendant
Hofstede	René	Keygene	Netherlands	Attendant
Holterman	Martijn	Solynta	Netherlands	Attendant
Holton	Nick	Leaf Expression Systems	UK	Attendant
Hoopes	Genevieve	Michigan State University	USA	Attendant
Hsieh	Chenyun	Utrecht university	Netherlands	Attendant
Hu	Courtney	BASF Vegetable Seeds	USA	Attendant
Hu	Guojian	University of Toulouse, INPT	France	Attendant
Hu	Zhangjian	Zhejiang University	China	Attendant
Huercano Rubens	Carolina	Universidad de Málaga	Spain	Poster Presenter (DEVp03)
Humphry	Matthew	Aardevo BV	Netherlands	Attendant
Hunter	Ben	Bayer Crop Science	NA	Attendant
Hunziker	Johan	University of Tsukuba	Japan	Oral Presenter (BIOo02)
Ibañez	Ana	Instituto Multidisciplinario de Biología Vegetal (CONICET-UNC)	Argentina	Attendant
Ibañez	Verónica Noé	IBAM- CONICET/UNCuyo	Argentina	Attendant
Iglesias	Ariadna	Centre for Research in Agricultural Genomics (CRAG)	Spain	Attendant
Ikeda	Hiroki	Utsunomiya University	Japan	Attendant
Imerovski	Ivana	HZPC	Netherlands	Attendant
Iqbal	Md. Asif	Lal Teer Seed Ltd.	Bangladesh	Attendant
Irfan	Mohammad	Rutgers, The State University of New Jersey	USA	Attendant
Israeli	Alon	The Hebrew University of Jerusalem	Israel	Attendant
Iwai	Yumi	Japan Tobacco Inc.	Japan	Attendant
Jacobs	Joseph	HM-Clause	USA	Attendant
Jacobs	Jeanne	AgResearch	New Zealand	Attendant
Jacobsen	Deidra	University of Utah	USA	Poster Presenter (EVOp07)
Jakobson	Liina	Eesti Taimekasvatuse Instituut	Estonia	Attendant
Jayakody	Thilani	Michigan State University	USA	Attendant
Jeridi	Roua	INRAE	France	Attendant
Jetti	Sri Madhulika	NA	NA	Attendant
Jewehan	Ahmad	Szent Istvan University	Hungary	Attendant
Jha	Sarita	National Institute of Plant Genome Research, New Delhi, India	India	Poster Presenter (STRp13)
Jiang	Xiaobing	Wageningen University & Research	Netherlands	Poster Presenter (DEVp04)
Jimenez	Randi	California Department of Agriculture	USA	Attendant
Jimenez-Gomez	Jose	INRAE	France	Chair (NET)
Jinying	Luo	NA	China	Attendant

Jobson	Emma	Boyce Thompson Institute	USA	Attendant
Jones	Jonathan	Sainsbury Lab, Norwich, UK	UK	Attendant
Joshi	Vijay	Texas A&M AgriLife Research	USA	Attendant
Juranic	Martina	Wageningen University & Research	Netherlands	Attendant
K	Princy	University of Hyderabad	India	Attendant
Kabir	Lutful	Lal Teer Seed Ltd.	Bangladesh	Attendant
Kacheyo	Olivia	Solynta	Netherlands	Attendant
Kahlon	Parvinderdeep	Technical University of Munich	Germany	Oral Presenter (STRop)
Kaiser	Natalie	Michigan State University	USA	Oral Presenter (BREo05)
Kaiser Schnitzler	Carolina	Universidade Federal do Rio Grande do Sul (UFRGS)	Brazil	Attendant
Kalisvaart	Jonathan	Rijk Zwaan Breeding B.V.	Netherlands	Attendant
Kamalachandran	Dharani	Utrecht University	Netherlands	Attendant
Kaminski	Kacper	Philip Morris International R&D (PMI)	Switzerland	Attendant
Kamiyoshihara	Yusuke	Nihon University	Japan	Attendant
Kano	Akihito	Takii Seed	Japan	Attendant
Kaplan	Boaz	Nirit Seeds Ltd.	Israel	Attendant
Kappers	Iris	Wageningen University & Research	Netherlands	Attendant
Karasov	Talia	University of Utah	USA	Attendant
Kariyat	Rupesh	The University of Texas Rio Grande Valley	USA	Attendant
Karlova	Rumyana	Wageningen University & Research	Netherlands	Attendant
Karniel	Uri	Hazera Seeds Ltd.	Israel	Attendant
Kaur	Livleen	Punjab Agricultural University	India	Attendant
Kayikci	Halim	Bati Akdeniz Agricultural Research Institute	Turkey	Attendant
Keren	Alexandra	Agricultural Research Organization (ARO) Volcani Center	Israel	Attendant
Kerlan	Marie-Claire	INRAE	France	Attendant
Ketelaars	Frans	Rijk Zwaan Breeding B.V.	Netherlands	Attendant
Keyhaninejad	Neda	The University of Georgia	USA	Attendant
Khanal	Samjhana	Wageningen University & Research	Netherlands	Attendant
Kharshiing	Eros V	St. Edmund's College, Shillong	India	Poster Presenter (DEVp05)
Khosa	Jiffinvir	Punjab Agricultural University	India	Attendant
Kim	Chami	University of Florida	USA	Attendant
Kim	Heejin	Postech	South Korea	Attendant
Kim	Youngin	East West Seed Company	Bangladesh	Attendant
King	Kevin	United Genetics Seeds Co.	USA	Attendant
Kirschke	Elaine	Apeel Sciences	USA	Attendant
Kitahara	Naoto	Nippon Del Monte Corporation	Japan	Attendant
Klap	Chen	Agricultural Research Organization (ARO) Volcani Center	Israel	Attendant
Knapp	Sandra	Natural History Museum	UK	Chair (EVO)
Kneib	Raquel	EMBRAPA - The Brazilian Agricultural Research Corporation	Brazil	Poster Presenter (BREp11)
Knoch	Eva	GMI/RIKEN	Japan	Oral Presenter (BIOo03)
Koch	Amit	The Hebrew University of Jerusalem	Israel	Attendant
Komatsu	Hiroki	Kagome co.,LTD	Japan	Attendant
Kondhare	Kirtikumar	CSIR- National Chemical Laboratory Pune	India	Attendant
Konishi	Chiaki	Kikkoman Corp.	Japan	Attendant
Konkina	Anna	Mediterranean Agronomic Institute of Chania	Grece	Attendant
Kontbay	Kübra	Max Planck Institute of Molecular Plant Physiology (MPIPZ)	Germany	Attendant
Koropacka	Kamila	Axia Vegetable Seeds	Netherlands	Attendant
Kortbeek	Ruy	University of Amsterdam	Netherlands	Attendant
Koseoglou	Eleni	Wageningen University & Research	Netherlands	Poster Presenter (STRp15)

Kouiho	Sehou Romaric	Wageningen University & Research	Netherlands	Attendant
Koumproglou	Rachil	Semillas Fitó	Spain	Attendant
Koussevitzky	Shai	Limagrain Vegetable Seeds	Israel	Attendant
Kozub	Carolina	CONICET Argentina	Argentina	Attendant
Kressin	Jonathan	East West Seed Company	Thailand	Attendant
Kulkarni	Gopal	East West Seed Company	India	Attendant
Kumari	Dr Aradhna	COA, JNKVV, GANJ BASODA	India	Attendant
Kyriakidou	Maria	McGill University	Canada	Poster Presenter (BREp12)
L C	Sushmitha	IARI	India	Attendant
Lagarrigue	David	Aardevo BV	Netherlands	Attendant
Langedijk	Nathalia	Enza Zaden	Netherlands	Attendant
Lanteri	Sergio	University of Turin	Italy	Poster Presenter (STRp04)
Lapidot	Moshe	Agricultural Research Organization (ARO) Volcani Center	Israel	Attendant
Laursen	Tomas	University of Copenhagen	Denmark	Attendant
Lazzaro	Mark	College of Charleston	USA	Attendant
Le Bec	Nolwenn	RHUL	UK	Attendant
Lebeigle	Ludivine	University of Laussane (UNIL)	Switzerland	Attendant
Lee	Je Min	Kyungpook National University	South Korea	Attendant
Lee	Kang Min	Chonbuk National University	South Korea	Attendant
Lee	Sarah	Michigan State University	USA	Attendant
Lefebvre	Véronique	INRAE	France	Attendant
Leniak	Ewa	Max Planck Institute of Molecular Plant Physiology (MPIPZ)	Germany	Attendant
Lerner	Alon	Top Seeds International LTD	Israel	Attendant
Levin	Ilan	Agricultural Research Organization (ARO) Volcani Center	Israel	Attendant
Lewis	Esther	Royal Holloway University of London	UK	Attendant
Lewis	Mark	Sakata Seed America	USA	Attendant
Li	Jie	John Innes Centre	UK	Attendant
Li	Jinhua	Southwest University	China	Attendant
Li	Linge	Utrecht University	Netherlands	Poster Presenter (STRp16)
Li	Qiang	Shandong Agricultural University	China	Poster Presenter (DEVp06)
Li	Ruiling	University of Turin	Italy	Poster Presenter (BIOp04)
Li	Tianrun	University of California, Davis	USA	Attendant
Li	Xin	Institute of Vegetables and Flowers, Chinese Academy of Agricultural Sciences	China	Attendant
Li	Yue	Northeast Agricultural University	China	Attendant
Lian	Jiajie	Shandong Agricultural University	China	Attendant
Liard	Louison	Enza Zaden	Netherlands	Attendant
Lichtenstein	Gabriel	Weizmann Institute of Science	Israel	Attendant
Lieberman Lazarovich	Michal	Agricultural Research Organization (ARO) Volcani Center	Israel	Attendant
Liedl	Barbara	West Virginia State University	USA	Attendant
Liedschulte	Verena	Philip Morris International R&D (PMI)	Switzerland	Attendant
Lima	Natércia	EMBRAPA - The Brazilian Agricultural Research Corporation	Brazil	Attendant
Limoey	Daniel	The Hebrew University of Jerusalem	Israel	Attendant
Lin	Wanping	Agricultural Research Organization (ARO) Volcani Center	Israel	Attendant
Lindhout	Pim	Solynta	Netherlands	Attendant
Linssen	Freek	Wageningen University & Research	Netherlands	Attendant
Lionneton	Eric	HM-Clause	France	Attendant
Lippman	Zach	Howard Hughes Medical Institute - Cold Spring Harbor Laboratory	USA	Attendant
Lippolis	Antonio	Wageningen University & Research	Netherlands	Attendant
Lira	Bruno Silvestre	Universidade de São Paulo	Brazil	Oral Presenter (DEVo02)

Liu	Guan	Heilongjiang University	China	Attendant
Liu	Haiping	Michigan Technological University	USA	Attendant
Liu	Sukuan	University Of Colorado Boulder	USA	Attendant
Löchli	Karin	Goethe University Frankfurt	Germany	Attendant
Lomas	Tomas	Bayer Crop Science	Netherlands	Attendant
Lombardo	Antonello	Università degli Studi della Tuscia	Italy	Attendant
Lombardo	Fabien	University of Tsukuba	Japan	Attendant
Londoño	Lina	Universidad Libre - Pereira	Colombia	Poster Presenter (NETp05)
López Martín	María Jesús	Instituto de Biologia Molecular y Celular de Plantas (IBMCP)	Spain	Attendant
Lorenzen	Jim	Bill & Melinda Gates Foundation	USA	Attendant
Lyngdoh Mawphlang	Ophilia Ibapalei	North Eastern Hill University	India	Attendant
Macias Gonzalez	Miguel	United Genetics Seeds Co.	USA	Attendant
Madlung	Andreas	University of Puget Sound	USA	Poster Presenter (NETp06)
Maeda	Tomohiro	Nippon Del Monte Corporation	Japan	Attendant
Mafireyi	Godwin	Starke Ayres	South Africa	Attendant
Magome	Hiroshi	Japan Tobacco Inc.	Japan	Attendant
Mahood	Elisabeth	Cornell University	USA	Attendant
Mainiero	Samantha	Boyce Thompson Institute	USA	Attendant
Maioli	Alex	University of Turin	Italy	Poster Presenter (BIOp05)
Makov	Tal	The Hebrew University of Jerusalem	Israel	Attendant
Mallard	Stephanie	Vilmorin	France	Attendant
Mane	Ramesh	HM-Clause	India	Attendant
Mangino	Giulio	COMAV, Universitat Politècnica de València	Spain	Poster Presenter (BREp13)
Manin	Sylvie	Vilmorin	France	Attendant
Mankare	Sandeep	East West Seed Company	India	Attendant
Manrique	Norma	International Potato Center (CIP)	Peru	Attendant
Manrique	Silvia	University of Milan	Italy	Attendant
Mao	Jingjing	Wageningen University & Research	Netherlands	Attendant
Marie-Hélène	Andrieu	INRAE	France	Attendant
Markova	Mira	University of Texas at Arlington	USA	Attendant
Marques Dos Santos	Bruna	University of Copenhagen	Denmark	Attendant
Marti Ferrando	Tatiana	Wageningen University & Research	Netherlands	Attendant
Martin	Greg	Boyce Thompson Institute	USA	Attendant
Martin Romero	Juan Antonio	Bayer Crop Science	Spain	Attendant
Martin-Rodriguez	Jose Angel	CEBAS-CSIC	Spain	Attendant
Martina	Matteo	University of Turin	Italy	Poster Presenter (BREp14, BREp15)
Martine	Chris	Bucknell University	USA	Oral Presenter (EVOop)
Martinez	Shantel	Bayer Crop Science	USA	Attendant
Martínez	Cristina	CEBAS-CSIC	Spain	Attendant
Martínez	María Carolina	INTA- CONICET	Argentina	Attendant
Martínez Melgarejo	Purificacion Andrea	CEBAS-CSIC	Spain	Attendant
Martinez-Sanchez	Marcela	Plant and Food Research NZ	New Zealand	Attendant
Masini	Laura	NA	Italy	Attendant
Mathur	Saloni	National Institute of Plant Genome Research, New Delhi, India	India	Oral Presenter (STRo03)
Matsumoto	Chihiro	Utsunomiya University	Japan	Attendant
Maxwell	Douglas	University of Wisconsin-Madison	USA	Attendant
Mazo	Carolina	Cornell University	USA	Attendant
Mazzucato	Andrea	University of Tuscia	Italy	Poster Presenter (STRp20)
Mcleod	Louis	INRAE	France	Attendant

Mcnulty	Michael	NA	NA	Attendant
Megias	Victor	Semillas Fitó	Spain	Attendant
Meijer	Wiebe	HZPC	Netherlands	Attendant
Meisenburg	Mara	Wageningen University & Research	Netherlands	Attendant
Mejía Solórzano	Anais	National University of San Marcos	Peru	Attendant
Melanson	Rebecca	Mississippi State University	USA	Attendant
Menda	Naama	Boyce Thompson Institute	USA	Attendant
Meng	He	Tobacco Research Institute, Chinese Academy of Agricultural Science	China	Attendant
Meng	Xiaoxi	University of Minnesota	USA	Attendant
Menisterio	Jeany Mae	East West Seed Company	Philippines	Attendant
Millenaar	Frank	Nunhems	USA	Attendant
Mizutani	Masaharu	Kobe University	Japan	Attendant
Moein	Fatemeh	University of Isfahan	Iran	Attendant
Moghe	Gaurav	Cornell University	USA	Attendant
Moglia	Andrea	University of Turin	Italy	Attendant
Molina-Hidalgo	Francisco Javier	VIB-Ghent University	Belgium	Poster Presenter (BIOp06)
Monforte	Antonio J.	Instituto de Biologia Molecular y Celular de Plantas (IBMCP)	Spain	Attendant
Monino Lopez	Daniel	Wageningen University & Research	Netherlands	Poster Presenter (STRp17)
Montoro	Teresa	Enza Zaden	Spain	Attendant
Moré	Marcela	Instituto Multidisciplinario de Biología Vegetal (CONICET-UNC)	Argentina	Attendant
Morelli	Luca	Centre for Research in Agricultural Genomics (CRAG)	Spain	Attendant
Moret	Aubry	BioBased Economy group	Netherlands	Attendant
Motenko	Etel	Agricultural Research Organization (ARO) Volcani Center	Israel	Attendant
Mouden	Sanae	Wageningen University & Research	Netherlands	Attendant
Mouton	Pauline	Mme	France	Attendant
Movilli	Andrea	University of Milan	Italy	Attendant
Moyle	Leonie	Indiana University	USA	Attendant
Mueller-Roeber	Bernd	University of Potsdam	Germany	Attendant
Munir	Shoaib	Huazhong Agricultural University	China	Poster Presenter (BIOp07)
Munoz	Lina	Technical University of Munich	Germany	Poster Presenter (NETp07)
Murata	Emi	ADNdiagnóstico	NA	Attendant
Murúa Carrizo	Francisco	National University of Catamarca	Argentina	Poster Presenter (EVOp08)
Muskens	Marielle	Agrico Research	Netherlands	Attendant
Mythri	Bikkasani	Kerala Agricultural University	India	Poster Presenter (STRp18)
Nadakuduti	Satya Swathi	University of Florida	USA	Attendant
Nago	Eman	Top Seeds International LTD	Israel	Attendant
Naguvanahally Chandrashekara	Surakshitha	Max Planck Institute of Molecular Plant Physiology (MPIPZ)	Germany	Attendant
Nagy	Natalia	NA	NA	Attendant
Nair	Aditi	University of Hyderabad	India	Attendant
Najmim	Fatema	Lal Teer Seed Ltd.	Bangladesh	Attendant
Nambeesan	Savithri	The University of Georgia	USA	Attendant
Namphengsone	Natacha	The University of Georgia	USA	Poster Presenter (DEVp07)
Nashilevitz	Shai	Hazera Seeds Ltd.	Israel	Attendant
Nativ- Aharoni	Rotem	Erma Zaden	Israel	Attendant
Nayak	Aditya	Plantik Biosciences	France	Attendant
Negin	Boaz	Weizmann Institute of Science	Israel	Attendant
Neves	Catarina	Universidade de Lisboa	Portugal	Attendant
Nguyen Quoc	Linh	NA	NA	Attendant
Nichodemus	Cornelius Onyedikachi	University of Port Harcourt	Nigeria	Poster Presenter (EVOp09)

Nicolao	Rodrigo	UFPel	Brazil	Poster Presenter (BREp16)
Nicolas	Philippe	Boyce Thompson Institute	USA	Attendant
Nicolia	Alessandro	Council for Agricultural Research and Economics (CREA)	Italy	Attendant
Nieuwenhuis	Ronald	Wageningen University & Research	Netherlands	Attendant
Nishida	Atsushi	Kyoto University	Japan	Attendant
Noman	Muhammad	Peking University	China	Attendant
Nomura	João	ESALQ/USP	Brazil	Attendant
Noureen	Azka	National Institute for Biotechnology and Genetic engineering Faislabad, Pakistan	Pakistan	Attendant
Nouri-Ellouz	Oumèma	University of Sfax	Tunisia	Attendant
Ntelkis	Nikolaos	University of Thessaly	Greece	Attendant
Nunome	Tsukasa	NIVFS,NARO	Japan	Attendant
Obaje	Joseph	Federal University of Technology Akure	Nigeria	Attendant
Ogundare	Goodluck	University of Ilorin	Nigeria	Attendant
Oi	Yuki	Kagome co.,LTD	Japan	Attendant
Olave	Andrea	The Sainsbury Laboratory, Norwich	UK	Attendant
Olegário Da Silva	Giovani	EMBRAPA - The Brazilian Agricultural Research Corporation	Brazil	Attendant
Oliveira	Maria José	Universidade de São Paulo	Brazil	Attendant
Olmstead	Richard	University of Washington	USA	Attendant
Omomoh	Bernard	Federal University of Technology Akure	Nigeria	Attendant
Oome	Stan	HZPC	Netherlands	Attendant
Orchard	Caleb	The Ohio State University	USA	Attendant
Ordoñez	Benny	University of California, Davis	USA	Attendant
Ortiz	Irma	University of California, Riverside	USA	Attendant
Orzaez	Diego	Instituto de Biologia Molecular y Celular de Plantas (IBMCP)	Spain	Poster Presenter (BIOp10)
Osorio	Jaime	Colombian Corporation for Agricultural Research - Agrosavia	Colombia	Attendant
Osvail De Oliveira Junior	Marcelo	Universidade de São Paulo	Brazil	Attendant
Ouyang	Bo	Huazhong Agricultural University	China	Attendant
Oved	Matan	The Hebrew University of Jerusalem	Israel	Attendant
Ozgoren	Burak	Manier	Turkey	Attendant
Pabón Mora	Natalia	Universidad de Antioquia	Colombia	Attendant
Padua	Jose	British American Tobacco (BAT)	Brazil	Attendant
Palombo	Nahuel	CONICET-UNC	Argentina	Attendant
Pamei	Injangbuanang	University of Hyderabad	India	Attendant
Pan	Zhechao	Yunnan Academy of Agricultural Sciences	China	Attendant
Pande	Makarand	East West Seed Company	India	Attendant
Pandita	Deepu	Government Department of School Education Jammu	India	Attendant
Paran	Ilan	Agricultural Research Organization (ARO) Volcani Center	Israel	Chair (BRE)
Parisi	Bruno	Council for Agricultural Research and Economics (CREA)	Italy	Attendant
Park	Suejin	University of California, Riverside	USA	Attendant
Peled	Elad	Top Seeds International LTD	Israel	Attendant
Perach	Omer	NA	NA	Attendant
Peralta	Iris Edith	National University of Cuyo	Argentina	Attendant
Percio	Francisco	Instituto de Hortofruticultura Subtropical y Mediterránea, (IHSM)	Spain	Poster Presenter (DEVp08)
Pereira	Arione	EMBRAPA - The Brazilian Agricultural Research Corporation	Brazil	Attendant
Pereira	Lara	The University of Georgia	USA	Oral Presenter (NETo02)
Pereira Da Costa	Javier	Universidad Nacional de Rosario (UNR)	Argentina	Attendant
Pereyra Bistraín	Leonardo Isaac	Instituto Potosino de Investigación Científica y Tecnológica A.C.	Mexico	Poster Presenter (STRp19)
Perez	Jose	NA	NA	Attendant
Perez Alfocea	Francisco	CEBAS-CSIC	Spain	Attendant

Pesce	Céline	HM-Clause	USA	Attendant
Peters	Sander	Wageningen University & Research	Netherlands	Attendant
Pezzi	Pedro	Universidade Federal do Rio Grande do Sul (UFRGS)	Brazil	Poster Presenter (EVOp11)
Philippe	Glenn	Cornell University	USA	Oral Presenter (DEVo01)
Picarella	Maurizio	University of Tuscia	Italy	Attendant
Pidon	Hélène	IPK Gatersleben	Germany	Attendant
Pineau	Aline	HM-Clause	France	Attendant
Pinna	Julia	Universidade de São Paulo	Brazil	Attendant
Pirrello	Julien	Toulouse-INP/ENSAT	France	Attendant
Plaisance	Stephane	VIB-Ghent University	Belgium	Attendant
Plissonneau	Clémence	Gautier Semences	France	Attendant
Pompili	Valerio	University of Turin	Italy	Attendant
Ponce	Olga	University of Birmingham	UK	Attendant
Ponukumatla	Dr. Rachana	Govt. Degree College (Science)	India	Attendant
Portis	Ezio	University of Turin	Italy	Attendant
Possenti	Marco	Council for Agricultural Research and Economics (CREA)	Italy	Attendant
Powell	Adrian	Boyce Thompson Institute	USA	Attendant
Pratta	Guillermo	IICAR-CONICET-UNR	Argentina	Poster Presenter (BREp03)
Pretz	Chelsea	University Of Colorado Boulder	USA	Attendant
Price	Hadas	Weizmann Institute of Science	Israel	Attendant
Prohens	Jaime	Universitat Politècnica de València	Spain	Chair (EVO), Oral Presenter (BREo03)
Provelengiou	Stella	NA	NA	Attendant
Pullaiahgari	Durgeshwar	University of Hyderabad	India	Attendant
Punder	Sathish	United Genetics Seeds Co.	India	Attendant
Qi	Shilian	Jiangsu Normal University	China	Attendant
Qin	Kezhen	Max Planck Institute of Molecular Plant Physiology (MPIPZ)	Germany	Attendant
Qin	Xiaoqiong	University of California, Davis	USA	Attendant
Qiu	Zhengkun	South China Agricultural University,	China	Attendant
Quiñones	Alejandra	Universidad Peruana Cayetano Heredia	Peru	Attendant
Quinteros	Gonzalo	National Institute of Agricultural Research	Argentina	Poster Presenter (DEVp09)
Rabanus-Wallace	Tim	IPK Gatersleben	Germany	Attendant
Rademacher	Eike	Rijk Zwaan Breeding B.V.	Netherlands	Attendant
Ragazzo	Gabriel	Universidade de São Paulo	Brazil	Attendant
Rahman	Md. Sajedur	Lal Teer Seed Ltd.	Bangladesh	Attendant
Ramirez	Lorena	Wageningen University & Research	Netherlands	Oral Presenter (BIOo04)
Ramirez Gaona	Miguel	Wageningen University & Research	Netherlands	Attendant
Ramírez Ojeda	Gabriela	Universidad Autónoma Chapingo	Mexico	Poster Presenter (EVOp12)
Ramos	Flavio	NA	NA	Attendant
Ranawaka	Buddhini	Queensland University of Technology (QUT)	Australia	Poster Presenter (EVOp13)
Randall	Linnell	Boyce Thompson Institute	USA	Attendant
Rao	Sombir	National Institute of Plant Genome Research, New Delhi, India	India	Poster Presenter (STRp21)
Rashid	Muhammad Abdul Rehman	Yunnan Academy of Agricultural Sciences	China	Poster Presenter (EVOp14)
Raz	Amit	Agricultural Research Organization (ARO) Volcani Center	Israel	Attendant
Razifard	Hamid	University of Massachusetts	USA	Attendant
Redkar	Amey	Universidad de Cordoba	Spain	Attendant
Reeves	Patrick	USDA	USA	Attendant
Ren	Panrong	Institute of Genetics and Developmental Biology Chinese Academy of Sciences	China	Attendant
Rezaei Cherati	Sajedeh	University of Arkansas at Little Rock	USA	Attendant
Rhodes	Jack	TSL, Norwich	UK	Attendant

Richael	Craig	JR Simplot Company--Plant Sciences Division	USA	Attendant
Rigano	Maria Manuela	University of Naples Federico II	Italy	Poster Presenter (STRp06)
Rimon Knopf	Ronit	Hazera Seeds Ltd.	Israel	Attendant
Roberts	Miles	Michigan State University	USA	Attendant
Roberts	Robyn	Colorado State University	USA	Attendant
Robertson	Colby	NA	NA	Attendant
Rochsar	Edan	The Hebrew University of Jerusalem	Israel	Attendant
Roda	Federico	Universidad Nacional de Colombia	Colombia	Attendant
Rodriguez	Gustavo	IICAR-CONICET-UNR	Argentina	Attendant
Rodriguez-Concepcion	Manuel	Instituto de Biologia Molecular y Celular de Plantas (IBMCP)	Spain	Attendant
Rohr	Angela	EMBRAPA - The Brazilian Agricultural Research Corporation	Brazil	Attendant
Rombauts	Stephane	VIB-Ghent University	Belgium	Attendant
Romero-Rodríguez	Beatriz	Instituto de Hortofruticultura Subtropical y Mediterránea, (IHSM)	Spain	Attendant
Roque	Edelin	Instituto de Biologia Molecular y Celular de Plantas (IBMCP)	Spain	Attendant
Rosa-Martínez	Elena	Instituto de Conservación y Mejora de la Agrodiversidad Valenciana (COMAV), Universitat Politècnica de València	Spain	Poster Presenter (STRp23)
Rosati	Carlo	ENEA	Italy	Attendant
Rose	Jocelyn	Cornell University	USA	Attendant
Rosenkranz	Remus	Goethe University Frankfurt	Germany	Attendant
Rossi	Magdalena	Universidade de Sao Paulo	Brazil	Attendant
Rotem	Yaniv	Hazera Seeds Ltd.	Israel	Attendant
Rotino	Giuseppe Leonardo	Council for Agricultural Research and Economics (CREA)	Italy	Attendant
Rozas López	José Antonio	Semillas Fitó	Spain	Attendant
Ruiz-Lopez	Noemi	Instituto de Hortofruticultura Subtropical y Mediterránea, (IHSM)	Spain	Attendant
Rutter	William	USDA	USA	Attendant
Sadder	Monther	University of Jordan	Jordan	Poster Presenter (STRp25)
Sadre	Radin	Michigan State University	USA	Attendant
Saeko	Areerat	East West Seed Company	Netherlands	Attendant
Saengnak	Vilasinee	Chia Tai Company Limited	Thailand	Attendant
Saha	Surya	Boyce Thompson Institute	USA	Attendant
Sahin	Ahmet	The Mediterranean Agronomic Institute of Zaragoza (IAMZ)	Spain	Attendant
Salas	Elisa	International Potato Center (CIP)	Peru	Attendant
Salazar-Sarasua	Blanca	Instituto de Biologia Molecular y Celular de Plantas (IBMCP)	Spain	Poster Presenter (DEVp10)
Salinier	Jérémy	UR GAFL INRAE	France	Attendant
Salleres-Neira	Belen	NA	NA	Attendant
Samach	Alon	The Hebrew University of Jerusalem	Israel	Attendant
Sanchez	Gabino	Hudson River Biotechnology	Netherlands	Attendant
Sánchez Prudencio	Ángela	CEBAS-CSIC	Spain	Attendant
Sanchez-Puerta	M. Virginia	IBAM-Universidad Nacional de Cuyo	Argentina	Attendant
Santillán Martínez	Miguel	Wageningen University & Research	Netherlands	Poster Presenter (STRp26)
Santos Monteiro	Scarlet	Universidade de São Paulo	Brazil	Attendant
Sapkota	Manoj	The University of Georgia	USA	Poster Presenter (BREp17)
Sari	Ugur	Çanakkale Onsekiz Mart Üniversitesi	Turkey	Attendant
Schaap	Paul	Solynta	Netherlands	Attendant
Schaareman	Rob	BASF Vegetable Seeds	Netherlands	Attendant
Schouten	Henk	Wageningen University & Research	Netherlands	Attendant
Schrader	Andrea	RWTH Aachen University	Germany	Poster Presenter (STRp14), Oral Presenter (STRo01)

Schuurink	Robert	University of Amsterdam	Netherlands	Attendant
Segatto	Ana Lúcia Anversa	Instituto Federal do Rio Grande do Sul - Campus Caxias do Sul	Brazil	Attendant
Seibert	Tanja	Max Planck Institute of Molecular Plant Physiology (MPIPZ)	Germany	Attendant
Selby	Jessica	Bayer Crop Science	NA	Attendant
Selda Rivarez	Mark Paul	National Institute of Biology, Slovenia	Slovenia	Attendant
Seo	Eunyoung	University of California, Berkeley	USA	Attendant
Sevilla	Myrna	BHN Research/BHN Seed	USA	Attendant
Shalit-Kaneh	Akiva	Agricultural Research Organization (ARO) Volcani Center	Israel	Attendant
Shalom	Liron	Top Seeds International LTD	Israel	Attendant
Shannon	Laura	University of Minnesota	USA	Attendant
Sharathkumar	Malleshaiah	Wageningen University & Research	Netherlands	Attendant
Sharma	Kapil	University of Hyderabad	India	Attendant
Sharma	Rameshwar	University of Hyderabad	India	Attendant
Sharma	Sanjeev	The James Hutton Institute	UK	Attendant
Sheedy	John	Chia Tai Company Limited	Thailand	Attendant
Shelef	Moran	Top Seeds International LTD	Israel	Attendant
Shen	Xuexue	Wageningen University & Research	Netherlands	Attendant
Shen	Zhengxing	USDA	USA	Attendant
Shi	Kai	Zhejiang University	China	Poster Presenter (STRp12)
Shi	Li	Wageningen University & Research	Netherlands	Attendant
Shimizu	Toshiro	Takii Seed	Japan	Attendant
Shiose	Lumi	Universidade de São Paulo	Brazil	Attendant
Shohael	Abdullah	Jahangirnagar University	Bangladesh	Attendant
Shohat	Hagai	The Hebrew University of Jerusalem	Israel	Poster Presenter (STRp27)
Shoji	Tsubasa	RIKEN Center for Sustainable Resource Science	Japan	Attendant
Silva	Carolina	ESALQ/USP	Brazil	Attendant
Silva-Arias	Gustavo A.	Technical University of Munich	Germany	Oral Presenter (NETo03)
Silvar	Cristina	University of Coruña	Spain	Poster Presenter (BREp18)
Simanowitz	Marc	The Hebrew University of Jerusalem	Israel	Attendant
Simbaqueba	Jaime	Colombian Corporation for Agricultural Research - Agrosavia	Colombia	Attendant
Simon	Reinhard	Wageningen University & Research	Netherlands	Attendant
Sinbunyama	Itsarayot	Chia Tai Company Limited	Thailand	Attendant
Singh	Dharmendra	ACT	NA	Attendant
Singh	Jasdeep	Punjab Agricultural University	India	Attendant
Singh	Pradeep Kumar	East West Seed Company	India	Attendant
Singh	Vikas	NA	NA	Attendant
Sjoberg	Stephanie	Bayer Vegetable Seeds	USA	Attendant
Skaliter	Oded	The Hebrew University of Jerusalem	Israel	Attendant
Slaman	Ellen	Wageningen University & Research	Netherlands	Attendant
Śliwka	Jadwiga	Plant Breeding and Acclimatization Institute - National Research Institute	Poland	Attendant
Smith	Patrick	National Institute of Agricultural Research	Argentina	Attendant
Smith	Stacey	University Of Colorado Boulder	USA	Attendant
Smits	Henrikje	Leibniz Institute of Plant Biochemistry	Germany	Attendant
Snouffer	Ashley	The University of Georgia	USA	Oral Presenter (DEVo04)
Soares	Flávio	BioISI-FCUL	Portugal	Poster Presenter (BREp19)
Soares	Luana	Universidade Federal do Rio Grande do Sul (UFRGS)	Brazil	Poster Presenter (EVOp15)
Sohrawardy	Hosaain	Lal Teer Seed Ltd.	Bangladesh	Attendant
Solo	Nejra	Enza Zaden	Netherlands	Attendant
Solomon	Emmanuel	Cranfield University	UK	Attendant

Soltani	Ali	Bayer Crop Science	NA	Attendant
Sonawane	Prashant	Weizmann Institute of Science	Israel	Attendant
Song	Chao	Ben-Gurion University of the Negev	Israel	Attendant
Song	Lin	University of Wisconsin-Madison	USA	Attendant
Song	Yang	Utrecht University	Netherlands	Attendant
Sonneveld	Devon	Wageningen University & Research	Netherlands	Attendant
Sorensen	Iben	Cornell University	USA	Attendant
Soyk	Sebastian	University of Laussane (UNIL)	Switzerland	Oral Presenter (DEVop)
Spiegelman	Ziv	Agricultural Research Organization (ARO) Volcani Center	Israel	Attendant
Sreelakshmi	Yellamaraju	University of Hyderabad	India	Attendant
Srivastava	Anjil	Durham University	UK	Attendant
Stam	Remco	Technical University of Munich	Germany	Oral Presenter (EVOo04)
Stein	Nils	IPK Gatersleben	Germany	Attendant
Stevens	Danielle	University of California, Davis	USA	Attendant
Stockem	Julia	Solynta	Netherlands	Attendant
Strickler	Susan	Boyce Thompson Institute	USA	Chair (STR)
Stromvik	Martina	McGill University	Canada	Attendant
Struss	Darush	East West Seed Company	Thailand	Attendant
Stuttmann	Johannes	Martin Luther University Halle	Germany	Attendant
Su	Ying	Solynta	Netherlands	Attendant
Subode	Su	The Ohio State University	USA	Attendant
Sulli	Maria	ENEA	Italy	Poster Presenter (BREp20)
Sullmann	Julia	University of Bologna	Italy	Attendant
Sunarti	Sri	Wageningen University & Research	Netherlands	Attendant
Surveswaran	Siddharthan	CHRIST Deemed to be University	India	Attendant
Suzuki	Shoichi	Japan Tobacco Inc.	Japan	Attendant
Swinnen	Gwen	University of Laussane (UNIL)	Switzerland	Attendant
Szechtman	Alejandro	Hazera Seeds Ltd.	Israel	Attendant
Szepesi	Ágnes	University of Szeged	Hungary	Poster Presenter (STRp29)
Tai	Helen	Agriculture and Agri-Food Canada	Canada	Chair (BRE)
Taitano	Nathan	The University of Georgia	USA	Attendant
Takakura	Yoshimitsu	Japan Tobacco Inc.	Japan	Attendant
Takeuchi	Takanori	Japan Tobacco Inc.	Japan	Attendant
Takisawa	Rihito	Ryukoku university	Japan	Attendant
Takova	Katerina	University of Plovdiv	Bulgaria	Poster Presenter (BIOp09)
Tamura	Izumi	Utsunomiya University	Japan	Attendant
Tanaka	Kiwamu	Washington State University	USA	Attendant
Tang	Yaping	Xinjiang Academy of Agricultural Sciences and Huazhong Agriculture University	China	Attendant
Tavares Flores	Estefania	West Virginia University	USA	Poster Presenter (BREp21)
Taylor	Mark	The James Hutton Institute	UK	Attendant
Tecle	Isaak Yosief	Boyce Thompson Institute	USA	Attendant
Tehawkho	Sophia	Top Seeds International LTD	Israel	Attendant
Teitelbaum	Eliya	The Hebrew University of Jerusalem	Israel	Attendant
Termolino	Pasquale	CNR-IBBR, UOS Portici	Italy	Attendant
Thapa	Shree	University of California, Davis	USA	Attendant
Thawko	Tina	Top Seeds International LTD	Israel	Attendant
Therezan	Rodrigo	University of Amsterdam	Netherlands	Attendant
Thoen	Manus	Enza Zaden	Netherlands	Attendant
Thole	Vera	John Innes Centre	UK	Attendant
Thoris	Kai	Wageningen University & Research	Netherlands	Attendant
Thurgood	Luke	J.R. Simplot Company	USA	Attendant

Tieman	Denise	University of Florida	USA	Attendant
Tikunov	Yury	Wageningen University & Research	Netherlands	Oral Presenter (BREo02)
Tipu	Mohammad Monirul Hasan	Bangladesh Agricultural Research Institute	Bangladesh	Attendant
Tissier	Alain	Leibniz Institute of Plant Biochemistry	Germany	Attendant
Tnani	Hédia	IPT	Tunisia	Attendant
Tongyoo	Pumipat	Kasetsart University	Thailand	Attendant
Topcu	Yasin	The University of Georgia	USA	Poster Presenter (BREp22)
Toppino	Laura	Council for Agricultural Research and Economics (CREA)	Italy	Attendant
Torgeman	Shai	The Hebrew University of Jerusalem	Israel	Attendant
Torres Ascurra	Yerisf Carla	Wageningen University & Research	Netherlands	Attendant
Torres Montilla	Salvador	Centre for Research in Agricultural Genomics (CRAG)	Spain	Oral Presenter (NETo04)
Toruno	Tania	University of California, Davis	USA	Attendant
Tourdot	Edouard	INRAE	France	Attendant
Trepat	Felipe	Universidad Nacional de Rosario (UNR)	Argentina	Attendant
Trinh	Jessica	University of California, Davis	USA	Attendant
Tripodi	Pasquale	Council for Agricultural Research and Economics (CREA)	Italy	Oral Presenter (EVOo02)
Tsampalla	Afroditi	ELGO-DIMITRA	Greece	Attendant
Udagawa	Hisashi	Japan Tobacco Inc.	Japan	Attendant
Ullrich	Sarah	Goethe University Frankfurt	Germany	Attendant
Umemoto	Naoyuki	RIKEN Center for Sustainable Resource Science	Japan	Attendant
Ünal	Ali	NA	NA	Attendant
Underwood	Charles	Max Planck Institute for Plant Breeding Research	Germany	Attendant
Usadel	Björn	HHU Düsseldorf University	Germany	Attendant
Vaikuntapu	Papa Rao	ICAR-DGR	India	Attendant
Vainer	Andrii	Weizmann Institute of Science	Israel	Poster Presenter (STRp30)
Van 'T Hof	Pieter	Universidad San Francisco de Quito (USFQ)	Ecuador	Attendant
Van Der Hulst	Ron	Solynta	Netherlands	Attendant
Van Der Knaap	Esther	The University of Georgia	USA	Chair (DEV)
Van Der Sluis	Iris	Takii seed	Netherlands	Attendant
Van Der Vlies	Pieter	HZPC Research b.v.	Netherlands	Attendant
Van Der Weerden	Gerard	Radboud University Nijmegen	Netherlands	Attendant
Van Dingenen	Judith	University of Gent	Belgium	Attendant
Van Dun	Kees	Rijk Zwaan Breeding B.V.	Netherlands	Attendant
Van Eck	Joyce	Boyce Thompson Institute	USA	Chair (BIO)
Van Eck	Herman	Wageningen University & Research	Netherlands	Attendant
Van Haperen	Pauline	Keygene	Netherlands	Attendant
Van Haperen	Pauline	Keygene	Netherlands	Attendant
Van Leeuwen	Karina	East West Seed Company	Thailand	Attendant
Van Oord	Amanda	Rijk Zwaan Breeding B.V.	Netherlands	Attendant
Van Os	Martha	University of Amsterdam	Netherlands	Attendant
Vargas	Eliana	CONICET Argentina	Argentina	Attendant
Vazquez	Dana Valeria	IICAR-CONICET-UNR	Argentina	Attendant
Vazquez-Vilar	Marta	Instituto de Biologia Molecular y Celular de Plantas (IBMCP)	Spain	Poster Presenter (DEVp11)
Vecchio	Franco	Nunhems Italy srl	Italy	Attendant
Veltkamp	Vera	Wageningen University & Research	Netherlands	Attendant
Verbakel	Henk	BASF Vegetable Seeds	Netherlands	Attendant
Verdier	Jerome	INRAE	France	Attendant
Verweij	Walter	Enza Zaden	Netherlands	Attendant
Vidavski	Favi	Tomatech	Israel	Attendant
Vidavski	Tomer	The Hebrew University of Jerusalem	Israel	Attendant

Visconti	Sabina	University of Rome Tor Vergata	Italy	Attendant
Visser	Richard	Wageningen University & Research	Netherlands	Attendant
Vogelaar	Aat	Rijk Zwaan Breeding B.V.	Netherlands	Attendant
Vossen	Jack	Wageningen University & Research	Netherlands	Attendant
Vriezen	Wim	BASF Vegetable Seeds	Netherlands	Attendant
Wahl	Vanessa	Max Planck Institute of Molecular Plant Physiology (MPIPZ)	Germany	Attendant
Wan	Hongjian	Zhejiang Academy of Agricultural Sciences	China	Attendant
Wang	Bingsen	Huazhong Agricultural University	China	Attendant
Wang	Keke	INT-ENSAT	France	Attendant
Wang	Lulu	Southwest University	China	Attendant
Wang	Lulu	Southwest University	China	Attendant
Wang	Luyang	Institute of Genetics and Developmental Biology Chinese Academy of Sciences	China	Attendant
Wang	Rufang	Wageningen University & Research	Netherlands	Attendant
Wang	Xingang	Cold Spring Harbor Laboratory (CSHL)	USA	Attendant
Wang	Xulan	Wageningen University & Research	Netherlands	Attendant
Waterhouse	Peter	Queensland University of Technology (QUT)	Australia	Oral Presenter (BIOo01)
Wenjing	Yang	CAS Center for Excellence in Molecular Plant Sciences	China	Attendant
Wheeler	Lucas	University Of Colorado Boulder	USA	Poster Presenter (NETp08)
Wolpe	Yochai	Top Seeds International LTD	Israel	Attendant
Wolter	Daiana	Universidade Federal de Pelotas	Brazil	Attendant
Wolters	Anne-Marie	Wageningen University & Research	Netherlands	Attendant
Wolters	Pieter Jacobus (Jaap)	Wageningen University & Research	Netherlands	Attendant
Wormit	Alexandra	RWTH Aachen University	Germany	Attendant
Wu	Cheng-Chiang	National Taiwan University	Taiwan	Attendant
Wu	Hermione	ShungFong Gene Editing Research Institute	China	Attendant
Wu	Raquel	Universidade de São Paulo	Brazil	Attendant
Wu	Yi	Wageningen University & Research	Netherlands	Poster Presenter (BREp23)
Xiangyang	Xu	Northeast Agricultural University	China	Attendant
Xiao	Mengyuan	University of California, Davis	USA	Poster Presenter (BREp24)
Xico	Carlos Manuel	Bejo Guatemala	Guatemala	Attendant
Yada	Haruna	Utsunomiya university	Japan	Attendant
Yadav	Sunil Kumar	HM-Clause	India	Attendant
Yadgary	Liran	Hazera Seeds Ltd.	Israel	Attendant
Yamazaki	Akira	Kyoto University	Japan	Attendant
Yamazaki	Muneo	National Agriculture and Food Research Organization	Japan	Attendant
Yan	Zhe	Wageningen University & Research	Netherlands	Attendant
Yanar	Ertuğrul Gazi	NA	NA	Attendant
Yañez	Anahi	CIGEBIO- UNSJ/CONICET	Argentina	Attendant
Yang	Guoqian	Shanghai Jiao Tong university	China	Attendant
Yorinori	Newton	Cavendish Farms	Canada	Attendant
Yu	Jingwei	University of California, Davis	USA	Poster Presenter (BREp25)
Yuan	Guoliang	Beijing Academy of Agricultural and Forestry Sciences	China	Attendant
Zahn	Iris	Wageningen University & Research	Netherlands	Poster Presenter (DEVp12)
Zamanova	Gergana	CPSBB	Bulgaria	Attendant
Zamir	Dani	The Hebrew University of Jerusalem	Israel	Oral Presenter (BREop)
Zamora Zaragoza	Jorge	Rijk Zwaan Breeding B.V.	Netherlands	Attendant

Zebell	Sophia	Cold Spring Harbor Laboratory (CSHL)	USA	Attendant
Zelman	Alice	University of Connecticut	USA	Attendant
Zhang	Biyao	Beijing Institute of Genomics, CAS (China National Center for Bioinformation)	China	Attendant
Zhang	Lei	The University of Georgia	USA	Poster Presenter (BREp26)
Zhang	Ning	Boyce Thompson Institute	USA	Attendant
Zhang	Xiaoyue	Institute of Genetics and Developmental Biology Chinese Academy of Sciences	China	Attendant
Zhang	Yingying	Inner Mongolia University	China	Attendant
Zheng	Hui	Zhejiang University	China	Attendant
Zheng	Shuangshuang	Institute of Genetics and Developmental Biology Chinese Academy of Sciences	China	Attendant
Zhou	Enbai	CAS Center for Excellence in Molecular Plant Sciences	China	Attendant
Zhou	Jiaqi	University of California, Davis	USA	Poster Presenter (STRp31)
Zhou	Ming	Beijing Vegetable Research Center, Beijing Academy of Agriculture and Forestry	China	Attendant
Zhu	Jie	University of California, Davis	USA	Attendant
Zimnoch-Guzowska	Ewa	Plant Breeding and Acclimatization Institute - National Research Institute	Poland	Attendant
Zocca	Pietro	University of Amsterdam	Netherlands	Attendant
Zoli	Lisa	Consorzio Sativa Soc. Coop. Agricola	Italy	Attendant
Zouine	Mohamed	Toulouse-INP/ENSAT	France	Attendant