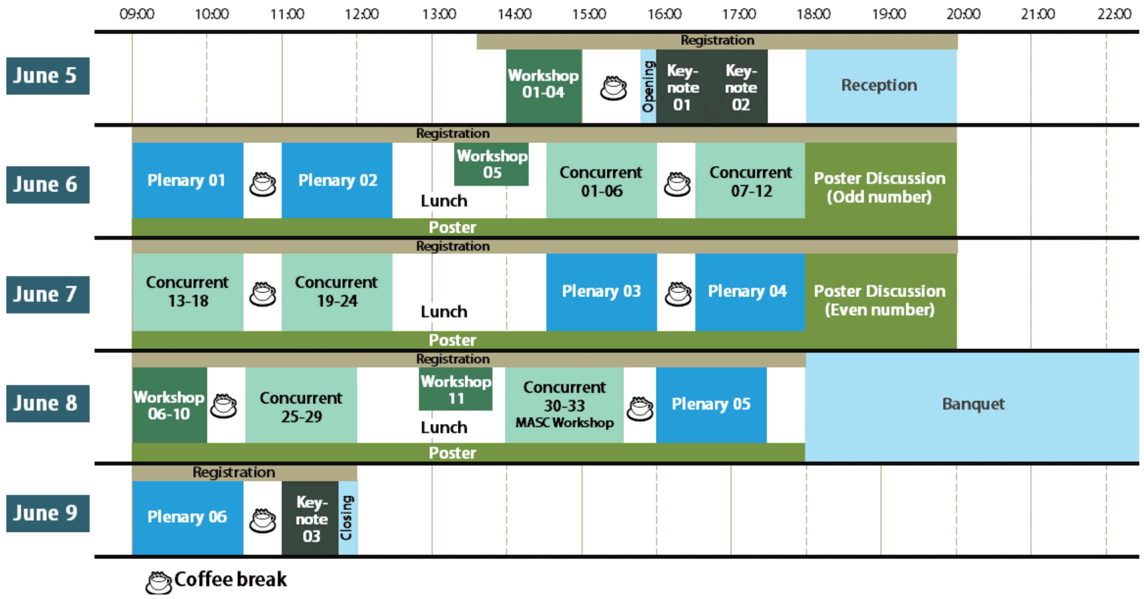
The 33rd International Conference on Arabidopsis Research



09:00 10:00 11:00 12:00 13:00 14:00 15:00 16:00 17:00 18:00 19:00 20:00 21:00 22:00

June 5	Registration Workshop 01-04 ☕ Opening Key-note 01 Key-note 02 Reception
June 6	Registration Plenary 01 ☕ Plenary 02 Lunch Workshop 05 Concurrent 01-06 ☕ Concurrent 07-12 Poster Discussion (Odd number) Poster
June 7	Registration Concurrent 13-18 ☕ Concurrent 19-24 Lunch Plenary 03 ☕ Plenary 04 Poster Discussion (Even number) Poster
June 8	Registration Workshop 06-10 ☕ Concurrent 25-29 Workshop 11 Lunch Concurrent 30-33 MASC Workshop ☕ Plenary 05 Banquet Poster
June 9	Registration Plenary 06 ☕ Key-note 03 Closing

☕ Coffee break

Day 1 (Mon. Jun. 5)

Workshop 01 Integration of engineering, plant sciences, and agricultural research for translational research

Application#: W04

Day 1: Mon. Jun. 5

Organized by: Ross Sozzani (North Carolina State University), Lucia Strader (Duke Universtiy)

This workshop focuses on the integration of engineering and biology for plant improvement. Networks of scientists that conduct basic and applied research are critical for advancing this field. The workshop aims to cover data acquisition, data intergration,and data mining while promoting knowledge transfer and skill sharing. Biotech-enabled plant advances incorporating whole-plant structure and physiology will be essential to solve global agriculture problems.

14:00 - 14:03 Opening remarks

14:03 - 14:18 **Integrating Engineering, Plant Sciences, and Agricultural Research for Translational Research: An Introduction to the Workshop and Case Study Presentation**
Ross Sozzani (North Carolina State University, USA) on-site, C000811

14:19 - 14:34 **Multi-scale modeling approaches for understanding plant and agronomic systems across biological scales**
Cranos Williams (North Carolina State University, USA) on-site, C000792

14:35 - 14:50 **The nexus of plant peptide-receptor modules and environmental adaptation**
Akie Shimotohno (Nagoya University, Japan) on-site, C000363

14:50 - 15:00 Closing remarks

Workshop 02 Coordinating and utilizing the rapidly growing collection of independently assembled Arabidopsis genomes

Application#: W07

Day 1: Mon. Jun. 5

Organized by: Magnus Nordborg (Gregor Mendel Institute, Austrian Academy of Sciences), Detlef Weigel (Max Planck Institute for Biology, Tübingen)

Advances in long-read sequencing technology have made it possible to complement the Arabidopsis reference genome with hundreds of independently assembled genomes. For these data to be useful to the community they need to be integrated with previously existing resources from the 1001 Genomes Project. We will discuss how this can be accomplished, and what we can learn from complete genome information on species-wide scale.

14:00 - 14:01 Opening remarks

14:01 - 14:10 **Rapid cycles of satellite homogenization and retrotransposon invasion drive Arabidopsis pancentromere evolution**
Ian Henderson (University of Cambridge, United Kingdom) on-site, C000775

14:11 - 14:20 **The pan-genome and local adaptation of Arabidopsis thaliana**
Jianquan Liu (Lanzhou University, China) on-site, C000629

14:21 - 14:30 **Assembling and Annotating Arabidopsis Genomes to Model Protein Abundance**
Richard Mott (University College London, United Kingdom) on-site, C000753

14:31 - 14:40 **The Actual Mobilome of Arabidopsis thaliana**
Anna Igolkina (GMI, Austria) on-site, C000536

14:41 - 14:50 **Benchmarking graph building pipeline on plant genome assemblies**
Zhigui Bao (Max Planck Institute for Biology Tübingen, Germany) on-site, C000511

14:51 - 15:00 **Challenges of annotating complex genes in the Arabidopsis long read genome collection**
Luisa Teasdale (Max Planck Institute - Department of Biology, Germany) on-site, C000688

Workshop 03 Systems biology of plant-microbes interactions

Application#: W08 Organized by: Shahid Mukhtar (University of Alabama at Birmingham)
Day 1: Mon. Jun. 5

A systems perspective on mechanisms of pathogen infection and plants' responses to such biotic stresses can lead to significant advances in plant biology and agriculture in general. This session will highlight exciting new discoveries being made in plant-pathogen interactions by leveraging functional genomics and systems biology approaches in the model system Arabidopsis and agronomically important crop plants. We will seek topics pertinent to plant receptor networks to perceive diverse pathogens, transcriptional gene regulatory networks at different scales (e.g. tissue/single cell), mechanisms of pathogen manipulation of host plants, and systemic outcomes of infection.

14:00 - 14:02 Opening remarks
14:02 - 14:15 **Spatial and systems biology of plant-microbe interactions**
Shahid Mukhtar (University of Alabama at Birmingham, USA) on-site, C000819
14:16 - 14:29 **MAMP and DAMP signalling contributes resistance to Fusarium graminearum in Arabidopsis**
Gopal Subramaniam (Agriculture and Agri-Food Canada, Canada) on-site, C000777
14:30 - 14:43 **Attraction of Herbivores for Survival from Virulent Pathogens in Arabidopsis**
Kazuha Mori (Nagoya University, Japan) on-site, C000658
14:44 - 14:57 **Functional or NAT? RNA control of receptor expression**
Adam Mott (University of Toronto - Scarborough, Canada) on-site, C000144
14:57 - 15:00 Closing remarks

Workshop 04 Molecular dialogues in reproductive development

Application#: W09 Organized by: Julia Santiago (University of Lausanne), Tetsuya Higashiyama (University of Tokyo)
Day 1: Mon. Jun. 5

The workshop will cover different aspects of molecular dialogues controling reproduction in plants.

14:00 - 14:01 Opening remarks
14:01 - 14:19 **Cell wall recognition and patterning by a sensor complex coordinates cell wall architecture and drives pollen tube expansion**
Julia Santiago (University of Lausanne, Switzerland) on-site, C000716
14:20 - 14:38 **Turning up the volume on intercellular communication during pollen tube reception**
Sharon Kessler (Purdue University, USA) on-site, C000353
14:39 - 14:57 **Multiple roles of aspartic endopeptidases ECS1 and ECS2 in fertilization**
Meng-xiang Sun (Wuhan University, China) on-site, C000229
14:57 - 15:00 Closing remarks

Opening

15:50 - 16:00 Representative of the ICAR2023 Organizing Committee

Keynote 01

16:00 - 16:45 **Transcriptional regulatory network of plant abiotic stress responses**
Kazuko Yamaguchi-Shinozaki (Tokyo University of Agriculture, Japan) on-site, I000014
Chaired by Motoaki Seki (RIKEN CSRS)

Keynote 02

16:45 - 17:30 **Regulation of Arabidopsis leaf growth and applications in crops**
Dirk Inzé (VIB Center for Plant Systems Biology, Belgium) on-site, I000010
Chaired by Keiko Sugimoto (RIKEN CSRS)

Reception

18:00 - 20:00

Day 2 (Tue. Jun. 6)

Plenary 01	**From single cells to an organism**
9:00 - 9:30	**Fast and invasive cell growth requires resilient cell wall assembly** Anja Geitmann (McGill University, Canada) on-site, I000013 Chaired by Keiji Nakajima (Nara Institute of Science and Technology)
9:30 - 10:00	**Mechanical conflict and cell polarity in de novo shoot initiation** Kalika Prasad (Indian Institute of Science Education and Research, India) on-site, I000007 Chaired by Ikram Blilou (King Abdullah University of Science and Technology)
10:00 - 10:30	**Understanding vascular development using chemical and single cell biology** Bert De Rybel (VIB/Ghent University, Belgium) on-site, I000008 Chaired by Ken Birnbaum (New York University)

Plenary 02	**Interactions between organisms**
11:00 - 11:30	**Leveraging DANGEROUS MIX Autoimmunity to Understand Host-Microbe Interactions** Eunyoung Chae (National University of Singapore, Singapore) on-site, I000023 Chaired by Satoko Yoshida (Nara Institute of Science and Technology)
11:30 - 12:00	**Overlapping and distinct pathogen effector recognition specificities conferred by independently evolved NLR proteins in plants** Kee Hoon Sohn (Seoul National University, Korea) on-site, I000016 Chaired by Yasuhiro Kadota (RIKEN CSRS)
12:00 - 12:30	**Understanding environmental influence on plant-pathogen interactions** Xiufang Xin (Center for Excellence in Molecular Plant Sciences, Institute of Plant Physiology and Ecology, Chinese Academy of Sciences; CEPAMS, Chinese Academy of Sciences-John Innes Center joint program, China) on-site, I000011 Chaired by Kei Hiruma (University of Tokyo)

Workshop 05	**Science as stories: From data to presentations. The untold story of your research.**
Application#: W13 **Day 2: Tue. Jun. 6** 13:15 -	Organized by: Belén Moro (Centre for Research in Agricultural Genomics (CRAG)) *The aim of the workshop is to learn how to prepare scientific presentations that convey a clear message and maximize the output of your research. Our framework combines storytelling with how the brain process oral information along with images. We will dissect the anatomy of a presentation and discuss what makes it memorable.*

Concurrent 01 Advances in plant nutrition under changing environment

Application#: C04
Day 2: Tue. Jun. 6

Organized by: Hatem Rouached (Michigan State University), Benoit Lacombe (CNRS)

Plants have evolved highly effective transport, sensing and signaling systems to ensure acquisition of sufficient minerals for growth and development. This session aims to share new results on newly identified genes/regulatory pathways or metabolites involved in the regulation of ion homeostasis in plants. These include, but are not limited to: (i) effects of limitation or excess of various macro- and microelements on plant growth capacity; (ii) effects of components of global climate changes (drought, CO2, heat, etc.) on the regulation of ions transport and assimilation.

14:30 - 14:37 **Plant growth stimulation by elevated CO2 depends on phosphorus homeostasis in chloroplasts**
Hatem Rouached (Michigan State University, USA) on-site, C000178

14:38 - 14:48 **Nutritional interactions in plants (N x P) and new type of GWAS providing full epistatic maps with a gene resolution.**
Gabriel Krouk (CNRS, France) on-site, C000783

14:49 - 15:01 **Plasticity of root permeability for nutrient acquisition**
Marie Barberon (University of Geneva, Switzerland) on-site, C000209

15:02 - 15:14 **BUZZ: An essential gene in post-initiation root hair growth and root architecture in response to nitrate**
Karen Sanguinet (Washington State University, USA) on-site, C000813

15:15 - 15:27 **Live transcription imaging of plant Pi starvation response**
Laurent Nussaume (CEA, France) on-site, C000157

15:28 - 15:38 **Nitrogen signaling mechanisms modulating root gravitropism: involvement of flowering repressor and peptide hormone signaling**
Hideki Takahashi (Michigan State University, USA) on-site, C000266

15:39 - 15:46 **Histone chaperone NAP1 proteins are involved in plant growth under nitrogen deficient conditions in Arabidopsis thaliana [Short Talk]**
Jie Linnan (Hokkaido University, Japan) on-site, C000670

15:47 - 15:54 **The genetic diversity provided by natural Arabidopsis accessions to identify potentially adaptive differences in root morphology and soil resource capture [Short Talk]**
Christian Hermans (Université libre de Bruxelles (ULB), Belgium) on-site, C000545

Concurrent 02 The environmentally responsive plant epigenome

Application#: C19
Day 2: Tue. Jun. 6

Organized by: Hong Qiao (University of Texas at Austin), Mark Zander (Rutgers, State University of New Jersey)

The environmental responsiveness of the plant epigenome is an emerging and fascinating research area. To shed new light on the underlying mechanisms, our speaker list covers exciting topics ranging from immediate impacts of stress over vernalization to technologies capturing epigenome dynamics.

14:30 - 14:32 Opening remarks

14:32 - 14:48 **Jasmonate signaling through the lens of epigenomics**
Mark Zander (Rutgers University, USA) on-site, C000802

14:49 - 15:05 **(Re)programming Cell Identity and Function in Response to intrinsic and extrinsic cues**
Doris Wagner (University of Pennsylvania, USA) on-site, C000787

15:06 - 15:22 **A DNA element to remember 'winter cold' in Arabidopsis**
Yuehui HE (Peking University, China) on-site, C000630

15:23 - 15:39 **TANDEM ZINC-FINGER/PLUS3 integrates light and temperature signalling in plant nuclear hubs.**
Eirini Kaiserli (University of Glasgow, Scotland, United Kingdom) on-site, C000119

15:40 - 15:49 **Sensory plastids in growth- and defense-related epigenetic phenotype adjustment [Short Talk]**
Ha Eun Jeh (Pennsylvania State University, USA) on-site, C000030

15:50 - 15:59 **Epidermal Cell Type-Specific Chromatin Dynamics Underlying Arabidopsis Heat Stress Memory [Short Talk]**
Daniel Slane (The University of Tokyo, Graduate School of Frontier Sciences, Department of Integrated Sciences, Laboratory of Integrated Biology, Japan) on-site, C000307

15:59 - 16:00 Closing remarks

Concurrent 03 New tools and applications in plant molecular genetics

Application#: C07 Organized by: Eilon Shani (Tel Aviv University)
Day 2: Tue. Jun. 6

The session will focus on developing new genetic and biotechnological discoveries in plant biology. This year's outstanding achievements in CRISPR biology (e.g., cell-type-specific genome editing, genome-scale sgRNA libraries), imaging mass spectrometry, TF interactomics, Cryo-electron microscopy of membrane proteins, flux metabolomics, plant phenomics, root micro-fluidics, super-resolution microscopy, and single-cell methylation, spatial transcriptomics and more have gained significant success worldwide. The session will allow scientists to present their most advanced discoveries and discuss the cutting technologies transforming plant science.

14:30 - 14:32 Opening remarks
14:32 - 14:47 **Identifying Transcriptional Activation Domains**
Lucia Strader (Duke University, USA) on-site, C000832
14:48 - 15:03 **Natural and artificial regulation of plant cell states**
Ryan Lister (University of Western Australia, Australia) on-site, C000830
15:04 - 15:19 **Time to sow: In planta CRISPR screens are ready**
Thomas Jacobs (VIB-UGent Center for Plant Systems Biology, Belgium) on-site, C000803
15:20 - 15:32 **Location, location, location: a system-wide assesment of subcellular protein localization in Arabidopsis roots by mass-spectrometry [Short Talk]**
Monique van Schie (Wageningen University, Netherlands) on-site, C000334
15:33 - 15:45 **A single-nucleus transcriptome atlas of seed-to-seed development in Arabidopsis [Short Talk]**
Travis Lee (Salk Institute, USA) on-site, C000090
15:46 - 15:58 **Multi-Knock – a multi-targeted genome-scale CRISPR toolbox to overcome functional redundancy in plants**
Eilon Shani (Tel Aviv University, Israel) on-site, C000779
15:58 - 16:00 Closing remarks

Concurrent 04 Cellular reprogramming in regeneration and development

Application#: C17 Organized by: Idan Efroni (The Hebrew University), Alexis Maizel (Heidelberg University)
Day 2: Tue. Jun. 6

At the heart of plants' developmental plasticity is the broad ability of their cells to undergo rapid and coordinated changes in cell identity and function. This is manifested during post-embryonic formation of new organs and in their ability to repair damaged organs and tissues. The session will focus on the parallels and convergences in cellular reprogramming mechanisms during development and regeneration.

14:30 - 14:32 Opening remarks
14:32 - 14:48 **Specific regulation on diverse regenerative responses in Arabidopsis**
Momoko Ikeuchi (Nara Institute of Science and Technology, Japan) on-site, C000404
14:49 - 15:05 **Born Again: The Early Stages of Plant Cell Reprogamming**
Kenneth Birnbaum (New York University, USA) on-site, C000778
15:06 - 15:22 **A molecular framework for regeneration competency in plants**
Abdul Kareem (Swedish University of Agricultural Sciences, Uppsala, Sweden) on-site, C000737
15:23 - 15:34 **Transcriptional Regulation of Cell-cell Movement During Root Tip Regeneration [Short Talk]**
Itay Cohen (Hebrew University of jerusalem, Israel) on-site, C000493
15:35 - 15:46 **It's All in the Timing: Enhancing Regeneration Efficiency Using Morphogenic Factors [Short Talk]**
Bastiaan Bargmann (Virginia Tech, USA) on-site, C000351
15:47 - 15:58 **Leaf epidermal patterning and fate determination [Short Talk]**
Chin-Min Ho (Institute of plant and microbial biology, Academia Sinica, Taiwan) on-site, C000022
15:58 - 16:00 Closing remarks

Concurrent 05 Organelle-organelle communication under stress

Application#: C20

Day 2: Tue. Jun. 6

Organized by: Eunsook Park (University of Wyoming), Inge De Clercq (VIB Center for Plant Systems Biology, Ghent University)

Organelles coordinate the complex intracellular metabolism in eukaryotic cells by imposing a physical barrier to sequester metabolites and macromolecules. The intricate organization of organelle-organelle communication under biotic and abiotic stresses is a recently emerging research topic and highly relevant to understanding the plant's responses to the changing environment. In this concurrent session, we will highlight the recent findings in a broad range of inter-organellar communication pathways under various stresses.

14:30 - 14:32 Opening remarks

14:32 - 14:42 **Chloroplast-nuclear communication in plant immunity**
Eunsook Park (University of Wyoming, USA) on-site, C000348

14:43 - 14:58 **Energy Metabolism vs. Moonlighting: A Balancing Act To Prevent Oxidative Stress**
Jennifer Selinski (Christian-Albrechts University Kiel, Germany) on-site, C000719

14:59 - 15:14 **Investigating how chloroplast-initiated intracellular signals control intercellular trafficking mediated by plasmodesmata in Nicotiana benthamiana**
Andrea Zanini (Donald Danforth Plant Science Center, USA) on-site, C000537

15:15 - 15:25 **Light-induced chloroplast biogenesis: photobodies control alternative promoter selection as a mechanism of nucleus-chloroplast communication [Short Talk]**
Chan Yul Yoo (University of Utah, USA) on-site, C000611

15:26 - 15:36 **405nm Photostimulation of the Endoplasmic Reticulum-Chloroplast Contact Site in Arabidopsis Hypocotyls Causes Rapid Cytoskeletal Depolymerization, Elevated Cytoplasmic Calcium, and Elevated Organellar ROS [Short Talk]**
Sara Maynard (Texas A&M University, USA) on-site, C000764

15:37 - 15:47 **Fuctional characterization of Arabidopsis thaliana Synaptotagmin1 domains using Tricalbin3 chimeras in Saccharomyces cerevisiae. [Short Talk]**
Francisco Benitez-Fuente (UNIVERSIDAD DE MALAGA, CSIC (IHSM), Spain) on-site, C000471

15:48 - 15:58 **Elucidating organelle-organelle and organelle-to-nucleus signaling pathways during plant stress responses**
Inge De Clercq (Ghent University / VIB UGent Center for Plant Systems Biology, Belgium) on-site, C000804

15:58 - 16:00 Closing remarks

Concurrent 06 Plant proteostasis: The dynamic proteome in plant cell signalling

Application#: C35

Day 2: Tue. Jun. 6

Organized by: Uli Bechtold (Durham University), Ari Sadanandom (Durham University)

This ICAR session has a dual purpose in highlighting recent discoveries in plant Proteostasis as well as the tools that have been made available through the Plant Proteostasis community to enable new researchers to explore the role of proteostasis in diverse aspects of plant development and response to environment.

14:30 - 14:32 Opening remarks

14:32 - 14:48 **SUMOcode: Deciphering how SUMOylation enables plants to adapt to their environment.**
Ari Sadanandom (University of Durham, United Kingdom) on-site, C000823

14:49 - 15:05 **Regulation of proteostasis and activation of Ca2+ channels by two distinct receptor kinases in maintaining immune integrity**
Libo Shan (Texas A&M University, USA) on-site, C000340

15:06 - 15:22 **Proximity labeling proteomics identified an inner nuclear membrane protein degradation system in plants**
Yangnan Gu (University of California, Berkeley, USA) on-site, C000085

15:23 - 15:39 **Regulation of the homeostasis of immune signaling proteins through proteasome-mediated degradation**
Xin Li (University of British Columbia, Canada) on-site, C000540

15:40 - 15:49 **Identification of interacting factors of the TARANI/ Ubiquitin-specific protease 14 (UBP14) in Arabidopsis thaliana [Short Talk]**
Anjana Hegde (Indian Institute of Science, India) on-site, C000514

15:50 - 15:59 **Molecular mechanism for peroxisomal protein transport via the ubiquitin system [Short Talk]**
Shoji Mano (National Institute for Basic Biology, Japan) on-site, C000280

15:59 - 16:00 Closing remarks

Concurrent 07 Arabidopsis and its translational research in the Global South

Application#: C32

Day 2: Tue. Jun. 6

Organized by: Gabriela Auge (CONICET - iB3, University of Buenos Aires), José Estevez (Fundación Instituto Leloir - CONICET, Argentina / Universidad Andrés Bello, Chile)

Arabidopsis research globally has provided invaluable tools to understand the plant world at different biological scales. A sizable proportion of that research is carried out by researchers in the Global South (i.e. countries located around the tropics and the Southern hemisphere), even though these countries face many political and budget limitations for scientific endeavours. This symposium aims to highlight the work of researchers from the Global South, oftentimes under-represented in international conferences, to bring a more diverse perspective to the meeting.

16:30 - 16:32 Opening remarks

16:32 - 16:47 **The power of haploid genetics in plants - Lessons from Arabidopsis thaliana**
Ravi Maruthachalam (Indian Institute of Science Education and Research(IISER), Thiruvananthapuram, India) on-site, C000588

16:48 - 17:03 **Plants to humans: Arabidopsis for translational research**
Sridevi Sureshkumar (Monash University, Australia) on-site, C000109

17:04 - 17:19 **TOC1 is a direct regulator of the Arabidopsis defence response against necrotrophic pathogens**
Robert Ingle (University of Cape Town, South Africa) on-site, C000495

17:20 - 17:29 **Role of the Arabidopsis AtbZIP63 transcription factor stability in energy management [Short Talk]**
Pamela Carlson (University of Campinas, Brazil) on-site, C000141

17:30 - 17:39 **NLP7 is a central integrator of transcription networks in nitrogen signaling and drought stress [Short Talk]**
Jose Alvarez (Centro de Biotecnologia Vegetal, Facultad de Ciencias de la Vida, Universidad Andres Bello, Santiago 8370186, Chile) on-site, C000520

17:40 - 17:49 **A B-Box protein suppresses flowering in Arabidopsis through multi-level regulation of the photoperiod pathway [Short Talk]**
Rahul Puthan Valappil (Indian Institute of Science Education and Research (IISER), India) on-site, C000350

17:50 - 17:59 **What did the grasses gain by losing PEAPOD? Evolution and conserved functionality of organ size and shape regulator PEAPOD [Short Talk]**
Ruth Cookson (AgResearch Ltd / University of Waikato, New Zealand) on-site, C000277

17:59 - 18:00 Closing remarks

Concurrent 08 Understanding circadian regulation in unpredictable environments

Application#: C05

Day 2: Tue. Jun. 6

Organized by: Antony Dodd (John Innes Centre), Tokitaka Oyama (Kyoto University)

Circadian clocks provide a temporal structure within plants, which contributes their responses to the fluctuating environment. Understanding how the circadian clock adapts plant physiology and development to environmental fluctuations forms a crucial part of forecasting the responses of plants-including crops- to an increasingly unpredictable climate.

16:30 - 16:32 Opening remarks

16:32 - 16:46 **Integration of circadian and environmental cues**
Antony Dodd (John Innes Centre, United Kingdom) on-site, C000793

16:47 - 17:01 **Behaviors of cell-autonomous- and non-cell-autonomous circadian rhythms in the plant body**
Tokitaka Oyama (Kyoto University, Graduate School of Science, Japan) on-site, C000833

17:02 - 17:16 **A spatial model of the plant clock reveals design principles for coordinated timing under noisy environments**
James Locke (University of Cambridge, United Kingdom) online, C000746

17:17 - 17:31 **Gene expression noise reduction for a robust circadian clock in Arabidopsis**
Shu-Hsing Wu (Institute of Plant and Microbial Biology, Academia Sinica, Taiwan) on-site, C000628

17:32 - 17:46 **Molecular mechanisms underlying light-induced resetting of the circadian clock in the green alga Chlamydomonas**
Takuya Matsuo (Nagoya University, Japan) on-site, C000720

17:47 - 17:57 **Quantity regulation of TOC1 and PRR5 for temperature compensation in the Arabidopsis circadian clock [Short Talk]**
Akari Maeda (Nagoya university, Japan) on-site, C000653

17:57 - 18:00 Closing remarks

Concurrent 09 Guard cell signalling and metabolism

Application#: C23
Day 2: Tue. Jun. 6

Organized by: Diana Santelia (ETH Zurich), Toshinori Kinoshita (Nagoya University)

Over the past few years, it has become evident that guard cell signalling and membrane ion transport are tightly coordinated with the metabolic changes occurring within the guard cells. How this intricate network is regulated at the molecular level is a fascinating question with global influence. In our session, we will discuss some of the most recent breakthrough discoveries on this topic.

16:30 - 16:32 Opening remarks

16:32 - 16:40 **Light regulation of stomatal movement and plasma membrane H+-ATPase in guard cells**
Toshinori Kinoshita (ITbM, Nagoya University, Japan) on-site, C000748

16:41 - 17:06 **Sugars are mesophyll messengers regulating stomatal opening under red light**
Yotam Zait (Hebrew University of Jerusalem, Israel) on-site, C000834

17:07 - 17:32 **Hydrogen peroxide promotes stomatal development and opening through inducing the nuclear localization of KIN10**
Mingyi Bai (Shandong University, China) on-site, C000231

17:33 - 17:41 **Investigating the Role of Carbohydrate Metabolism in Bacterial-Triggered Stomatal Movements Using the Model System Arabidopsis thaliana and Pseudomonas syringe pv tomato [Short Talk]**
Lucia Piro (ETH Zurich, Switzerland) on-site, C000435

17:42 - 17:50 **Phosphorylation of WD-repeat protein WDR by phototropins is essential for starch degradation to promote stomatal opening [Short Talk]**
Shota Yamauchi (Yamaguchi University, Japan) on-site, C000214

17:51 - 17:59 **Stomatal CO2/bicarbonate Sensor Consists of Two Interacting Protein Kinases HT1 and MPK4/12 in Arabidopsis [Short Talk]**
Yohei Takahashi (Nagoya University, Japan) on-site, C000543

17:59 - 18:00 Closing remarks

Concurrent 10 Development and environmental responses: What are kept and what are lost over the evolutionary history of land plants

Application#: C14
Day 2: Tue. Jun. 6

Organized by: Daisuke Urano (Temasek Life Sciences Laboratory), Kimitsune Ishizaki (Kobe University)

Developmental strategies for adaptations to ever-changing environment have been diversified during the long history of land plant evolution. This session focuses on developmental processes and stress responses commonly present or different between the bryophyte models and Arabidopsis, and discusses how the complexity, specificity, and divergence have evolved.

16:30 - 16:31 Opening remarks

16:31 - 16:49 **Adapting to Adversity: Evolutionary Insights into G-protein Networks and Stress Readiness in Land Plants**
Ting-Ying Wu (IPMB, AS, Taiwan) on-site, C000111

16:50 - 17:08 **Reproductive strategy control by a Marchantia GRAS transcriptional regulator**
Sebastian Schornack (University of Cambridge, Sainsbury Laboratory, United Kingdom) on-site, C000693

17:09 - 17:27 **Functional evolution of thermospermine in land plants**
Miguel Blázquez (IBMCP (CSIC-U Politècnica de València), Spain) on-site, C000776

17:28 - 17:46 **Cross-stress gene expression atlas of Marchantia polymorpha reveals the hierarchy and regulatory principles of abiotic stress responses**
Marek Mutwil (Nanyang Technological University, Singapore) on-site, C000270

17:47 - 17:59 **Analysis of stem cell-promoting CLE peptide signaling in the shoot apical meristems of land plants [Short Talk]**
Yuki Hirakawa (Gakushuin University, Japan) on-site, C000664

17:59 - 18:00 Closing remarks

Concurrent 11 Role of biomolecular condensates in abiotic stress signaling

Application#: C24

Organized by: Monika Chodasiewicz (King Abdullah University of Science and Technology (KAUST)), Emilio Gutierrez-Beltran (University of Sevilla)

Day 2: Tue. Jun. 6

The session focuses on the role of biomolecular condensates in abiotic stress response. Abstracts related to BMC, formation mechanism, composition of BMC under abiotic stress are very welcome.

16:30 - 16:35 Opening remarks

16:35 - 16:55 **Functional idling in membrane-bound condensates**
Panagiotis Moschou (University of Crete, Greece) on-site, C000243

16:56 - 17:16 **Uncovering the function of FLOE1, a phase separating and prion-like hydration sensor protein involved in seed germination**
Sterling Field (Carnegie Institution for Science, USA) on-site, C000805

17:17 - 17:30 **Control of meiosis under heat stress [Short Talk]**
Arp Schnittger (University of Hamburg, Germany) on-site, C000047

17:31 - 17:44 **Heat-regulated phosphorylation of TOT43 is a switch for stress granule association to contribute to heat tolerance in Arabidopsis [Short Talk]**
Shao-Li Yang (VIB-UGent Center for Plant Systems Biology, Belgium) on-site, C000046

17:45 - 17:58 **Characterization of Arabidopsis ECT family in stress tolerance and stress granules assembly [Short Talk]**
Nicolas Figueroa Fuentealba (King Abdullah University of Science and Technology (KAUST), Saudi Arabia) on-site, C000249

17:58 - 18:00 Closing remarks

Concurrent 12 Translation regulation in plants

Application#: C34

Organized by: Catharina Merchante (Universidad de Málaga), Gemma Sans-Coll (Universidad de Málaga), Jose Antonio Duarte-Conde (Universidad de Málaga)

Day 2: Tue. Jun. 6

Translation is an integral component of the Central Dogma of molecular biology. Although its general mechanism is relatively well understood, little is known about the selective translation of specific mRNAs and its regulation. The emergence of technologies that allow in-depth study of translation resulted in new plant-specific translation mechanisms being unveiled and translationally-regulated mRNAs have been found to be key in the plant's adaptational responses. Recent examples have demonstrated the biological significance of translational regulation in plants and its potential in the generation of new, powerful biotechnological tools.

16:30 - 16:32 Opening remarks

16:32 - 16:44 **Uncovering the Hidden Message of mRNAs: The Exploration of Alternative Translation Initiation Sites**
Ming-Jung Liu (Academia Sinica, Taiwan) on-site, C000454

16:45 - 16:57 **Diel and Circadian Dynamics of Translation in Arabidopsis via Ribosome Profiling**
Michael Ting (Max Planck Institute of Molecular Plant Physiology, Germany) on-site, C000427

16:58 - 17:10 **Dynamic regulation of translation upon pathogen infection**
Jinlong Wang (Duke University, USA) online, C000221

17:11 - 17:22 **NMD and translation of intergenic splicing-mediated polycistronic transcripts [Short Talk]**
Yukio Kurihara (Department of Life Sciences, Graduate School of Arts and Sciences, The University of Tokyo, Japan) on-site, C000390

17:23 - 17:34 **Plant miRNA-target 3′-end pairing affects miRNA-mediated translational repression [Short Talk]**
Ho-Ming Chen (Academia Sinica, Taiwan) on-site, C000247

17:35 - 17:46 **Deciphering the role of specialized ribosomes in plants´ translation efficiency [Short Talk]**
Jose Duarte-Conde (University of Málaga, Spain) on-site, C000512

17:47 - 17:58 **Translation-coupled Epigenetic Regulation of Transposable Elements in Plants [Short Talk]**
Zhen Lei (CAS Center for Excellence in Molecular Plant Sciences, China) on-site, C000064

17:58 - 18:00 Closing remarks

Poster discussion (Odd number)

18:00 - 20:00

Day 3 (Wed. Jun. 7)

Concurrent 13 Integration of Arabidopsis and crop research in plant biotic interactions

Application#: C33

Day 3: Wed. Jun. 7

Organized by: Yusuke Saijo (Nara Institute of Science and Technology), Kenichi Tsuda (Huazhong Agricultural University)

This session will present and discuss comparative and integrative studies on Arabidopsis and crop plants in different areas of plant biotic interactions. We hope this helps to stimulate a new way of thinking, elucidate new molecular principles and develop solutions for SDGs, in the research field and beyond.

Time	Program
9:00 - 9:01	Opening remarks
9:01 - 9:15	**Mitigation of plant growth-defense trade-off through damage-associated Pep peptides and receptors under phosphate deficiency** Yusuke Saijo (Nara Institute of Science and Technology, Japan) on-site, C000678
9:16 - 9:31	**Interactions between plants and root microbiome in rice and Arabidopsis** Yang Bai (Institute of Genetics and Developmental Biology, China) online, C000816
9:32 - 9:46	**RCR1, a pericycle-expressed ion channel, safe-guards the stele and confers broadspectrum resistance to clubroot** Wei Wang (Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, China) on-site, C000796
9:47 - 10:01	**Studying the genetic basis for plant-microbe associations using a synthetic biology approach [Short Talk]** Jose Dinneny (Stanford University, USA) on-site, C000591
10:02 - 10:13	**Drought Recovery Induced Immunity Confers Pathogen Resistance [Short Talk]** Natanella Illouz-Eliaz (Salk Institute, USA) on-site, C000252
10:14 - 10:29	**Plant immunity and microbiota tame potentially harmful commensal bacteria** Kenichi Tsuda (Huazhong Agricultural University, China) on-site, C000799
10:29 - 10:30	Closing remarks

Concurrent 14 Stress-induced signalling peptides

Application#: C36

Day 3: Wed. Jun. 7

Organized by: Nijat Imin (Western Sydney University), Cyril Zipfel (University of Zurich)

The workshop focuses on plant peptides and receptors, other components of signalling pathways and downstream signalling events in plant development, adaptation, and in particular plant response to the environment.

Time	Program
9:00 - 9:01	Opening remarks
9:01 - 9:15	**Regulation and execution of plant immunity by phytocytokines** Cyril Zipfel (Institute of Plant and Microbial Biology, University of Zurich, Switzerland) on-site, C000115
9:16 - 9:30	**TBA** (Alisa Huffaker) (TBA, TBA) TBA, TBA
9:31 - 9:45	**Elucidating the peptide-receptor signalling pathways that regulates root architecture and nitrogen acquisition** Nijat Imin (University of Auckland, New Zealand) on-site, C000684
9:46 - 10:00	**Coordination of cell surface immunity and N limitation by CEP-mediated signalling** Martin Stegmann (Technical University Munich, Germany) on-site, C000040
10:01 - 10:10	**A cell wall-modifying gene-dependent CLE peptide transport in conferring drought resistance [Short Talk]** Satoshi Endo (Kyoto University of Advanced Science, Japan) on-site, C000077
10:11 - 10:20	**An Evolutionarily Conserved Long-distance Migrating Peptide Regulates Lignin Biosynthesis Pathway and Plant Immunity [Short Talk]** Ying-Lan Chen (National Cheng Kung University, Taiwan) on-site, C000701
10:21 - 10:30	**The phytocytokine AtCAPE9 and its receptor AtCAPER1 functions on plant systemic stomatal immunity [Short Talk]** Chi-Hsin Chang (Agricultural Biotechnology Research Center, Academia Sinica, Taiwan) on-site, C000016

Concurrent 15 Arabidopsis relatives from laboratories to natural fields

Application#: C16 **Day 3: Wed. Jun. 7**	Organized by: Kentaro K. Shimizu (University of Zurich), Hiroshi Kudoh (Kyoto University) *The phenotype of wild-type and mutants in natural fields is often distinct from that in regulated laboratory conditions. Recently, Arabidopsis and its relatives are emerging as model systems to understand gene function in naturally fluctuating environments, which is coined in natura. The workshop will welcome researchers from diverse disciplines including long-term regular monitoring of gene expression, epigenome and phenome in natura, predicting plant responses to global climate changes, ecological networks of diverse herbivores and pathogens, laboratory experiments capturing natural complexity such as the food web.*
9:00 - 9:03	Opening remarks
9:03 - 9:22	**A keystone genes underlies the persistence of an experimental food web** Matthew Barbour (Université de Sherbrooke, Canada) on-site, C000770
9:23 - 9:42	**Seasonality of virus-host interactions between Turnip mosaic virus and Arabidopsis halleri during the long-term infection in a natural environment** Mie Honjo (Center for Ecological Research, Kyoto University, Japan) on-site, C000402
9:43 - 10:02	**Keystone pairs of Arabidopsis accessions increase plant resistance to field herbivory** Yasuhiro Sato (University of Zurich, Switzerland) on-site, C000118
10:03 - 10:14	**Rapid evolution in Arabidopsis thaliana in global field experiments in the pan-genomic era [Short Talk]** Xing Wu (Carnegie Institution for Science, USA) on-site, C000635
10:15 - 10:26	**Time-series field phenotyping system PlantServation using machine learning revealed seasonal pigment fluctuation trends in diploid and polyploid Arabidopsis [Short Talk]** Toshiaki Tameshige (KIBR, Yokohama City Univ., Japan) on-site, C000567
10:26 - 10:30	Closing remarks

Concurrent 16 Plant epigenetics and chromatin dynamics

Application#: C01 **Day 3: Wed. Jun. 7**	Organized by: Robert Schmitz (University of Georgia), Xuehua Zhong (Washington University, St. Louis) *Chromatin modifications have emerged as an important regulatory mechanism for versatile biological processes. Although the DNA in each nucleus of an individual is essentially identical, the manner in which it is interpreted by the cell is dependent on its spatial and environmental context. Research incorporating innovative methods to unravel these mechanisms as well as those that incorporate the study of histone and DNA modifications, transcription factor dynamics, small RNAs, and chromatin structure will be featured within this session.*
9:00 - 9:01	Opening remarks
9:01 - 9:15	**Molecular basis of non-CG methylation landscape in plants** Xuehua Zhong (Washington University in St. Louis, USA) on-site, C000145
9:16 - 9:30	**Dynamic regulatory mechanism of H3K27me3 demethylase REF6 responding to environment** Xiaofeng Cao (Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, China) on-site, C000861
9:31 - 9:45	**Crosstalk among epigenetic marks during establishment of heterochromatin** Taiko To (The University of Tokyo, School of Science, Japan) on-site, C000376
9:46 - 10:00	**An evolutionary epigenetic clock in plants** Frank Johannes (Technical University of Munich, Germany) on-site, C000233
10:01 - 10:10	**Distinct chromatin signatures in the Arabidopsis male gametophyte [Short Talk]** Zhe Wu (Southern University of Science and Technology, China) on-site, C000336
10:11 - 10:20	**Erasure of Epigenetic Memory in Arabidopsis Flowering Control [Short Talk]** Toshiro Ito (Nara Institute of Science and Technology, Japan) on-site, C000580
10:21 - 10:30	**Temporal expression of BLADE-ON-PETIOLE 1 and 2 in successive leaves define the shape of their lamina [Short Talk]** Mingli Xu (University of South Carolina, USA) on-site, C000099

Concurrent 17 Hidden messages of RNAs for environmental responses

Application#: C22
Day 3: Wed. Jun. 7

Organized by: Ming-Jung Liu (Academia Sinica), Misato Ohtani (University of Tokyo)

How do the regulatory networks between environmental factors and RNA molecules trigger plant physiological and stress responses? This concurrent session will feature the recent advances in RNA sequences- and structure-based strategies for regulating gene expression. How plant mRNAs produce novel proteins, how non-coding RNAs and RNA-binding proteins regulate RNA fates, and how RNA functionalities are diversified both at genome-wide and single-molecule levels will be discussed.

9:00 - 9:02	Opening remarks
9:02 - 9:15	**Long non coding RNAs modulate the transcriptome by modifying alternative splicing regulations in Arabidopsis** Martin Crespi (Institute of Plant Sciences Paris Saclay IPS2, France) online, C000417
9:16 - 9:29	**Plants can sense and respond to environmental stress via pre-mRNA splicing regulation** Misato Ohtani (The University of Tokyo, Japan) on-site, C000416
9:30 - 9:43	**RNA structure, a hidden regulator in living cells** Yiliang Ding (John Innes Centre, United Kingdom) on-site, C000060
9:44 - 9:57	**Prevalent Unannotated ORFs Revealed by Improved Super-Resolution Ribosome Profiling** Polly Hsu (Michigan State University, USA) online, C000530
9:58 - 10:11	**Ribosomal RNA turnover and cellular homeostasis** Gustavo MacIntosh (Iowa State University, USA) on-site, C000747
10:12 - 10:19	**Arabidopsis DXO1, a decapping enzyme for NAD-capped RNAs, activates RNMT1 to methylate the mRNA guanosine cap [Short Talk]** Chen Xiao (HongKong Baptist University, Hong Kong) on-site, C000342
10:20 - 10:27	**siRNAs derived from nitrate reductases, NIA1 and NIA2, play vital roles in growth and stress adaptation [Short Talk]** Yan Yan (Southern University of Science and Technology, China) on-site, C000171
10:27 - 10:30	Closing remarks

Concurrent 18 Making contacts: Membrane contact sites between plant organelles

Application#: C08
Day 3: Wed. Jun. 7

Organized by: Joe McKenna (University of Warwick), Emily Breeze (University of Warwick)

Membrane contact sites (MCSs) are defined as areas of close apposition and tethering between the membranes of two organelles but crucially, the membranes do not fuse. These sites function as specific microdomains for the bi-directional exchange of molecular cargo and are linked to the propagation of intracellular signals enabling a coordinated cellular response to internal and external cues. This session will bring together plant cell biologists researching the molecular mechanisms of MCS tethers using new experimental tools and imaging techniques, with plant physiologists and pathologists interested in the wider role of MCSs in developmental and stress signalling.

9:00 - 9:02	Opening remarks
9:02 - 9:20	**Near-UV light signaling at the chloroplast-endoplasmic reticulum-plasma membrane contact site.** Lawrence Griffing (Texas A&M University, USA) on-site, C000762
9:21 - 9:39	**Plant endoplasmic reticulum-membrane contact sites and selective autophagy** Pengwei Wang (Huazhong Agricultural University, China) on-site, C000444
9:40 - 9:58	**Lipid transport at chloroplast-mitochondria contact sites in Arabidopsis thaliana** Morgane Michaud (Laboratoire de Physiologie Cellulaire et Végétale, CNRS, UGA, INRAE, CEA, France) on-site, C000438
9:59 - 10:17	**Structure and functions of plant synaptotagmins** Miguel Botella (Instituto de Hortofruticultura Subtropical y Mediterránea UMA-CSIC, Spain) on-site, C000329
10:18 - 10:23	**SEED LIPID DROPLET PROTEIN 1 and 2 and LD-PLASMA MEMBRANE ADAPTOR form a lipid droplet-plasma membrane contact site that might play a role under stress [Short Talk]** Janis Dabisch (Uni Münster, Germany) on-site, C000486
10:24 - 10:29	**The role of DGK1 and DGK2 in Membrane Contact Sites and Stress Tolerance [Short Talk]** Selene Garcia-Hernandez (Universidad de Malaga Spain, Spain) on-site, C000522
10:29 - 10:30	Closing remarks

Concurrent 19 Temporal regulation of environmental responses, growth, and development

Application#: C09

Day 3: Wed. Jun. 7

Organized by: Takato Imaizumi (University of Washington), Dawn Nagel (University of California, Riverside)

Plant cells respond to the same types of stimuli differently depending on when (time of the day, season, developmental ages, etc.), how often (frequency, gradual changes, and stochasticity), and how long (duration – secs, mins, hours, days, etc. - and kinetics) they were given. In this session, we will discuss plant responses (from cellular to developmental) that are impacted by environmental stress and regulated by time in different scales and context.

11:00 - 11:02	Opening remarks
11:02 - 11:17	**The induction of florigen FLOWERING LOCUS T gene is controlled by phytochrome A high-irradiance response and external coincidence mechanism under natural long-day conditions** Takato Imaizumi (University of Washington, USA) on-site, C000184
11:18 - 11:33	**Cold tolerance of membranes is a matter of timing and metabolic state – not just a saturation story** Rebecca Roston (University of Nebraska-Lincoln, USA) on-site, C000539
11:34 - 11:49	**Circadian effects in seconds, minutes, hours, weeks and months.** Alex Webb (University of Cambridge, United Kingdom) on-site, C000106
11:50 - 11:59	**Phloem cells - from single cell transcriptomics to development and function [Short Talk]** Jiyun Kim (Heinrich Heine University Düsseldorf, Germany) on-site, C000504
12:00 - 12:09	**Nitrogen-responsive SnRK1-FBH4 module affects flowering time and metabolism in Arabidopsis [Short Talk]** Miho Sanagi (Hokkaido University, Japan) on-site, C000021
12:10 - 12:19	**Rational approaches to synchronizing germination in seed populations [Short Talk]** Liam Walker (University of Warwick, United Kingdom) on-site, C000453
12:20 - 12:29	**A Comparative Study of Adaptive Stress Tolerance in the Brassicaceae Family [Short Talk]** Andrea Ramirez (Stanford University, USA) on-site, C000050
12:29 - 12:30	Closing remarks

Concurrent 20 Interdisciplinary approaches applied to plasmodesmata research

Application#: C15

Day 3: Wed. Jun. 7

Organized by: Yoselin Benitez-Alfonso (Centre for Plant Sciences. University of Leeds)

Plasmodesmata provide a route for the transport of signalling proteins and RNAs, metabolites and hormones to coordinate cellular functions within tissues and across distant organs. This session aims to uncover the broad range of interdisciplinary approaches that have been recently applied to understand plasmodesmata formation and function. We will hear from researchers combining genetic and bioorthogonal chemistry approaches, and physico mechanical models to dissect plasmodesmata function as well as developing new devices and using interfamily grafts and bryophytes to follow Plasmodesmata development and their role in multicellularity. We will also discuss the potential of engineering this mechanism to improve crops in a changing environment

11:00 - 11:01	Opening remarks
11:01 - 11:15	**Plasmodesmata walls: a study of the mechanical and structural properties that control their biological function** Yoselin Benitez-Alfonso (Centre for Plant Sciences. University of Leeds, United Kingdom) on-site, C000349
11:16 - 11:30	**The development of a microfluidic chip for entrapping tobacco BY-2 cells has enabled the analysis of plasmodesmata permeability using cultured cells in real-time.** Ken-ichi Kurotani (Nagoya Univ. Bioscience and Biotechnology Center, Japan) on-site, C000478
11:31 - 11:45	**Regulation of brassinosteroid homeostasis in the Arabidopsis root** Jenny Russinova (VIB-UGent, Belgium) on-site, C000468
11:46 - 12:00	**Environmental fluctuation and regulation of intercellular communication in the moss, Physcomitrium patens** Tomomichi Fujita (Hokkaido University, Japan) on-site, C000738
12:01 - 12:10	**A long-distance top-down movement of a transcription factor regulating the root phloem development [Short Talk]** Ji-Young Lee (Seoul National University, Republic of Korea) on-site, C000204
12:11 - 12:20	**A novel mechanism for plasmodesmata mediated cell-cell communication in plants [Short Talk]** Marija Smokvarska (CNRS, France) on-site, C000028
12:21 - 12:30	**Cellular adaptations for long-distance transport through the phloem sieve tube [Short Talk]** Lothar Kalmbach (University of Lausanne, Department of Plant Molecular Biology, Switzerland) on-site, C000519

Concurrent 21 Molecular signaling in plant-insect interactions

Application#: C13

Organized by: Jyothilakshmi Vadassery (National Institute of Plant Genome Research (NIPGR)), Gen-Ichiro Arimura (Tokyo University of Science)

Day 3: Wed. Jun. 7

Molecular signaling in plant defense against herbivory is an emerging area of study with identity of receptors, channels and early signaling genes that connects it to jasmonate pathway relatively unknown. The regulation of phytohormone and glucosinolate pathway by various signaling components are also unexplored. The session will cover the latest discoveries in the field

11:00 - 11:01 Opening remarks

11:01 - 11:17 **Geographic, Ecological and Transcriptional Forces Shaping Glucosinolate Defense Metabolite Variation**
Daniel Kliebenstein (University of California, Davis, USA) on-site, C000185

11:18 - 11:34 **Plant defense system in arabidopsis-Spodoptera interactions**
Gen-ichiro Arimura (Tokyo University of Science, Japan) on-site, C000023

11:35 - 11:51 **Hunting for insect secreted proteins that modulate plant immunity: Spodoptera litura- Arabidopsis interaction as a model system**
Jyothilakshmi Vadassery (National Institute of Plant Genome Research(NIPGR), Delhi, India) on-site, C000483

11:52 - 12:08 **Damage-activated proteolysis as a potential key player in the plant wound response**
Simon Stael (Swedish University of Agricultural Sciences, Sweden) on-site, C000319

12:09 - 12:18 **CIRCADIAN CLOCK-ASSOCIATED1 (CCA1) controls resistance to aphid by altering indole glucosinolate production [Short Talk]**
Keyan Salzman (Texas A&M University, USA) on-site, C000237

12:19 - 12:28 **Is Ca2+-induced activation of Arabidopsis lipoxygenase 2 involved in green leaf volatile burst? [Short Talk]**
Kenji Matsui (Yamaguchi University, Japan) on-site, C000489

12:28 - 12:30 Closing remarks

Concurrent 22 Molecular condensation for reproductive and biotic stress regulation: From cell biology to biophysical mechanism

Application#: C03

Organized by: Yansong Miao (Nanyang Technological University), Yangnan Gu (University of California Berkeley)

Day 3: Wed. Jun. 7

Biomolecular condensation (BMC) has emerged as a critical regulatory mechanism that dynamically tunes the constituents and biophysical properties of signaling complexes during plant response to diverse developmental and environmental cues. This session focuses on BMC-mediated signaling research that integrates advanced imaging, biochemical, biophysical, and mathematical approaches to understand the spatiotemporal regulation of plant immune responses and reproduction.

11:00 - 11:13 **Molecular Condensation at Host-Pathogen Interface for Plant Immunity**
Yansong Miao (Nanyang Technological University SIngapore, Singapore) on-site, C000123

11:14 - 11:34 **Formation of NPR1 condensates promotes cell survival during the plant immune response**
Xinnian Dong (Howard Hughes Medical Institute and Duke University, USA) on-site, C000790

11:35 - 11:50 **Dynamic proteostasis and protein condensation in malectin-like receptor kinase-mediated activation of an intracellular immune receptor**
Ping He (Texas A&M University, USA) on-site, C000347

11:51 - 12:06 **Phenolic acid-induced stress granule formation mediates plant interspecific competition**
Wei Wang (Peking University, China) on-site, C000045

12:07 - 12:22 **The compaction of flowering plant sperm through chromatin phase separation**
Xiaoqi Feng (Institute of Science and Technology, Austria, Austria) on-site, C000772

12:23 - 12:30 **AGO2 condensates behavior after bacterial inoculation [Short Talk]**
Moriaki Saito (University of California, Riverside, USA) on-site, C000690

Concurrent 23 A systems perspective: Omics integration and modeling

Application#: C25

Day 3: Wed. Jun. 7

Organized by: Lisa Van den Broeck (North Carolina State University), Antoni Garcia (Centre for research in agricultural Genomics)

The characterization and quantification of interconnections among molecules is fundamental to providing a systemic view about how plants integrate, attenuate, and respond to developmental and environmental cues. Complementary, predictive modeling of gene regulatory networks, phosphorylation cascades, hormone signaling, or metabolic pathways are powerful approaches to guide new hypotheses and base future experiments. This session will focus on studies that aim to integrate -omics datasets, unravel molecular networks, and elaborate predictive models to address functional questions in Arabidopsis.

11:00 - 11:03	Opening remarks
11:03 - 11:18	**Functional characterization of Arabidopsis protein-coding genes and lincRNAs using multi-omics networks** Klaas Vandepoele (VIB-UGent Center for Plant Systems Biology, Belgium) on-site, C000107
11:19 - 11:34	**A quantitative model of carbon partitioning during plant cold acclimation** Anastasia Kitashova (LMU Munich, Germany) on-site, C000142
11:35 - 11:50	**Modelling hormone transport within the Arabidopsis root** Kristian Kiradjiev (University of Nottingham, United Kingdom) on-site, C000490
11:51 - 12:06	**Understanding the Molecular Mechanisms Underlying FERONIA Receptor Kinase-mediated Signalling Using Multiomics Approach** Hongqing Guo (Iowa State University, USA) on-site, C000754
12:07 - 12:17	**New elements of cis-regulatory code of plant genes revealed by deep learning models [Short Talk]** Jedrzej Szymanski (Forschungszentrum Jülich GmbH & Leibniz Institute of Plant Genetics and Crop Plant Research, Germany) on-site, C000456
12:18 - 12:28	**Assessing the impacts of genetic defects on starch metabolism in Arabidopsis plants using the carbon homeostasis model [Short Talk]** Shuichi Kudo (Graduate School of Systems Life Sciences, Kyushu University, Japan) on-site, C000223
12:28 - 12:30	Closing remarks

Concurrent 24 Transposable elements, epigenetics, and environmental adaptation

Application#: C28

Day 3: Wed. Jun. 7

Organized by: Leandro Quadrana (Institut of Plant Science Paris-Saclay (IPS2)), Eriko Sasaki (Kyushu University)

This concurrent session will cover multiple aspects of epigenetic regulation and its role in environmental adaptation: DNA methylation, chromatin modifications, transposon control, reproduction, transgenerational epigenetics, and population epigenomics.

11:00 - 11:01	Opening remarks
11:01 - 11:13	**The genetic basis of non-CG transposon methylation variation in Arabidopsis thaliana** Eriko Sasaki (Kyushu University, Japan) on-site, C000321
11:14 - 11:26	**Transposable element sequences and their epigenetic control in plants: engines of rapid adaptation?** Pierre Baduel (CNRS / ENS - PSL, France) on-site, C000496
11:27 - 11:39	**Novel mechanism of transposon repression by histone deacetylases** Hidetaka Ito (Hokkaido University, Japan) on-site, C000189
11:40 - 11:52	**Targeted integrations of retrotransposons into centromeric regions in Arabidopsis** Sayuri Tsukahara (The University of Tokyo, Japan) on-site, C000498
11:53 - 12:05	**Targeted Transposition in Arabidopsis** Richard Keith Slotkin (Danforth Plant Science Center & University of Missouri, USA) on-site, C000026
12:06 - 12:18	**Unique aspects of transposable element silencing in duckweeds (lemnaceae)** Arturo Mari-Ordonez (Gregor Mendel Institute (GMI), Austria) on-site, C000801
12:19 - 12:24	**RNA deadenylation pathway suppresses transposable elements in Arabidopsis [Short Talk]** Ling Wang (CAS Center for Excellence in Molecular Plant Sciences / Institute of Plant Physiology and Ecology, China) on-site, C000092
12:25 - 12:30	**Gene-transposon transcripts can be epigenetically regulated and impact gene response to stress conditions in Arabidopsis thaliana [Short Talk]** Jeremy Berthelier (Okinawa Institute of Science and Technology, Japan) on-site, C000474

Plenary 03 Sustainable society and plants

14:30 - 15:00 **Plant environmental memory: adaptive plasticity in the context of climate change**
Gabriela Auge (Consejo Nacional de Investigaciones Científicas y Tecnologicas (CONICET), South America) on-site, I000012
Chaired by Minako Ueda (Tohoku University)

15:00 - 15:30 **Investigating the role of Wall-associated kinases (WAKs) during secondary wall development**
Kim Johnson (La Trobe University, Australia) on-site, I000006
Chaired by Taku Demura (Nara Institute of Science and Technolgy)

15:30 - 16:00 **The parasitic plant (Striga) and sorghum arms race**
Steven Maina Runo (Kenyatta University, Kenya) on-site, I000019
Chaired by Miyo Terao-Morita (National Institute for Basic Biology)

Plenary 04 Functional metabolomics

16:30 - 17:00 **How do Plants Evolve Specialized Metabolites and Pathways?**
Asaph Aharoni (Weizmann Institute of Science, Israel) on-site, I000026
Chaired by Mami Yamazaki (Chiba University)

17:00 - 17:30 **Dissecting gene-metabolite relationships in the legume terpenome**
Sibongile Mafu (University of Massachusetts Amherst, USA) on-site, I000018
Chaired by Miyako Kusano (University of Tsukuba)

17:30 - 18:00 **Exploring plant metabolite functions beyond the conventional view**
Masami Yokota Hirai (RIKEN Center for Sustainable Resource Science, Japan) on-site, I000021
Chaired by Yuki Nakamura (RIKEN CSRS)

Poster discussion (Even number)

18:00 - 20:00

Day 4 (Thu. Jun. 8)

Workshop 06 Single cell technologies and its diversity of applications

Application#: W10

Day 4: Thu. Jun. 8

Organized by: Ao Liu (HHMI-Stanford University), Bruno Guillotin (NYU-Center of Genomics and Systems Biology)

The fast development of single cell technology is revolutionizing the field of omics study. In the past few years, plant biologists have successfully adopted single cell technology and generated multiple plant cell atlases. These datasets allow us to capture the transcriptomic diversity in different cell types and help us understand cellular heterogeneity, as well as the basis of cell identity and cell fate transitions. For this session, we would like to focus on the most recent advances in the application of single cell technologies.

9:00 - 9:02 Opening remarks
9:02 - 9:15 **Origin and diversification of the cell types of the flower**
Luke Nikolov (Indiana University, USA) on-site, C000809
9:16 - 9:29 **Constructing an Arabidopsis Embryonic Expression Atlas using snRNA-seq**
Ping Kao (Graduate School of Life Sciences, Tohoku University, Japan, Japan) on-site, C000322
9:30 - 9:43 **Cell Cycle Dynamics During Plant Cell Reprogramming**
Laura Lee (New York University, USA) on-site, C000509
9:44 - 9:57 **Time-resolved single-cell and spatial gene regulatory atlas of plants under pathogen attack**
Tatsuya Nobori (Salk Institute, USA) on-site, C000125
9:57 - 10:00 Closing remarks

Workshop 07 Watching and quantifying biochemical processes in intact plants

Application#: W03

Day 4: Thu. Jun. 8

Organized by: Cheng-Hsun Ho (ABRC, Academia Sinica)

The understanding of signaling and metabolic processes in multicellular organisms requires knowledge of the spatial dynamics of small molecules and the activities of enzymes, transporters and other proteins in vivo, as well as biophysical parameters inside cells and across tissues. Genetically encoded sensors are engineered fluorescent proteins that have been developed for a wide range of small molecules, such as ions and metabolites, or to report biophysical processes, such as transmembrane voltage or tension.

9:00 - 9:02 Opening remarks
9:02 - 9:17 **Live show of nitrate dynamics in root nd developemt of Arabidopsis**
Ho Cheng-Hsun (Academia Sinica, Taiwan) on-site, C000122
9:18 - 9:38 **Towards Soil-on-a-Chip — structured micro-environments for root science**
Guido Grossmann (Heinrich-Heine-University Duesseldorf, Germany) on-site, C000824
9:39 - 9:59 **CO2 Sensing and Signaling Components are Required for Stomatal Responses to Elevated Temperatures**
Nattiwong Pankasem (University of California San Diego, USA) on-site, C000359
9:59 - 10:00 Closing remarks

Workshop 08 Spatiotemporal dynamics of protein and protein complexes in the cell

Application#: W06

Day 4: Thu. Jun. 8

Organized by: Hisashi Koiwa (Texas A&M University), Libo Shan (Texas A&M University), Juan Dong (Rutgers University)

Recent advances in biochemistry and biophysics, plant molecular and cell biology revealed that the differential fate of proteins in cell space including transport, modification, and even aggregation leads to contrasting cellular output in abiotic and biotic defense responses and plant development. Hence, the need for the detection and visualization of protein complex dynamics in living cells has become the technology of utmost importance. This workshop aims to showcase cutting-edge technologies and findings in spatiotemporal dynamics of cellular proteins and protein complexes.

9:00 - 9:02 Opening remarks
9:02 - 9:15 **Tandem fluorescent timer in Plants: A Tool for Acquiring Spatiotemporal Information about Proteins**
Yukihiro Nagashima (Texas A&M University, USA) on-site, C000535
9:16 - 9:29 **Ironing out the issues: protein dynamics in response to iron deficiency**
Terri Long (North Carolina State University, USA) on-site, C000749
9:30 - 9:43 **Plant plasma membrane nano-organization and cell polarization**
Xue Pan (University of Toronto Scarborough, Canada) on-site, C000513
9:44 - 9:57 **Unraveling the molecular and cellular mechanisms underlying a MLR-NLR complex-regulated autoimmunity**
Fausto Andres Ortiz Morea (Texas A&M University / Universidad de la Amazonia, USA) online, C000756

9:57 - 9:58 Closing remarks

Workshop 09 Arabidopsis small RNA biology

Application#: W01
Day 4: Thu. Jun. 8

Organized by: Keith Slotkin (Donald Danforth Plant Science Center & University of Missouri)

This workshop will focus on newly discovered roles of small RNAs, highlighting two hot areas of research in the field: 1) The function of small RNAs that are generated only in very specific reproductive cells, and 2) The role of small RNA warfare during the Arabidopsis-pathogen/pest interaction.

9:00 - 9:01 Opening remarks

9:01 - 9:12 **Mating system influences the requirement for RdDM during reproduction in Brassicaceae**
Rebecca Mosher (University of Arizona, USA) on-site, C000533

9:13 - 9:24 **Interspecies regulatory small RNAs in plant-parasite interactions**
Saima Shahid (Oklahoma State University, USA) on-site, C000608

9:25 - 9:36 **Translation-dependent epigenetic silencing of transposon**
Jungnam Cho (Chinese Academy of Sciences, China) on-site, C000097

9:37 - 9:48 **Reproductive barriers established by epigenetic mechanisms in the endosperm**
Claudia Köhler (Max Planck Institute of Molecular Plant Physiology, Germany) on-site, C000767

9:49 - 10:00 **Regulating Pol-IV to generate epigenetic diversity**
Julie Law (Salk Institute for Biological Studies, USA) on-site, C000785

Workshop 10 Arabidopsis bioinformatics

Application#: W05
Day 4: Thu. Jun. 8

Organized by: Nicholas Provart (University of Toronto), Tanya Berardini (Phoenix Bioinformatics)

This workshop will feature updates and introductions of online resources that are part of the Arabidopsis scientist's modern research toolkit, just like laboratory equipment, enzymes, and buffers. Essential resources like TAIR and BAR will be revisited in addition to highlighting resources created and maintained by community members in the Asia Pacific region that are of global importance.

9:00 - 9:02 Welcome

9:02 - 9:14 **Updates to the Bio-Analytic Resource**
Nicholas Provart (University of Toronto / BAR, Canada) on-site, C000795

9:15 - 9:27 **To integrate or not to integrate: how to collaborate with conversational AI programs**
Masanori Arita (RIKEN Center for Sustainable Resource Science, Japan) on-site, C000820

9:28 - 9:40 **Complete sequence assembly of Arabidopsis ribosomal DNA (rDNA) arrays provides insight into rDNA variation, epigenetic regulation and large scale recombination**
Ramya Enganti (HHMI/Indiana University, USA) on-site, C000711

9:41 - 9:53 **The 2023 TAIR update: From basics to the progress with the community-developed v12 of the genome**
Tanya Berardini (The Arabidopsis Information Resource/Phoenix Bioinformatics, USA) on-site, C000791

9:53 - 10:00 Discussion/Q&A/Questions for all speakers

Concurrent 25 The road to recovery: Elucidating stress recovery pathways and reversing stress effects

Application#: C21
Day 4: Thu. Jun. 8

Organized by: Natanella Illouz-Eliaz (Salk Intitute), Travis Lee (Salk Institute)

Plants manifest a plethora of responses from the molecular to the phenotypic level when exposed to different environments. For example, plants under water deprivation often develop smaller and darker leaves than their well-watered counterparts. Extensive empirical work has shown that gene expression is a key determinant of the physiological and developmental responses of plants to environmental cues. Further, the return to homeostasis following environmental challenges can be associated with processes distinct from the stressor proper, yet are of equal importance for plant survival. In this session, we will focus on the frontier between stress tolerance and recovery to understand mechanisms affecting reproductivity and yield after encountering stress. Although some studies consider stress recovery, it is mostly presented as a control that stressful conditions have relieved. In order to reshape a plant's ability to cope with stress and recovery responses and to enhance plant performance under fluctuating environments there is a need to gain a greater understanding of the margin between the stress, differences in response to various stress severities, and stress recovery as a process that can be studied and improved.

10:30 - 10:35 Opening remarks

10:35 - 10:55 **Conflicts in phenotypic natural selection constrain adaptation to climate change in Arabidopsis thaliana**
Moi Exposito-Alonso (Carnegie Institution for Science, Stanford University, USA) on-site, C000550

10:56 - 11:16 **Molecular and evolutionary basis of selective autophagy-mediated heat stress recovery in plants**
Yasin Dagdas (Gregor Mendel Institute, Austria) on-site, C000136

11:17 - 11:37 **Leveraging ecological specialization to understand plant drought tolerance strategies and their genetic modulation: a focus on ecological divergent Arabidopsis species**
Juliette de Meaux (University of Cologne, Germany) online, C000839

11:38 - 11:48 **Transcription factor and chromatin-based heat memory in plants [Short Talk]**
Nobutoshi Yamaguchi (Nara Institute of Science and Technology, Japan) on-site, C000226

11:49 - 11:59 **Response of Arabidopsis thaliana to flooding with physical flow [Short Talk]**
Nobuhiro Suzuki (Sophia University, Japan) on-site, C000596

Concurrent 26 Receptor kinase signaling in development

Application#: C12
Day 4: Thu. Jun. 8

Organized by: Christian Hardtke (University of Lausanne), Jamie Van Norman (UC Riverside)

In recent years, receptor kinase pathways have gained prominence in developmental processes. This session features the latest developments in their characterization in phenomena as diverse as polarity, cell division orientation or regeneration.

10:30 - 10:31 Opening remarks

10:31 - 10:50 **Which side are you on? Linking polarized receptor kinases to root cell division control**
Jaimie Van Norman (University of California, Riverside, USA) on-site, C000572

10:51 - 11:10 **Beyond stem cells: Novel roles for CLE peptide signaling in shoot apical meristems and the environmental control of plant growth.**
Zachary Nimchuk (University of North Carolina at Chapel Hill, USA) on-site, C000354

11:11 - 11:30 **CLE-BAM/CIK signaling in root vascular patterning**
Pingping Qian (Osaka University, Japan) on-site, C000424

11:31 - 11:40 **Coordinating root system architecture: the intersection of CEP and Cytokinin hormone pathways in Arabidopsis [Short Talk]**
Michael Taleski (Australian National University, Australia) on-site, C000696

11:41 - 11:50 **Stomata-derived intercellular signaling that directs mesophyll air space formation [Short Talk]**
Yuki Yoshida (Kumamoto University, Japan) on-site, C000712

11:51 - 12:00 **A phosphoinositide hub connects CLE peptide signaling and polar auxin efflux regulation [Short Talk]**
Qian Wang (DBMV, University of Lausanne, Switzerland) on-site, C000096

Concurrent 27 Chemical priming as a sustainable tool for improved productivity under stress conditions

Application#: C30
Organized by: Vassilis Fotopoulos (The Cyprus University of Technology), Khurram Bashir (Lahore University of Management Sciences)

Day 4: Thu. Jun. 8

Chemical biology could contribute towards crop improvement while improving farmers' income and ultimately contributing towards good health and sustainable agricultural practices. This could also help achieve sustainable development goals (SDGs) such as SDG1: No Poverty (Through improving farmers' income) SDG2: Zero hunger (Through enhanced crop production) SDG3: Good Health and Well-being (Through improved nutritional quality) The session would provide an opportunity to share the latest trends in the chemical biology of plants.

10:30 - 10:31 Opening remarks
10:31 - 10:46 **Signalling and epigenetic maintenance of plant immune memory by chemical priming agents.**
Jurriaan Ton (University of Sheffield, United Kingdom) on-site, C000829
10:47 - 11:02 **Employment of functionalized nanoparticles and polymers towards climate-smart crops**
Vasileios Fotopoulos (Cyprus University of Technology, Cyprus) on-site, C000827
11:03 - 11:18 **Ethanol-mediated chemical priming to mitigate drought stress in plants**
Khurram Bashir (Lahore University of Management Sciences, Pakistan) on-site, C000160
11:19 - 11:30 **Screening chemicals regulating ion channels and modulating plant growth mechanism**
Nobuyuki Uozumi (Tohoku University, Japan) on-site, C000153
11:31 - 11:42 **VDAL, a new protein biostimulant from Verticillium dahliae and its applications in Agriculture**
Zhizhong Gong (China Agricultural University, China) on-site, C000784
11:43 - 11:51 **Chemical biology study of jasmonate signaling by development of a biased agonist derived from stereoisomers of coronatine [Short Talk]**
Kengo Hayashi (Tohoku University, Japan) on-site, C000261
11:52 - 12:00 **Identification of new targets for improving abiotic stress tolerance in plants [Short Talk]**
María del Rosario González Bermúdez (Student, Spain) on-site, C000218

Concurrent 28 Cross-kingdom RNA communications and innovative Eco-friendly disease control solutions

Application#: C02
Organized by: Hailing Jin (University of California, Riverside)

Day 4: Thu. Jun. 8

Cross-kingdom RNA communications between plants and interaction organisms is a newly emerging field. Understanding the molecular mechanisms and regulatory pathways underlying the RNA communications will help us design RNA-based new generation of plant protection solutions that are more effective and environmentally friendly.

10:30 - 10:32 Opening remarks
10:32 - 10:52 **Cross-kingdom RNA trafficking between plants and fungal pathogens**
Hailing Jin (University of California, Riverside, USA) on-site, C000826
10:53 - 11:13 **Expanding the Universe of Sprayable RNAs – Current Challenges and Prospects for the Future**
Aline Koch (University of Regensburg, Gemany) on-site, C000864
11:14 - 11:34 **TBA**
(Lionel Navarro) (TBA, TBA) , TBA
11:35 - 11:45 **Proof of concept: circular antisense RNAs (caRNAs) as a new mode of action for RNA-based plant protection [Short Talk]**
Timo Schlemmer (University of Regensburg, Germany) on-site, C000757
11:46 - 11:56 **The role of plant extracellular vesicles in mRNA intercellular trafficking [Short Talk]**
Huan-Chi Tien (Institute of Plant and Microbial biology, Academia Sinica, Taiwan) on-site, C000211
11:56 - 12:00 Closing remarks

Concurrent 29

Visualizing the dynamics of the circadian clock

Application#: C27
Day 4: Thu. Jun. 8

Organized by: Chin-Mei Lee (National Taiwan University), Huang-Lung Tsai (National Taiwan University)

Plant circadian clocks continuously adjust their rhythm in accordance with the ever-changing environments at different temporal and spatial levels. The advance in techniques and imaging systems along with the development of algorithms allow us to visualize the circadian clock interacting with environments at a whole plant to single-cell levels.

10:30 - 10:31 Opening remarks
10:31 - 10:46 **Investigating the dynamic regulation of stress-responsive genes in plants.**
Dawn Nagel (University of California, Riverside, USA) on-site, C000806
10:47 - 11:02 **Variation in internal timekeeping alters abiotic stress response**
Kathleen Greenham (University of Minnesota, USA) on-site, C000743
11:03 - 11:18 **Characterization of the long-distance circadian communication through micro-grafting techniques**
Nozomu Takahashi (Nara Institute of Science and Technology, Japan) on-site, C000683
11:19 - 11:31 **Microfocus X-ray CT Analysis of Arabidopsis Petioles for Leaf Movement [Short Talk]**
Maika Hayashi (Nara institute of science and technology, Japan) on-site, C000577
11:32 - 11:44 **Identification of LWD1-interacting proteins reveals novel regulators for Arabidopsis circadian clock [Short Talk]**
Chun-Kai Huang (Institute of Plant and Microbial Biology, Academia Sinica, Taiwan, ROC, Taiwan) on-site, C000200
11:45 - 11:51 **Long-distance circadian coordination via a phloem-delivered mobile transcript [Short Talk]**
András Székely (Max Planck Institute of Molecular Plant Physiology, Germany) on-site, C000473
11:51 - 11:52 Closing remarks

Workshop 11

Diversity and inclusion for excellence in science

Application#: W11
Day 4: Thu. Jun. 8

Organized by: Joanna Friesner (North American Arabidopsis Steering Committee, USA), Yoselin Benitez-Alfonso (Leeds University), Kanako Bessho-Uehara (Tohoku University)

Research and training using Arabidopsis has been vital to the success of plant science due, in large part, to sustained global collaborations in the plant science community. While recent studies indicate clear benefits of diversity and inclusion, progress in these areas is slow and has been driven by a few countries. This moderated workshop will feature a panel of plant biology faculty that will provide diverse perspectives on the challenges of working within academia, and the benefits of creating and sustaining a diverse community to achieve excellence.

12:45 - Moderator:
Keiko Torii (HHMI/UT Austin/Nagoya University, USA/Japan)
Panelists:
Gabriela Auge (CONICET, University of Buenos Aires, Argentina)
Yoselin Benitez-Alfonso (Leeds University, United Kingdom)
Kanako Bessho-Uehara (Tohoku University, Japan)
Jose Dinneny (Stanford University, USA)
Terri Long (NCSU, USA)
Keith Slotkin (DDPSC & University of Missouri, USA)
Hironaka Tsukagoshi (Meijo University, Japan)

Concurrent 30 Living on the edge: Adaptation of Arabidopsis extremophyte relatives to harsh environments

Application#: C10

Day 4: Thu. Jun. 8

Organized by: Maheshi Dassanayake (Louisiana State University), Simon Barak (Jacob Blaustein Institutes for Desert Research, Ben-Gurion University of the Negev)

Extremophytes, plants that inhabit harsh environments, represent novel genetic resources underexplored for their adaptations to multiple environmental stresses. Specifically, extremophytes that are closely related to Arabidopsis are ideal models for comparative multi-level analyses. This session will focus on systems biology research of Arabidopsis extremophyte relatives from physiological through molecular, “omics”, evolutionary, and ecological studies to elucidate mechanisms allowing these intriguing plants to survive the most extreme environments on the planet.

14:00 - 14:01 Opening remarks

14:01 - 14:15 **A counterintuitive conundrum: Salt inhibition of halophytic seed germination**
Simon Barak (Ben-Gurion University of the Negev, Israel) online, C000828

14:16 - 14:30 **Role and Functional Differences of HIGH-AFFINITY K+ TRANSPORTER1 (HKT1)-Type Transporters in Plants under Salt Stress**
Dae-Jin Yun (Konkuk University, Republic of Korea) on-site, C000163

14:31 - 14:45 **Exploring plant adaptations to aquatic environments: A study of Rorippa aquatica, an amphibious plant living at the edge of the water**
Seisuke Kimura (Kyoto Sangyo University, Japan) on-site, C000324

14:46 - 15:00 **Discovering how evolutionary innovations in growth regulation contribute to plant stress tolerance**
Prashanth Ramachandran (Stanford University, USA) on-site, C000594

15:01 - 15:10 **Enhanced Salt Tolerance by an Antarctic moss gene [Short Talk]**
NoA Bae (Sogang university, Republic of Korea) on-site, C000579

15:11 - 15:20 **Altitudinal genetic differentiation in the leaf wax-mediated flowering bud protection against frost in an early-spring flowering herb, Arabidopsis halleri [Short Talk]**
Hiroshi Kudoh (Center for Ecological Research, Kyoto University, Japan) on-site, C000599

15:21 - 15:30 **Seasonal dynamics of epigenome in a natural population of Arabidopsis halleri [Short Talk]**
Haruki Nishio (Shiga University, Japan) on-site, C000529

Concurrent 31 Short and long range signaling by RNA

Application#: C26

Day 4: Thu. Jun. 8

Organized by: Dave Jackson (Cold Spring Harbor Laboratory), Margaret Frank (Cornell University), Fritz Kragler (Max Planck Institute of Molecular Plant Physiology), Michitaka Notaguchi (Nagoya University)

Plant development, physiology and defense are controlled by several classes of mobile RNAs that move both cell-to-cell, through plasmodesmata, and into the phloem for systemic movement. Mobile mRNAs control meristem, leaf and tuber development, among other processes. Small RNA silencing signals and miRNAs also move systemically through plasmodesmata and the phloem, for example, to control nutrient homeostasis. The workshop will present new findings in this exciting emerging area of plant biology research.

14:00 - 14:02 Opening remarks

14:02 - 14:16 **Deciphering signals from the noise in the mRNA mobileome using comparative Solanaceae genomics**
Margaret Frank (Cornell University, USA) on-site, C000794

14:17 - 14:31 **An RNA exosome subunit promotes cell-to-cell trafficking of a homeobox mRNA via plasmodesmata**
Munenori Kitagawa (College of Horticulture & Forestry Sciences, Huazhong Agricultural University, China) on-site, C000051

14:32 - 14:46 **Investigation of mRNAs that move long-distance**
Michitaka Notaguchi (Nagoya University, Japan) on-site, C000398

14:47 - 15:01 **Lost in translation? The long-distance travel of messenger RNAs**
Friedrich Kragler (Max-Planck-Institute of Molecular Plant Physiology, Germany) on-site, C000139

15:02 - 15:10 **Investigating the role of the Arabidopsis ROTAMASE CYCLOPHILIN gene family in organelle-mediated mobile mRNAs transport [Short Talk]**
Yu-Hsien Chang (Institute of Plant and Microbial Biology, Academia Sinica, Taiwan) on-site, C000167

15:11 - 15:19 **A cell wall-modifying enzyme controls symplastic movement of RNA silencing in aerial Arabidopsis tissues [Short Talk]**
Florence Brioudes (ETH Zürich, Switzerland) on-site, C000315

15:20 - 15:28 **Dose-dependent long-distance movement of microRNA399 duplex regulates phosphate homeostasis in Arabidopsis [Short Talk]**
Chih-Pin Chiang (Agricultural Biotechnology Research Center, Academia Sinica, Taiwan) on-site, C000656

15:28 - 15:30 Closing remarks

Concurrent 32 Mechanisms and functions of endocytosis in plants

Application#: C18

Day 4: Thu. Jun. 8

Organized by: Jenny Russinova (VIB-UGent Center for Plant Systems Biology), Takashi Ueda (NIBB)

Plant endocytosis underlies a plethora of biological processes including nutrient uptake, signal transduction, development, polarity and tropic growth, immunity and responses to abiotic stress. However, the molecular machinery of endocytosis, its regulation and exact biological impacts are only beginning to be understood in plants. This session will cover the following topics (1) Molecular mechanisms of endocytosis in plants; (2) Endocytosis and plant polarity, development and nutrient uptake; (3) Endocytosis and plant-pathogen interactions; (4) Endocytosis and cell wall biogenesis; (5) Crosstalk between endocytosis, exocytosis and autophagy

14:00 - 14:02 Opening remarks

14:02 - 14:20 **Mechanistic insight into plant endocytosis**
Daniel Van Damme (Ghent University Department of Plant Biotechnology and Bioinformatics and VIB Center for Plant Systems Biology, Belgium) on-site, C000637

14:21 - 14:30 **Mechanisms underlying polar membrane targeting of SOSEKI protein [Short Talk]**
Andriy Volkov (Laboratory of Biochemistry, Wageningen University, Netherlands) on-site, C000541

14:31 - 14:49 **A novel reciprocal regulation mechanism for SH3P2 in crosstalk between endocytosis and autophagy**
Xiaohong Zhuang (The Chinese University of Hong Kong, Hong Kong) on-site, C000034

14:50 - 14:59 **Brassinosteroid receptor BRI1 deubiquitination by UBP12/UBP13 fine-tunes plant growth [Short Talk]**
Yongming Luo (VIB-UGent Center for Plant Systems Biology, Belgium) on-site, C000098

15:00 - 15:18 **Understanding the Evolution of Endosomal Sorting Mechanisms in Plants**
Marisa Otegui (University of Wisconsin-Madison, USA) on-site, C000032

15:19 - 15:28 **Ca2+-induced removal of inner vegetative plasma membrane in Arabidopsis sperm cells [Short Talk]**
Naoya Sugi (Yokohama City University, Japan) on-site, C000382

15:28 - 15:30 Closing remarks

Concurrent 33 Front-line of plant genome engineering

Application#: C31

Day 4: Thu. Jun. 8

Organized by: Daisuke Miki (Center of Excellence for Molecular Plant Sciences, Chinese Academy of Sciences), Masaki Endo (National Agriculture and Food Research Organization (NARO)), Yuriko Osakabe (School of Life Science and Technology, Tokyo Institute of Technology)

Genome engineering are revolutionizing life sciences and plant biotechnology that seek to develop new technologies for the precise manipulation of genes and genomes in vivo. In addition to its use for advancing our understanding of basic biology, genome engineering has numerous applications for improving agronomically traits. In this session, we will present and discuss recent advances in nuclear and organelle genome engineering approaches, novel tools and delivery system.

14:00 - 14:01 Opening remarks

14:01 - 14:18 **Genome engineering for plastid and mitochondria**
Shin-ichi Arimura (University of Tokyo, Japan) on-site, C000254

14:19 - 14:36 **Towards versatile plant gene editing systems: the wisker-based direct delivery method and small-size Cas protein**
Shigeo Sugano (National Institute of Advanced Industrial Science and Technology (AIST), Japan) on-site, C000660

14:37 - 14:54 **CRISPR/Cas-meditated Chromosome and Tissue Engineering in Arabidopsis**
Holger Puchta (Karlsruhe Institute of Technology, Germany) online, C000075

14:55 - 15:12 **Gene editing in Arabidopsis using RNA viruses**
Daniel Voytas (University of Minnesota, USA) online, C000369

15:13 - 15:21 **Insights into tRNA-like structures (TLS) as motifs facilitating long-distance transport of mRNAs [Short Talk]**
Eleftheria Saplaoura (Max Planck Institute for Molecular Plant Physiology, Germany) on-site, C000497

15:22 - 15:29 **Single-cell targeted chemical or genetic boosting of genome editing in maize [Short Talk]**
Ling Meng (KWS Group, USA) on-site, C000079

15:29 - 15:30 Closing remarks

Workshop 12 MASC: Arabidopsis for SDGs/4th Decadal Vision

Application#: W14
Day 4: Thu. Jun. 8

Organized by: Nicholas Provart (University of Toronto), Masatomo Kobayashi (RIKEN BRC)

The theme of this year's ICAR is Arabidopsis for Sustainable Development Goals. Participants will discuss how research in Arabidopsis can be leveraged to help achieve some of the United Nation's 17 SDGs, especially in the area of zero hunger, climate action, and life on land. In addition, participants will discuss how Arabidopsis research can help address important plant science questions (such as those posed in Armstrong et al., 2023; doi. 10.1111/nph.18771) and the kinds of international projects that might be considered as part of a 4th decadal vision for Arabidopsis research, following on from successful collaborations that have arisen from 3 decades of coordinated efforts.

14:00 -

Panelists:
Cris Argueso (Colorado State Univ., NAASC, USA)
Gabriela Auge (CONICET, Univ. of Buenos Aires, Argentina)
Sureshkumar Balasubramanian (Monash Univ, Australia)
Dirk Inze (VIB, Belgium)
Kazuki Saito (RIKEN CSRS, Japan)

Plenary 05 Evolution and ecology

16:00 - 16:30 **Adaptation in natural populations of outcrossing Arabidopsis species**
Filip Kolář (Charles University, Czech Republic) on-site, I000025
Chaired by Takashi Tsuchimatsu (University of Tokyo)

16:30 - 17:00 **The Mendelian and polygenic bases of weedy Arabidopsis thaliana evolution**
Cheng-Ruei Lee (National Taiwan University, Taiwan) on-site, I000015
Chaired by Eriko Sasaki (Kyushu University)

17:00 - 17:30 **All bullseyes great and small: Eco-Evo-Devo of petal patterning in Hibiscus**
Edwige Moyroud (University of Cambridge, UK) on-site, I000017
Chaired by Vincent Castric (CNRS - University of Lille)

Banquet

18:00 - 22:30

Day 5 (Fri. Jun. 9)

Plenary 06 Integration of environmental cues

9:00 - 9:30 **“To GROW or not to GROW”: molecular mechanism of cell elongation at low temperature in single plant cells.**
José M. Estevez (CBV-UNAB/Fundación Instituto Leloir-IIBBA, Chile/Argentina) on-site, I000009
Chaired by Jian-Kang Zhu (Southern University of Science and Technology)

9:30 - 10:00 **Integrating osmotic potential with Jasmonate-mediated plant acclimation**
Debora Gasperini (Leibniz Institute of Plant Biochemistry (IPB) , Germany/Croatia) on-site, I000020
Chaired by Shu-Hsing Wu (Academia Sinica)

10:00 - 10:30 **Peptide signal-mediated adaptation to spatially and temporally fluctuating environments in plants**
Yoshikatsu Matsubayashi (Nagoya university, Japan) on-site, I000024
Chaired by Tomonao Matsushita (Kyoto University)

Keynote 03

11:00 - 11:45 **Deconstructing Plant Processes: Cell by Cell**
Joseph Ecker (Salk Institute for Biological Studies, USA) on-site, I000022
Chaired by Tetsuya Higashiyama (University of Tokyo)

Closing and Introduction of ICAR2024

11:45 - 12:00 Representatives of the Organizing Committees of ICAR2023 and ICAR2024

Poster presentations

01 Abiotic response (salt/dehydration/water)

PO-001	**Overexpression of soybean Class II acyl-CoA-binding proteins unveils an oxylipin signaling mechanism in salt-stressed Arabidopsis** *Terry Shiu-Cheung Lung (School of Biological Sciences, The University of Hong Kong, Pokfulam, Hong Kong, China)*
PO-002 CC30	**Enhanced Salt Tolerance by an Antarctic moss gene** *NoA Bae (Sogang university, Korea)*
PO-003	**Chenopodium quinoa as a model plant to study salt stress** *Lucia Acosta-Gamboa (Donald Danforth Plant Science Center)*
PO-004	**Investigation of heterosis in the salinity tolerance of intraspecific hybrid in Arabidopsis thaliana** *Yoshiki Kamiya (Kobe University, Japan)*
PO-005	**Overexpression of eelgrass Rare Cold Inducible 2 (RCI2) encoding a small-membrane protein maintains chlorophyll content in Arabidopsis subjected to high salinity and dehydration** *Hajime Shiota (Yokohama City Univ., Japan)*
PO-006	**Arabidopsis APYs interact with PATL4 and co-regulate stress response in plants** *Jia-Hong Tang (National Taiwan University, Taiwan)*
PO-007	**Physiological and molecular alterations in Schrenkiella parvula under mild salt stress** *Keriman Şekerci (Tohoku University, Graduate School of Life Sciences)*
PO-008 CC19	**A Comparative Study of Adaptive Stress Tolerance in the Brassicaceae Family** *Andrea Ramirez Ramirez (Stanford University)*
PO-009	**A Ca2+ sensor switch for SOS1 Na+/H+ antiporter activation confers tolerance to elevated salt stress in Arabidopsis** *Joerg Kudla (Institut für Biologie und Biotechnologie der Pflanzen, Westfälische Wilhelms-Universität Münster, 48149 Münster, Germany)*
PO-010	**Dissecting genetic mechanism of natural variation in salt tolerance among Arabidopsis thaliana** *Takuma Kajino (Dept. of Bioscience, Tokyo Univ. of Agriculture)*
PO-011	**Analyses of salt susceptibility of Arabidopsis inositol transporter (INT) loss-of-function mutants** *Li See Ng (National Chung Hsing University, Taiwan)*
PO-012	**Soybean acyl-CoA-binding proteins modulate the activity of their protein interactor lipoxygenase in transgenic Arabidopsis during salinity stress** *Mee-Len Chye (University of Hong Kong)*
PO-013	**Identification of proteins interacting with CBL4 using a proximity biotinylation enzyme, AirID** *Akira Nozawa (Ehime University)*
PO-014	**Phosphorylation of Arabidopsis Glycine-Rich RNA-Binding Protein 8 by ABA-non-activated SnRK2s triggers its localization to the stress granules upon salinity stress by promoting its liquid-liquid phase separation** *Adrian Mateusz Kasztelan (Institute of Biochemistry and Biophysics, Polish Academy of Sciences, Poland)*
PO-015	**Defects in Arabidopsis N-Acetylglucosamine-1-P Uridylyltransferase Expression Impairs Protein N-glycosylation and Induces ABA-Mediated Salt Sensitivity** *Ya-Huei Chen (Institute of Plant and Microbial Biology, Academia Sinica, Taipei, Taiwan)*
PO-016	**HAT22/ABIG1 represses the transcription of AtERF71/HRE2 through a HD-Zip II-binding-like cis-regulatory element in Arabidopsis** *Md Bayzid (Pusan National University, Republic of Korea)*
PO-017	**From root to leaf: The effects of high soil salinity on the defense mechanisms of the phyllosphere** *Paula Collado Cordon (Duke University)*
PO-018	**proline content alterative 8 (pca8) acts as a suppressor mutant of atrzf1 (Arabidopsis thaliana ring zinc finger 1) to regulate dehydration and abscisic acid responses in Arabidopsis** *Ying Gong (Department of Applied Biology, Chonnam National University, Gwangju 61186, Korea)*
PO-019	**Pectin lyase 1 (PEL1) and Arabidopsis thaliana Ring Zinc Finger 1 (AtRZF1) coordinately regulate osmotic stress response to control vascular development** *CHORONG PARK (Department of Applied Biology, Chonnam National University, Gwangju 61186, Republic of Korea)*
PO-020	**Functional characterization of Glycine max RING Zinc Finger-Like 1 (GmRZFL1) and Solanum lycopersicum RING Zinc Finger-Like 1 (SlRZFL1) regulates dehydration sensitivity in Arabidopsis thaliana** *Cheol Soo Kim (Department of Applied Biology, Chonnam National University, Gwangju 61186, Republic of Korea)*
PO-021	**Meta-Analysis of Public RNA Sequencing Data of Multiple Abiotic Stresses in Arabidopsis thaliana Provides New Insights into both ABA-Dependent and ABA-Independent Stress Responsive Genes** *Mitsuo Shintani (Hiroshima University, Japan)*
PO-022	**Analysis of the transcription factor SGR5 that functions in the drought resistance mechanism** *Moeca Arai (Bioproduction Research Institute, AIST)*
PO-023	**An NPH3 domain protein mediates safe proline accumulation and drought resistance via function in intra-cellular trafficking.** *Neha Upadhyay Tiwari (IPMB, Academia Sinica, Taipei, Taiwan)*

PO-024	**Improving plant productivity and drought tolerance by regulating the NAD salvage pathway in Arabidopsis** *Zarnab Ahmad (Plant Genomic Network Research Team, RIKEN Center for Sustainable Resource Science (CSRS), Yokohama 230-0045, Japan)*
PO-025	**Identification of upstream kinases that regulate SnRK2 kinases in Arabidopsis** *Fumiyuki Soma (Institute of Crop Science, National Agriculture and Food Research Organization)*
PO-026	**Functional Analyses of Arabidopsis bZIP Transcription Factor Involved in Drought Tolerance** *Yoshimi Nakano (National Institute of Advanced Industrial Science and Technology (AIST))*
PO-027	**Hyperosmolarity-induced suppression of Raf-like protein kinase modulates physiological trade-off between growth and stress responses in Arabidopsis.** *Yoshiaki Kamiyama (Tokyo Univ. Agric. Tech., Japan)*
PO-028	**SnRK2-substrate 1 is phosphorylated in response to drought stress and accumulated to maintain plant growth.** *Sotaro Katagiri (Tokyo Univ. of Agric. and Thec., Japan)*
PO-029 CC27	**Identification of new targets for improving abiotic stress tolerance in plants** *María del Rosario González Bermúdez (Instituto de Biologia Molecular y Celular de Plantas (IBMCP-UPV-CSIC), Universitat Politècnica de València (UPV), Consejo Superior de Investigaciones Científicas (CSIC), 46022, Spain.)*
PO-030	**Plant GSK-like kinase partcipates in the activation the B-RAF kinase under osmotic stress in Arabidopsis** *Zhen Lin (Southern University of Science and Technology, China)*
PO-031	**Diverse transcriptional regulation in response to drought in Brachypodium distachyon ecotypes** *Anzu Minami (RIKEN Center for Sustainable Resource Science, Japan)*
PO-032	**Ethanol treatment enhances drought stress avoidance in cassava (Manihot esculenta Crantz)** *Anh Thu Vu (Plant Genomic Network Research Team, CSRS, RIKEN, Japan)*
PO-033	**1-Butanol treatment enhances drought stress tolerance in Arabidopsis thaliana** *Quynh Thi Nhu Do (Plant Genomic Network Research Team, RIKEN Center for Sustainable Resource Science, Japan)*
PO-034	**Physiological responses of drought tolerant and sensitive Kimchi cabbage varieties during seedling stage drying exposure** *Yoonah Jang (National Institute of Horticulral and Herbal Science, Republic of Korea)*
PO-035	**Using Thermal Imaging to Assess the Water Status of Rice** *Yan-Ci Zhang (Department of Agronomy, National Chung Hsing University, Taiwan)*
PO-036	**Determining the Levels of Water Deficiency in Oryza sativa by Using Remote Sensor** *Tzu-Chiao Liao (Department of Agronomy, National Chung Hsing University, Taiwan)*
PO-037	**Phenome analysis focusing on small open reading frames found an Arabidopsis-specific emerged de novo gene enhancing drought tolerance.** *Tomoyuki Takeda (Kyushu Institute of Technology, Japan)*
PO-038	**Characterization and molecular improvement of isothiocyanate-based inhibitors on stomatal opening that act as drought tolerance-conferring agrochemicals** *Yusuke Aihara (ITbM, Nagoya Univ., Japan)*
PO-039	**SnRK2 mediates SIZ1 phosphorylation and global SUMOylation increment upon osmotic stresses** *sang tian (SUSTC, China)*
PO-040	**Molecular Characterization and Expression Analysis of Nuclear Factor Y in wheat (Triticum aestivum L.)** *Ji woo Kim (Division of Life Sciences, Jeonbuk National University, Republic of Korea)*
PO-041 CC25	**Response of Arabidopsis thaliana to flooding with physical flow** *Nobuhiro Suzuki (Sophia University, Japan)*
PO-042	**A translational agricultural study from Arabidopsis to cabbage: determination of mechanisms enhancing submergence tolerance in cabbage (Brassica oleracea L. var. capitata)** *Fu-Chiun Hsu (National Taiwan University, Taiwan)*
PO-043 CC13	**Drought Recovery Induced Immunity Confers Pathogen Resistance** *Natanella Illouz-Eliaz (Salk Institute)*

02 Abiotic response (temperature)

PO-044	**Latitudinal gradient of molecular phenology unravels the physiological mechanism of bud dormancy** *Atsuko Miyawaki Kuwakado (Kyushu University, Japan)*
PO-045	**Analysis of transcriptional regulations of temperature-stress inducible genes mediated by clock-related transcription factors in Arabidopsis** *Satoshi Kidokoro (Sch. of Life Sci. and Tech., Tokyo Tech, Japan)*
PO-046	**SMAX1 potentiates phytochrome B-mediated hypocotyl thermomorphogenesis** *Chung-Mo Park (Seoul National University, Korea)*
PO-047	**Genome-wide epigenetic changes by warm temperature trigger developmental reprogramming in Arabidopsis** *Junghyun Kim (The University of Texas at Austin, USA)*
PO-048	**Evolution of plant responses to elevated ambient temperature** *Alvaro Montiel Jorda (School of Biological Sciences, University of Bristol, Bristol BS8 1TQ, United Kingdom)*

PO-049	**Genetic determinants of thermal response** *Sourav Mukherjee (School of Biological Sciences, Monash University, VIC 3800, AUSTRALIA)*
PO-050	**Thermosensory Transcription Factors Activate Thermoresponsive Gene Expression by Forming Biomolecular Condensates with the Mediator Complex** *Yongjian Qiu (The University of Mississippi, USA)*
PO-051	**Memory of 5-min heat stress is associated with pathogen defense mechanisms in Arabidopsis** *Rio Shimizu (Sophia University, Japan)*
PO-052	**BrbZIP-S, a bZIP transcription factor from Brassica rapa, enhanced stress tolerance in Nicotiana benthamiana.** *Tae Kyung Hyun (Department of Industrial Plant Science and Technology, Chungbuk National University)*
PO-053 CC25	**Transcription factor and chromatin-based heat memory in plants** *Nobutoshi Yamaguchi (Nara Institute of Science and Technology)*
PO-054	**Sensitized expression of LEARNED HEAT MEMORY 1 through histone modification confers thermotolerance in Arabidopsis thaliana.** *xuejing wang (Nara institute of science and technology, Japan)*
PO-055	**Maintenance of abiotic stress memory in plants: Lessons learned from heat acclimation** *Yee-yung Charng (Agricultural Biotechnology Research Center, Academia Sinica, Taiwan)*
PO-056 CC02	**Epidermal Cell Type-Specific Chromatin Dynamics Underlying Arabidopsis Heat Stress Memory** *Daniel Slane (Department of Integrated Biosciences, Graduate School of Frontier Sciences, The University of Tokyo, 5-1-5 Kashiwanoha, Kashiwa, Chiba, 277-8562, Japan)*
PO-057	**Regulatory roles of microRNA164 enhanced thermotolerance** *JENG-SHANE LIN (National Chung Hsing University)*
PO-058	**The Regulated Mechanism of miR163 and Its Target Genes on Plant Thermotolerance** *ZHEN YUAN KOK (National Chung Hsing University, Taiwan)*
PO-059	**Deciphering the role of the conserved microRNA169 in enhancing yield and thermotolerance in Arabidopsis** *Apoorva Gupta (National Institute of Plant Genome Research (NIPGR), New Delhi, India)*
PO-060 CC11	**Characterization of Arabidopsis ECT family in stress tolerance and stress granules assembly** *Nicolas Figueroa Fuentealba (King Abdullah University of Science and Technology (KAUST), Saudi Arabia)*
PO-061	**Prolonged Exposure to High Temperature Inhibits Shoot Primary and Root Secondary Growth in Panax ginseng** *Jeongeui Hong (Chungbuk National University, Republic of Korea)*
PO-062	**Identification of Protein Kinases Involved in the Post-translational Regulation of the Stress-Responsive Transcription Factor DREB2A** *Junya Mizoi (Graduate School of Agricultural and Life Sciences, The University of Tokyo, Japan)*
PO-063	**atDjB3, a class II J-domain protein, regulates heat stress response in Arabidopsis thaliana** *Gouri Satheesh (Indian Institute of Science Education and Research, Bhopal, India)*
PO-064	**Arabidopsis F-box protein EID1 regulates acquired thermotolerance through post-translational modification of HEAT SHOCK FACTOR BINDING PROTEIN** *GUAN-LIN CHUO (National Taiwan Univeristy, Taiwan)*
PO-065 CC11	**Heat-regulated phosphorylation of TOT43 is a switch for stress granule association to contribute to heat tolerance in Arabidopsis** *Shao-Li Yang (Department of Plant Biotechnology and Bioinformatics, Ghent University, Ghent, Belgium)*
PO-066	**On the mechanism of maintaining heat acclimation memory by the HSP101-HSA32 module in Arabidopsis** *Suma Mitra (Agricultural Biotechnology Research Center (ABRC), Academia Sinica, Taipei)*
PO-067	**Ethanol treatment induces heat tolerance in plants** *Daisuke Todaka (Plant Genomic Network Research Team, RIKEN CSRS, Japan)*
PO-068	**Phototropin mediates periodic cold priming in Arabidopsis** *Minoru Noguchi (Utsunomiya University, Japan)*
PO-069	**REVEILLE2 Thermosensitive Splicing: A Molecular Basis for the Integration of Nocturnal Temperature Information by the Arabidopsis Circadian Clock** *Matt Jones (University of Glasgow)*
PO-070	**Role of thioredoxins and regulation of carbon metabolism in acclimation to low temperatures** *David Gonzalez-Campo (LMU Munich)*
PO-071 Online-only	**Revealing the role of GNOM ARF-GEF in regulating cold stress response through a comparative proteomic approach** *Sumaiya Jannat Tapati (The United Graduate School of Agricultural Sciences, Iwate University, Morioka 020-8550, Japan)*
PO-072 Online-only	**Exploration of functional short peptides for protection against protein aggregation and instability in plants** *Hidefumi Hamasaki (Riken Yokohama Institute)*

03 Abiotic response (others)

PO-073	**Forward genetic screens to elucidate the molecular mechanism of alternative promoter selection in plants and yeasts** *Yoshiro Murakami (Kyoto University, Japan)*
PO-074	**Stomatal characteristics of an Arabidopsis: Natural accession with high sensitivity to increased CO2 concentration** *Tomoki Shuno (Dept. Biol., Fac. Sci., Univ. Kyushu)*
PO-075 CC09	**Stomatal CO2/bicarbonate Sensor Consists of Two Interacting Protein Kinases HT1 and MPK4/12 in Arabidopsis** *Yohei Takahashi (University of California San Diego, USA)*
PO-076	**Analysis of the role of RLDs in the gravity response of shoot using Arabidopsis thaliana** *Takeshi Nishimura Nishimura (National Institute for Basic Biology)*
PO-077	**LZY3 is localized on the plasma membrane to transduce the gravity signal in columella cells** *Hiromasa Shikata (National Institute for Basic Biology, NINS, Japan)*
PO-078	**The role of LAZY1-LIKE 4 in the signaling process in the gravity sensing cells in root gravitropism** *Miyo Terao Morita (National Institute for Basic Biology, Japan)*
PO-079	**Genetic framework for the coordination of shoot gravitropic setpoint angle by TILLER ANGLE CONTROL1** *Nozomi Kawamoto (National Institute for Basic Biology)*
PO-080	**Nicotianamine secretion for Zinc tolerance** *Kuo-Chen Yeh (Academia Sinica)*
PO-081	**Overexpression of a Tagetes patula Ascorbate peroxidase 1 in Arabidopsis enhances cadmium tolerance** *Chwan-Yang Hong (National Taiwan University, Taiwan)*
PO-082	**Environmental pH governs the phospho-switching of major plasma-membrane transporters** *Dharmesh Jain (Molecular and Biological Agricultural Sciences Program, Taiwan International Graduate Program, Academia Sinica and National Chung-Hsing University, Taipei 11529, Taiwan)*
PO-083	**Reconfiguration of central metabolites during abiotic stress periods modulate defense to pathogens in Arabidopsis** *ANTONI GARCIA-MOLINA (CENTER OF RESEARCH IN AGRIGENOMICS (CRAG))*
PO-084	**Meta-Analysis of RNA Sequencing Data of Arabidopsis and Rice under Hypoxia** *Keita Tamura (Hiroshima University, Japan)*
PO-085	**Abiotic Stress Modulated Plant U-Box Ubiquitin Ligases – Expression, Phenotype and Regulation** *Dudy Bar-Zvi (Ben-Gurion University of the Negev)*

04 Pathogen & insect response/Immunity

PO-086	**Characterisation of a TIR-NLR mediated immune activation with an alpha/beta-hydrolase fold protein** *Yi Yun Tan (National University of Singapore, Singapore)*
PO-087	**Transcriptome Analysis of Dangerous Mix Autoimmunity in A. thaliana** *Donghui HU (National University of Singapore, Singapore)*
PO-088	**Characterization of an antagonistic NLR pair in plant autoimmunity** *Yin Yin Liew (National University of Singapore)*
PO-089	**Genetic Requirements of DM10-DM11 Autoimmunity in Arabidopsis thaliana** *Jinge Wang (National University of Singapore, Singapore)*
PO-090	**Highly variable plant immune receptors share distinct genomic and epigenomic features** *Ksenia Krasileva (University of California, Berkeley)*
PO-091	**A Self-Compartmentalized Alpha/Beta Hydrolase Complex Participates in NLR-mediated Immunity in Plants** *Wei-Lin Wan (National University of Singapore, Singapore)*
PO-092	**2D-Phase separation of pathogen effectors subverts plant defence** *xinlu zhu (School of Biological Sciences, Nanyang Technological University, 637551,Singapore)*
PO-093	**Bacterial effector hopAM1 activity reconfigures ETI responses.** *Nestoras Kargios (University of Warwick, UK)*
PO-094	**A plant defence metabolite disarms bacterial type III injectisome assembly** *Pei Miao (Institute of Genetics and Developmental Biology, Beijing)*
PO-095	**Bacteria Pathogen Subvert Plant Innate Immunity via Phase Separating Effectors** *Yi Xie (School of Biological Sciences, Nanyang Technological University, Singapore)*
PO-096	**Deciphering SA-triggered plant stress responses through epitranscriptomic m6A regulation in cytosolic condensates** *Kaiwei Liu (Center for Plant Stress Biology, Center for Excellence in Molecular Plant Sciences (CEMPS), Chinese Academy of Sciences, Shanghai, China)*
PO-097	**Study on the interaction between Ralstonia solanacearum effector RsT3E-P and ACC oxidases in pattern-triggered immunity** *YU CHUAN CHANG (Institute of Plant Biology and Department of Life Science, National Taiwan University, Taipei, Taiwan)*
PO-098	**The effector protein RipBJ of Ralstonia solanacearum elicits plant immunity** *Chun yu Kuo (Institute of Plant Biology, National Taiwan University, Taipei, Taiwan)*

PO-099	**Bacterial pathogens deliver water/solute-permeable channels as a virulence strategy** *Kinya Nomura (Howard Hughes Medical Institute, Duke University, USA)*
PO-100	**Identification of yeast-secreted proteins to induce plant immune responses** *Chian Kwon (Dankook University, Korea)*
PO-101	**Characterization of high mobility group box proteins as conserved plant damage-associated molecular patterns** *Yukihisa Goto (Institute of Plant and Microbial Biology, Zürich-Basel Plant Science Center, University of Zürich, Zürich, Switzerland)*
PO-102	**Functional study on roles of Solyc12gA-interacting proteins in plant innate immunity** *Yu Chuan Chiu (Institute of Plant Biology, National Taiwan University)*
PO-103	**Assessing the Impact of Plant Immunity on Agrobacterium-Mediated Transformation by Floral Inoculation: Insights from the EFR Gene in Arabidopsis** *Mao-Sen Liu (Institute of Plant and Microbial Biology, Academia Sinica, Taipei, Taiwan)*
PO-104	**A bacterial typeⅢ effector requires the LRR-RK KIN7 to negatively regulate FLS2 homeostasis in Arabidopsis thaliana** *Yasuhiro Kadota (RIKEN Center for Sustainable Resource Science (CSRS))*
PO-105	**Valinomycin, a putative bi-directional natural compound with antifungal and immune-priming activity** *Nayeon Yoo (Department of Plant Biotechnology, Korea University, Seoul 02841, Republic of Korea)*
PO-106	**Gene regulatory network induced by Western flower thrips** *Saskia van Wees (Utrecht University)*
PO-107	**Effects of Turnip mosaic virus on Arabidopsis halleri-aphid interaction and the exploration of its causal genes in a natural environment.** *Miyabi Otsubo (Center for Ecological Research, Kyoto University, Japan)*
PO-108	**Quantitative analysis of the feeding behavior of herbivorous insects on Arabidopsis leaves reveals detailed mechanisms of trichomes contribution to plant defense** *Naoyuki Sotta (The University of Tokyo, Japan)*
PO-109	**Decision factors of morphological diversity in insect galls** *Kanako Bessho-Uehara (Tohoku University)*
PO-110	**Wound induced small-peptide mediated signalling cascade regulated by a receptor like kinase- RLK1 dictates growth vs defense decision in rice** *HARSHITH CHITHAVALLI YOGESH GOWDA (National Centre For Biological Sciences, TIFR, India, 560065)*
PO-111	**Small cyclic peptides that enhance disease resistance in Arabidopsis thaliana and Brachypodium distachyon** *Yoshiteru Noutoshi (Okayama University)*
PO-112	**Defense signal sensitization in response to damage-associated Pep peptides during phosphate starvation response** *Natsuki Tsuchida (Nara Institute of Science and Technology)*
PO-113	**XCP1 cleaves Pathogenesis-related protein 1 into CAPE9 for systemic immunity in Arabidopsis** *Yu-Hsuan Huang (Agricultural Biotechnology Research Center, Academia Sinica, Taiwan)*
PO-114	**14-3-3 proteins facilitate the activation of MAP kinase cascades by upstream immunity-related kinases** *Xiaojing Dong (Institute of Genetics and Developmental Biology)*
PO-115	**Dimerization and activation of Arabidopsis MAPKKKs in chitin-induced immunity.** *Koji Yamaguchi (Grad. Sch. Agri., Kindai Univ)*
PO-116	**Time-resolved MAPK activation shapes dynamics of defense responses in Arabidopsis** *Hoo Sun Chung (Ghent University Global Campus, South Korea)*
PO-117	**Bacterial effectors disrupt host chloroplast functions for virulence** *Charles Roussin-Leveillee (Universite de Sherbrooke, Canada)*
PO-118	**Receptor-like cytosolic kinase RIPK confers broad-spectrum disease resistance without yield penalties** *Yan Liang (Zhejiang University, China)*
PO-119	**The perception of quinones and reactive oxygen species by CARD1/HPCA1 in Arabidopsis** *Anuphon Laohavisit (Institute of Transformative Bio-Molecules, Nagoya University, Japan)*
PO-120	**The cytosolic thiol peroxidase PRXIIB is an intracellular sensor for H2O2 that regulates plant immunity through a redox relay** *Man Hu (Institute of Genetics and Developmental Biology, Chinese Academy of Sciences)*
PO-121	**Conserved molecular regulatory mechanism of the ROS-producing activity of RBOHs by phosphorylation and Ca2+ binding in land plants** *Takafumi Hashimoto (Tokyo University of Science, Japan)*
PO-122	**Oomycete effector AVRblb2 inhibits Ca2+ influx by targeting cyclic nucleotide-gated channel through Ca2+ sensors to suppress immune response** *Soeui Lee (Plant Immunity Research Center, Plant Genomics and Breeding Institute, Seoul National University, Seoul, 08826, Republic of Korea)*
PO-123	**Involvement of two cyclic nucleotide-gated ion channel subunits in jasmonic acid-mediated immune signaling** *Hyunsuh Lee (University of Toronto, Canada)*
PO-124	**An Interactor of CYCLIC NUCLEOTIDE-GATED ION CHANNEL 12 enhances downstream immune signaling events** *Robin Hon Ming Goh (Department of Cell & Systems Biology, University of Toronto)*

PO-125	**An attractive case of plant-virus coevolution supports the idea that non-canonical nucleotides within the host play an antiviral role** *Adrian Alejandro Valli (Spanish National Centre for Biotechnology (CNB-CSIC))*
PO-126	**Ethylene signal modulates survival of leaf explants in Arabidopsis** *Chae-min Lee (Plant Systems Engineering Research Center, Korea Research Institute of Bioscience and Biotechnology, Korea)*
PO-127	**Molecular mechanism of tenoxicam that inhibits plant immune responses** *Nobuaki Ishihama (RIKEN CSRS, Japan)*
PO-128	**Extracellular NAD(P) is a central signaling molecule of systemic acquired resistance** *Zhonglin Mou (Department of Microbiology and Cell Science, University of Florida, USA)*
PO-129	**Identification of epigenetically regulated genes in plant-virus interaction** *Regis Lopes Correa (Institute for Integrative Systems Biology (I2SysBio), Consejo Superior de Investigaciones Cientificas (CSIC) and Universidad de Valencia, Spain)*
PO-130	**A novel function for transcriptional regulators IBM2 and EDM2 as limiters of salicylic acid-dependant defence genes in Arabidopsis.** *Leonardo Furci (OIST)*
PO-131	**ELF18 INDUCED LONG NONCODING RNA 2 regulates the defense response by modulating CHITINASE expression** *Jun Sung Seo (Institution of GreenBio Science and Technology, Seoul National University, Republic of Korea)*
PO-132	**Identification of binding proteins of long non-coding RNA that act in plant infection defense** *HUIYUAN JIA (Nagoya City University, Japan)*
PO-133 CC22	**AGO2 condensates behavior after bacterial inoculation** *Moriaki Saito (Department of Microbiology and Plant Pathology, Center for Plant Cell Biology, Institute for Integrative Genome Biology, University of California, Riverside, USA)*
PO-134	**Translational control of pathogen-triggered gene expression in the Arabidopsis root: global and gene-specific approaches** *Wolfgang Dröge-Laser (University of Würzburg)*
PO-135	**Translation dynamics of the plant-virus interaction** *Gemma Sans-Coll (Instituto de Hortofruticultura Subtropical y Mediterránea “La Mayora”, Universidad de Málaga-Consejo Superior de Investigaciones Científicas (IHSM-UMA-CSIC))*
PO-136	**Translation initiation landscape profiling reveals hidden open-reading frames required for the pathogenesis of tomato yellow leaf curl Thailand virus** *Chin-Wen Chiu (The Agricultural Biotechnology Research Center of Academia Sinica, Taiwan)*
PO-137	**DNA binding activity of CAMTA3 is essential for its function: Identification of critical amino acids for its transcriptional activity** *KASAVAJHALA V.S.K. Prasad (Department of Biology, Colorado State University, Fort Collins, CO-80526, USA)*
PO-138	**Subgenome-dominant expression and alternative splicing in response to Sclerotinia infection in polyploid Brassica napus and progenitor species** *Keith Adams (University of British Columbia)*
PO-139	**Should I stay or should I go: nuclear mRNA retention during plant defense** *Tessa Visscher (Plant-Microbe Interactions, Utrecht University, the Netherlands)*
PO-140	**The Role of Nuclear Pore during Effector-triggered Immunity** *Xing Zhang (Howard Hughes Medical Institute and Duke University)*
PO-141	**Novel eINTACT system dissects bacterial exploitation of plant osmosignaling to promote disease** *Yuan You (Technical University of Munich, Germany)*
PO-142	**Proteomic analysis to understand chloroplast-nucleus communication in plant immunity.** *Seungmee Jung (Department of Molecular Biology, College of Agriculture, Life Sciences and Natural Resources, University of Wyoming, Laramie, WY USA.)*
PO-143	**Toward identification of host cell death-inducing genes of Colletotrichum higginsianum via transient gene expression in Arabidopsis thaliana leaves** *Katsuma Yonehara (RIKEN, Japan)*
PO-144	**Dynamics of Plasma Membrane Nanodomains during Disease Response in Arabidopsis thaliana** *Saki Takayama (Ritsumeikan University, Japan)*
PO-145	**Microbiota-mediated immunocompetence in Arabidopsis** *Bradley C. Paasch (Duke University, USA)*
PO-146	**The gene regulatory network in roots that create a disease suppressive soil** *Run Qi (Plant-Microbe Interactions, Department of Biology, Faculty of Science, Utrecht University, Utrecht, Netherlands)*
PO-147	**Functional analysis of rym-mediated resistance against Barley yellow mosaic virus infection to root and leaf in barley** *Hongjing Zhu (Institute of Crop Science, National Agriculture and Food Research Organization (NARO), Tsukuba, Japan)*
PO-148 CC21	**Is Ca2+-induced activation of Arabidopsis lipoxygenase 2 involved in green leaf volatile burst?** *Kenji Matsui (Yamaguchi University, Japan)*
PO-149	**Functions of Green Leaf Volatiles in Direct and Indirect Defense of Plants against Herbivores** *Rika Ozawa (Kyoto University, Japan)*
PO-150	**Real-time visualization of green leaf volatile-sensory Ca2+ signaling in Arabidopsis** *Masatsugu Toyota (Saitama University)*

PO-151	**Single-cell gene expression profiles of glucosinolate-myrosinase defense system-associated cells** *Taro Maeda (Keio University, Japan)*
PO-152 CC14	**The phytocytokine AtCAPE9 and its receptor AtCAPER1 functions on plant systemic stomatal immunity** *Chi-Hsin Chang (Agricultural Biotechnology Research Center, Academia Sinica, Taiwan)*
PO-153 CC09	**Investigating the Role of Carbohydrate Metabolism in Bacterial-Triggered Stomatal Movements Using the Model System Arabidopsis thaliana and Pseudomonas syringe pv tomato** *Lucia Piro (ETH Zurich)*
PO-154	**High humidity-induced abscisic acid catabolism critical for plant resistance against bacterial water acquisition and pathogenesis** *Shigetaka Yasuda (Nara Institute of Science and Technology, Japan)*
PO-155	**Preserving salicylic acid-mediated plant immunity in a warming climate** *Jonghum Kim (Department of Biology, Duke University, USA)*

05 Symbiosis/Parasitism

PO-156	**Iron effects on prehaustorium formation in Phtheirospermum japonicum** *MOHD HAFIFI BIN ABU BAKAR (Nara Institute of Science and Technology)*
PO-157	**A role for phytocytokines during parasitic plant haustorium formation** *Maxwell Fishman (RIKEN Center for Sutainable Resource Science)*
PO-158	**snRNA-seq reveals the transcriptional landscape for host-regulated vascular connections in Arabidopsis and parasitic plant interaction.** *Mengqi Cui (Nara Institute of Science and Technology)*
PO-159	**Characterization of rhizobacteria-induced immunity using Arabidopsis** *Mack Loranger (Department of Cell & Systems Biology, University of Toronto)*
PO-160 CC13	**Studying the genetic basis for plant-microbe associations using a synthetic biology approach** *Jose R Dinneny (Stanford University)*
PO-161	**Involvement of receptor proteins for peptidoglycans in mediation of growth promoting effects by Bacillus pumilus TUAT1 in Arabidopsis thaliana.** *Md Monirul Islam (Institute of Food and Radiation Biology, Bangladesh Atomic Energy Commission, Dhaka-1207, Bangladesh.)*
PO-162	**The missing link between Casparian strip integrity and rhizobacterial colonization** *Huei-Hsuan Tsai (University of Lausanne, Switzerland)*
PO-163	**Rhizobium vitis VAR03-1 enhances Arabidopsis thaliana primary root growth under nutrient-limited conditions** *Niarsi Merry Hemelda (Okayama University)*
PO-164	**A plant endophytic bacterium, Burkholderia sp. strain 869T2, promotes plant growth of Arabidopsis, lettuces, and several other vegetables** *Hau-Hsuan Hwang (Department of Life Sciences, National Chung Hsing University, Taichung, Taiwan 402)*
PO-165	**Deciphering the molecular mechanism of plant growth-promoting rhizobacterium Pseudomonas sp. CM11 on plant promotion** *Zhuang Yang (Cluster of Plant Developmental Biology, Wageningen University and Research, Netherlands)*
PO-166	**Dissecting bacterial root colonization strategies using complex synthetic communities on diverse hosts** *Gijs Selten (Utrecht University)*
PO-167	**Designing the assessment platform for determining the impacts of microbes to plant stress resilience** *Tao-Ho Chang (Academy of Circular Economy, National Chung Hsing University, Taiwan)*
PO-168	**Microbiome colonization leads to emergent plant phenotypes at elevated temperature.** *Hannah M. McMillan (Department of Biology, Duke University, Durham, NC 27708, USA)*
PO-169	**Root endophyte Colletotrichum tofieldiae promotes plant growth and recruits beneficial bacteria to roots under laboratory and field conditions with nitrogen deficiency** *Kei Hiruma (The University of Tokyo)*
PO-170 Online-only	**Root ER bodies and tryptophan derived secondary metabolites modulate root microbiota assembly** *Arpan Kumar Basak (Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University, Krakow, Poland)*

06 Epigenetics

PO-171	**Site-specific epigenetic regulation-mediated plant defense resposne** *Yuan Wang Wang (Institute of Genetics and Developmental Biology, Chinese Academy of Sciences)*
PO-172	**Elucidation of molecular mechanism underlying the antagonistic roles of class I and II RPD3-like histone deacetylases in response to environmental stresses** *Minoru Ueda (Plant Genomic Network Research Team, RIKEN CSRS, Japan)*
PO-173	**Hi-C Analyses Reveal Altered Chromatin Conformation Under Elevated CO2** *Scott Lewis (Donald Danforth Plant Science Center, MO, USA)*
PO-174	**Regulatory mechanism of heat-active retrotransposons by SET Domain Proteins SUVH2** *Niu Xiaoying (Hokkaido university, Japan)*

PO-175	**Compensation of H2A.Z and Polycomb Repressive Complex 2 in Determining Plant Cell Fate under Low Ambient Temperature** *Kehui Zhu (Key Laboratory of Plant Cell and Chromosome Engineering, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing)*
PO-176	**Epigenetic regulation by a long-term environment-responsive promoter of Arabidopsis halleri** *Hanako Shimizu (Kyoto University, Japan)*
PO-177	**Co-transcriptional regulation of VIN3 expression by a RNA binding protein during vernalization** *Yusheng Zhao (CAS, institute of genetics and developmental biology)*
PO-178	**A coiled-coil protein associates Polycomb Repressive Complex 2 with KNOX/BELL transcription factors to maintain silencing of cell differentiation-promoting genes in the shoot apex** *Wentao Wang (Huazhong Agricultural University)*
PO-179	**Down to earth: VAL1 and VAL2 affect root development in Arabidopsis** *José María Olvera Herrera (Laboratorio de Genética Molecular, Epigenética, Desarrollo y Evolución de plantas. Instituto de Ecología, Universidad Nacional Autónoma de México, México)*
PO-180	**Chromatin remodeling in the regulation of somatic genome integrity and meiotic inheritance in Arabidopsis** *Wen Hui Shen (IBMP-CNRS, 12 rue du Général Zimmer, 67084 Strasbourg, France)*
PO-181	**Transposition and silencing mechanisms of Tpn1 family transposable elements in the Japanese morning glory** *Yuki Mizunaru (Grad. Sch. of SLS., Kyushu Univ.)*
PO-182	**Effect of transposon mobilization on genomic imprinting in Arabidopsis** *Gerardo del Toro de León (Max Planck Institute of Molecular Plant Physiology)*
PO-183	**Antagonistic regulation of endosperm development by maternally and paternally imprinted genes in Arabidopsis thaliana** *Yuko Wada (Nara Inst. of Sci. and Tech., Japan)*
PO-184	**Dissecting parent-of-origin allele specific expression in Arabidopsis hybrids using fluorescence-activated nuclear sorting** *Ida Velle Myking (University of Oslo, Norway)*
PO-185	**Upstream regulator of genomic imprinting in rice is a small RNA-associated chromatin remodeler** *Avik Kumar Pal (National Centre for Biological Sciences, Tata Institute of Fundamental Research, GKVK Campus, Bangalore 560 065, India)*
PO-186	**Sbf I-based DNA double-strand breaks induce histones H4K16ac and H2A.Z deposition at multiple cleavage sites in Arabidopsis thaliana** *Kohei Kawaguchi (Kyoto Prefectural University, Kyoto, Japan)*
PO-187	**Single-molecule Targeted Accessibility and Methylation Sequencing of Centromeres, Telomeres, and rDNAs in Arabidopsis** *Weipeng Mo (Department of Biology, School of Life Sciences, Southern University of Science and Technology, Shenzhen 518055, China)*
PO-188	**Cotranscriptional demethylation induces global loss of H3K4me2 from active genes in Arabidopsis** *Shusei Mori (The University of Tokyo, Japan)*
PO-189	**Regulatory mechanisms and roles of centromere arrangement in Arabidopsis thaliana** *Takuya Sakamoto (Fac. Sci. Tech., Tokyo Univ. Sci., Japan)*
PO-190	**Transition of histone H2A.Z distribution on the genic region in the evolution of Arabidopsis** *Soichirou Satoh (Kyoto Prefectural University, Kyoto, Japan)*
PO-191 CC24	**Gene-transposon transcripts can be epigenetically regulated and impact gene response to stress conditions in Arabidopsis thaliana** *Jeremy Berthelier (Plant Epigenetics Unit, Okinawa Institute of Science and Technology (OIST), Okinawa, Japan)*
PO-192	**Investigating small RNA-mediated silencing mechanisms in duckweeds** *Veronica Barragan-Borrero (Gregor Mendel Institute of Molecular Plant Biology, Vienna, Austria)*
PO-193 CC12	**Translation-coupled Epigenetic Regulation of Transposable Elements in Plants** *Zhen Lei (CAS Center for Excellence in Molecular Plant Sciences)*
PO-194 CC24	**RNA deadenylation pathway suppresses transposable elements in Arabidopsis** *Ling Wang (CAS Center for Excellence in Molecular Plant Sciences / Institute of Plant Physiology and Ecology)*
PO-195	**RNA-directed DNA Methylation promotes genome integrity in Arabidopsis epiRILs** *ATSUSHI SHIMADA (Okinawa Institute of Science and Technology, Japan)*
PO-196	**Identification of underlying mechanisms involved in transposon activity and distribution in natural accessions of Arabidopsis thaliana** *Laura Diezma Navas (Gregor Mendel Institute (GMI), Vienna, Austria)*
PO-197	**Comprehensive characterization of transposable element-encoded genes and their function in Arabidopsis thaliana** *Carles Borredá (Institute of Plant Sciences Paris-Saclay (IPS2), Université Paris-Saclay, INRAE, Université Evry, Université Paris Diderot)*
PO-198	**The roles of histone H2A variants for the establishment of transposon-specific silent modification in Arabidopsis** *Shoko Oda (The University of Tokyo)*
PO-199	**Induction of T-DNA amplification by retrotransposon-derived sequences** *Wenxin Yuan (Yale University, Department of Molecular, Cellular and Developmental Biology, New Haven, Connecticut, USA)*

PO-200	**Molecular mechanisms on the maintenance of epigenetic silent marks regulated by histone variant H2A.W and chromatin remodeler DDM1** *Akihisa Osakabe (Department of Biological Sciences, The University of Tokyo, Japan)*
PO-201	**Re-analysis of publicly available methylomes using signal detection yields new information** *Alenka Hafner (Pennsylvania State University)*
PO-202	**High parent dominance of trimethylation of lysine 27 of histone H3 level in intraspecific hybrids of Arabidopsis thaliana** *Ryo Fujimoto (Kobe University, Japan)*
PO-203	**The Influence of loss of DECREASE IN DNA METHYLATION 1 function on heterosis in Arabidopsis** *Keita Nishimura (Kobe University, Graduate School of Agricultural Science, Kobe, Japan)*
PO-204	**Contribution of epigenetic mutations to the adaptive evolution of plant by regulating specialized** *Kazumasa Shirai (Kyushu Institute of Technology, Japan)*
PO-205	**Live-cell imaging of H3K4me3 in Arabidopsis thaliana** *Megumi Matsuoka (Department of Integrative Biosciences, The University of Tokyo, Japan)*
PO-206	**Enzyme-based fluorescence labeling of DNA methylation on a chromosome scale** *Min Jeong Kim (Department of Agriculture, Forestry and Bioresources, Seoul National University, Seoul 08826, Korea)*
PO-207	**Real-time visualization of somatic retrotransposition reveals principles of genomic permissivity to transposon integration** *Jie Chu (National Key Laboratory of Plant Molecular Genetics, CAS Center for Excellence in Molecular Plant Sciences, Chinese Academy of Sciences, Shanghai 200032, China.)*
PO-208 Online-only	**A Novel strategy to enhance phenotypic variation in plants** *Hidayah Faisal Alotaibi (Doctor)*

07 RNA biology

PO-209	**RNA triple helical structure facilitates retrotransposon mobilization in Arabidopsis** *Hui Li (CAS Center for Excellence in Molecular Plant Sciences / Institute of Plant Physiology and Ecology)*
PO-210 CC28	**Proof of concept: circular antisense RNAs (caRNAs) as a new mode of action for RNA-based plant protection** *Timo Schlemmer (University of Regensburg, Regensburg)*
PO-211 CC17	**siRNAs derived from nitrate reductases, NIA1 and NIA2, play vital roles in growth and stress adaptation** *Yan Yan (Institute of Plant and Food Science, Department of Biology, Southern University of Science and Technology, Shenzhen, 518055, China)*
PO-212	**The negative effect of flavonoids against dsRNA-cleaving activities of Dicer-like proteins** *Midori Tabara (Ritsumeikan University)*
PO-213	**ARGONAUTE1 nuclear/cytoplasmic shuttling controls small RNA regulation in Arabidopsis thaliana.** *Belén Moro (Centre for Research in Agricultural Genomics (CRAG))*
PO-214	**Functions of Arabidopsis FHA2 in miRNA biogenesis** *Joong-Tak Yoon (Yonsei University, Republic of Korea)*
PO-215 CC12	**Plant miRNA-target 3′-end pairing affects miRNA-mediated translational repression** *Ho-Ming Chen (Academia Sinica, Taiwan)*
PO-216	**Forward genetics identifies a DEAD box RNA helicase and a DnaJ-domain chaperone as new miRNA biogenesis factors** *Florian Brioudes (Swiss Federal Institute of Technology (ETH), Zürich, Switzerland)*
PO-217	**Reevaluation of Intracellular DCL1 Localization of Wild-type and Mutant Alleles in Relevance to Functional Ability and Phenotypes** *Yuichiro Watanabe (Dept. of Life Sciences, Grad. School of Arts and Sciences, University of Tokyo)*
PO-218	**An Evolutionarily Conserved Secondary Structure motif regulates the miRNA cleavage** *Yueying Zhang (John Innes Centre,UK)*
PO-219	**Chromatin-associated microprocessor assembly is regulated by the U1 snRNP auxiliary protein** *Artur Jarmolowski (Department of Gene Expression, Faculty of Biology, Institute of Molecular Biology and Biotechnology, Adam Mickiewicz University, Poznan 61-614, Poland.)*
PO-220	**A mutation in the Arabidopsis tri-snRNP associated protein suppressesthe sta1-1 defects by restoring protein-protein interaction** *Heejin Kim (Sogang university, Korea)*
PO-221	**A U1 snRNP component regulates thermomorphogenesis through alternative RNA splicing in** *Geeng-Loo Chong (Institute of Plant and Microbial Biology, Academia Sinica, Taiwan)*
PO-222	**Dynamic RNA methylation modulates growth in response to light and temperature in Arabidopsis** *Ullas Pedmale (Cold Spring Harbor Laboratory)*
PO-223	**Minor-intron splicing is required for proper HSP-mediated plant response to heat shock** *Zofia Szweykowska Kulinska (Department of Gene Expression, Institute of Molecular Biology and Biotechnology, Faculty of Biology, Adam Mickiewicz University, Poznan, Poland)*
PO-224	**Serine/Arginine-rich 45-mediated Transcriptional and Splicing Regulation in Plant Immunity in Arabidopsis thaliana** *Xiao-Ning Zhang (St. Bonaventure University, USA)*

PO-225	**Cleavage Factor I is essential for maintaining the diversity at the 3' ends of mRNA in plants** *Tomohiko TSUGE (ICR, Kyoto University, Japan)*
PO-226	**Minor-intron splicing is important for nutrient-dependent growth regulation in plants** *Kodai Ishibashi (Grad. Sch. Front. Sci., Univ. Tokyo)*
PO-227	**Depletion of Arabidopsis APPAN causes pleiotropic defects in rRNA processing** *Ilyeong Choi (Yonsei university, Korea)*
PO-228	**Dissecting the molecular mode of action of Restorer-of-Fertility-like proteins in plant mitochondria** *Sang Dang Huynh (ARC Centre of Excellence in Plant Energy Biology - School of Molecular Sciences, The University of Western Australia)*
PO-229	**Interaction between polyadenylation and C-to-U editing of mitochondrial mRNA involved in cytochorome c maturation** *Akihito Mamiya (Dept. Biol. Sci., Grad. Sch. Sci., Univ. Tokyo)*
PO-230	**Suppression of the dwarf phenotype of acl5, a mutant defective in thermospermine biosynthesis by a single-base change in a uORF of SAC51** *Yuichi Nishii (Okayama University, Japan)*
PO-231	**Role of pre-mRNA splicing in lateral root morphogenesis regulated by plastid signal** *Natsu Takayanagi (The University of Tokyo, Japan)*
PO-232	**A GWAS-driven CROSS-SPECIES APPROCH TOWARDS A SPLICING CODE** *Sureshkumar Balasubramanian (School of Biological Sciences, Monash University, VIC 3800, AUSTRALIA)*
PO-233	**Arabidopsis mRNA decay landscape shaped by XRN 5′-3′ exoribonucleases** *Wan-Yin Han (Agricultural Biotechnology Research Center, Academia Sinica)*
PO-234 CC17	**Arabidopsis DXO1, a decapping enzyme for NAD-capped RNAs, activates RNMT1 to methylate the mRNA guanosine cap** *Chen Xiao (HongKong Baptist University, HongKong)*
PO-235	**Assessing global impact of alternative splicing using multi-omics strategy** *Andres Reyes (Department of Plant Biology, Carnegie Institution for Science, Stanford, CA, USA.)*
PO-236 CC12	**NMD and translation of intergenic splicing-mediated polycistronic transcripts** *Yukio Kurihara (The University of Tokyo, Japan)*
PO-237	**Structural feature and function of pre-tRNA splicing enzymes from Arabidopsis thaliana and rice** *Kazuhito Akama (Graduate School of Natural Science and Technology, Shimane University, Japan)*
PO-238	**Single-cell transcriptome map and distribution of mobile mRNAs in heterografted Arabidopsis thaliana in response to nutritional changes** *Yagmur Hasbioglu (Max Planck Institute of Molecular Plant Physiology, Potsdam-Golm, Germany)*
PO-239 CC31	**Dose-dependent long-distance movement of microRNA399 duplex regulates phosphate homeostasis in Arabidopsis** *Chih-Pin Chiang (Agricultural Biotechnology Research Center, Academia Sinica, Taiwan)*
PO-240	**The role of Arabidopsis Cold Shock Proteins in the regulation of RNA mobility** *Diego Pinheiro Brito (Max Planck Institute of Molecular Plant Physiology, Germany)*
PO-241	**The emergent complexity of systemic mRNA transport by m5C-methylation** *Ying Xu (Max Planck Institute of Molecular Plant Physiology)*
PO-242 CC33	**Insights into tRNA-like structures (TLS) as motifs facilitating long-distance transport of mRNAs** *Eleftheria Saplaoura (Max Planck Institute for Molecular Plant Physiology)*
PO-243 CC28	**The role of plant extracellular vesicles in mRNA intercellular trafficking** *HUAN-CHI TIEN (Institute of Plant and Microbial biology, Academia Sinica)*
PO-244	**Expanding the horizons of plant RNA research using single molecule FISH** *Susan Duncan (John Innes Centre)*
PO-245	**Simultaneous detection of miRNA and mRNA at the single-cell level in plant tissues** *Wen-Hsiung Li (Academia Sinica)*
PO-246 Online-only	**Transcripts with long or structured translated upstream open reading frames (uORFs) can escape nonsense-mediated mRNA decay (NMD) in plants** *Orit Shaul (Bar-Ilan University, Israel)*
PO-247 Online-only	**A defect in an RNA metabolic enzyme suppresses the adverse effect of the accumulation of polyadenylated mitochondrial mRNA in Arabidopsis.** *Takashi Hirayama (Okayama Univ. IPSR)*
PO-248 Online-only	**Cell-type specific mRNA delivery in heterografted Arabidopsis revealed by single-cell transcriptomics** *Federico Apelt (Max Planck Institute of Molecular Plant Physiology, Germany)*

08 Translation

PO-249	**The phosphorylation of carboxyl-terminal eIF2α by SPA kinases contributes to enhanced translation efficiency during photomorphogenesis** *Hui-Hsien Chang (National Taiwan University, Taiwan)*
PO-250	**Functional study of PHYTOCHROME INTERACTING FACTOR in the translational regulation during photomorphogenesis** *Wei Lin (Department of Biochemical Science & Technology, National Taiwan University)*
PO-251	**Dynamic phosphorylation of ribosomal protein S6A ensures the successful development of young Arabidopsis seedlings** *Yueh Cho (Institute of Plant and Microbial Biology, Academia Sinica, Taiwan)*

PO-252	**Role of G3BP1 in Plant Stress Granules** *Fatimah Abdulhakim (Biological and Environmental Sciences and Engineering, King Abdullah University of Science and Technology, Thuwal, Saudi Arabia)*
PO-253	**Functional characterization of the deubiquitinase OTU2 role in Arabidopsis thaliana stress granules biology.** *Violeta Londono Velez (Center for Desert Agriculture, Biological and Environmental Science and Engineering Division, King Abdullah University of Science and Technology (KAUST), Thuwal, Saudi Arabia)*
PO-254 CC12	**Deciphering the role of specialized ribosomes in plants´ translation efficiency** *Jose Antonio Duarte-Conde (Instituto de Hortofruticultura Subtropical y Mediterránea, Universidad de Málaga-Consejo Superior de Investigaciones Científicas (IHSM-UMA-CSIC))*
PO-255	**Linking cold induced variation in RPL7 paralog abundances to the emergence of specialized ribosomes** *Dione Gentry Torfer (Max Planck Institute of Molecular Plant Physiology, Potsdam-Golm, Germany)*
PO-256	**Characterization of AtSQTL1, the Dedicated Chaperone of AtRPL10 in Arabidopsis** *Zhi Xing Lau (IPMB, Academia Sinica)*
PO-257	**Genome-wide identification of Arabidopsis non-AUG-initiated upstream ORFs with evolutionarily conserved regulatory sequences that control protein expression levels** *Yuta Hiragori (Graduate School of Agriculture, Hokkaido University)*
PO-258	**Modeling plant alternative translation initiation sites reveals evolutionarily conserved cis-regulatory codes in eukaryotes** *Ya-Ru Li (Biotechnology Center in Southern Taiwan, Academia Sinica, Taiwan)*

09 Nutrition

PO-259 CC07	**NLP7 is a central integrator of transcription networks in nitrogen signaling and drought stress** *Jose M Alvarez (Centro de Biotecnologia Vegetal, Facultad de Ciencias de la Vida, Universidad Andres Bello, Santiago 8370186, Chile)*
PO-260 CC19	**Nitrogen-responsive SnRK1-FBH4 module affects flowering time and metabolism in Arabidopsis** *Miho Sanagi (Hokkaido University, Japan)*
PO-261	**Coregulation of glutamine synthetase1;2 (GLN1;2) and NADH-dependent glutamate synthase (GLT1) gene expression in Arabidopsis roots in response to ammonium supply** *Soichi Kojima (Tohoku University)*
PO-262	**Nitrate fluctuation impacts cytokinin biosynthesis through modification of IPT3 chromatin profiles in Arabidopsis roots.** *Fanny Bellegarde (Nagoya University, Nagoya, Japan)*
PO-263 CC01	**Histone chaperone NAP1 proteins are involved in plant growth under nitrogen deficient conditions in Arabidopsis thaliana** *Jie Linnan (Hokkaido University)*
PO-264	**Elevated CO2 impairs Arabidopsis N nutrition through the inhibition of the root high-affinity nitrate uptake system** *Alain Gojon (IPSiM, Univ Montpellier, CNRS, INRAE, Institut Agro, Montpellier, France)*
PO-265	**Regulation of high-affinity nitrate uptake activity by NRT2.1 phosphorylation** *Yuri Ohkubo (Nagoya University, Japan)*
PO-266	**Role of potassium-dependent alternative splicing of MYB59 in maintenance of potassium concentration in shoots of Arabidopsis thaliana** *Sho Nishida (Faculty of Agriculture, Saga University, Japan)*
PO-267	**Glucosinolate catabolism maintains glucosinolate profiles and transport in sulfur-starved Arabidopsis** *Liu Zhang (Kyushu University, Japan)*
PO-268	**The Necessity of SLIM1 C-Terminal Region for Sulfur Deficiency Response** *Akiko Maruyama-Nakashita (Kyushu University, Japan)*
PO-269	**Plant iron nutrition: towards a new paradigm?** *Christian DUBOS (IPSiM, Univ Montpellier, CNRS, INRAE, Institut Agro, Montpellier, France)*
PO-270	**FEP/IMA peptides are required for Fe regulation in vascular plants.** *Aleksandr Sorokin (Group of Environmental Stress Response Systems, Institute of Plant Science and Resources, Okayama University, Okayama, Japan)*
PO-271	**The Effect of Chromatin Remodeling on Iron Homeostasis** *Justin Su (Department of Biology, Amherst College, USA)*
PO-272	**Investigating the Biological Role of Ferroportin 3** *Jeeyon Jeong (Department of Biology, Amherst College, USA)*
PO-273	**Identification of Sorghum bicolor iron transporter gene using Arabidopsis gene knockout line.** *Ryoichi Araki (Wakayama University, Japan)*
PO-274	**A novel Arabidopsis uptake transporter of coumarin plays a crucial role in root Fe uptake** *Shunsuke WATANABE (IPSiM, Univ Montpellier, CNRS, INRAE, Institut Agro, France)*
PO-275	**A FIT/WRKY complex modulates the biosynthesis of coumarins in response to environmental pH** *Jorge Enrique Salazar Henao (Institute of Plant and Microbial Biology, Academia Sinica, Taipei 11529, Taiwan)*

PO-276	**Coumarins delineate the cross-talk between manganese and iron uptake** *Yi-Hsiu Tsai (Institute of Plant Biology, National Taiwan University, Taiwan, R.O.C)*
PO-277	**Understanding the molecular mechanisms mediating the crosstalk between iron and sulfur networks in Arabidopsis.** *David Mendoza (University of Missouri)*
PO-278	**Global ribosome sequencing analysis of Arabidopsis mutant having mutation in a ribosomal protein uL13: boron-dependent growth change and expression of boron transporter genes** *Hirofumi Fukuda (Grad. Schl. Agr. Life Sci., Univ. Tokyo, Japan)*
PO-279	**Inhibition of TOR, a positive growth regulator, rescues root growth suppression under limited boron condition in Arabidopsis thaliana** *Ramita Jamornjureekul (Hokkaido University, Japan)*
PO-280	**Phosphorylation/Dephosphorylation-mediated Regulation of the Polar Localization of a Borate Transporter BOR1 in Arabidopsis thaliana** *Keita Muro (Osaka Metropolitan University, Japan)*
PO-281	**Functional Analysis of Arabidopsis Magnesium Ion Transporter AtMRS2-1** *Xiaoyu Yang (Graduate School of Agricultural and Life Sciences, The University of Tokyo)*
PO-282	**Defensin-like proteins induced by zinc deficiency are involved in Arabidopsis root elongation** *Yoichiro Fukao (Ritsumeikan University)*
PO-283	**Starvation-induced transcriptional control: metabolic signals, transmission via the central metabolic kinase SnRK1 and downstream gene regulation** *Jan Draken (Julius-Maximilians-University Würzburg Department of Pharmaceutical Biology, Germany)*
PO-284	**The Arabidopsis ACR9 protein is a repressor of the glucose signaling pathways** *Hong-Sheng Liao (Institute of Plant and Microbial Biology, Academia Sinica, Taipei 11529, Taiwan)*
PO-285	**Functional analysis of IDD4, a transcription factor which regulates root growth through sugar signaling in early developmental stages** *Ryoichi Shiroma (Shizuoka University, Japan)*
PO-286	**Nutrient sensing in plants by O-GlcNAcylation and O-Fucosylation** *Shouling Xu (Carnegie Institution at Stanford)*
PO-287	**bZIP1, 53 and 63 Transcription Factors are required in Starch Metabolism and Energy Homeostasis to maintain Vigorous Growth** *Raphael de Araújo Campos (University of Campinas)*
PO-288	**Mechanisms for phosphorylation and granule formation of a Raf-like kinase, PHOTOSYNTHESIS-RELATED RAF, in the liverwort Marchantia polymorpha** *Ryuichi Nishihama (Graduate School of Biostudies, Kyoto University, Japan)*
PO-289 Online-only	**Extrachromosomal circular DNA in response to phosphate starvation in Arabidopsis** *Monica Rojas-Triana (Section of Ecology and Evolution, Department of Biology, University of Copenhagen)*

10 Photosynthesis/Energy

PO-290	**The Zinc-Finger Thylakoid-Membrane Protein FIP in involved in photosynthesis apparatus adaptation to changing light condition** *Maciej Jerzy Bernacki (Department of Plant Genetics, Breeding and Biotechnology, Institute of Biology, Warsaw University of Life Sciences, Nowoursynowska Street 159, 02-776 Warsaw, Poland)*
PO-291	**The Role of NTRC, 2-Cys-Peroxiredoxins and thioredoxin f in photosynthesis in Arabidopsis thaliana when acclimated to different light conditions** *Louis Poeker (Ludwig-Maximilians-Universität München (LMU))*
PO-292	**Difference between leaf and single-plant photosynthesis of Arabidopsis thaliana under fluctuating light conditions** *Kazuma Sakoda (NTT Space Environment and Energy Laboratories)*
PO-293	**UV-B acclimation in Arabidopsis thaliana decreases the efficacy of the herbicide atrazine, which is mediated through the UVR8 signaling pathway** *Chris Groves (University of Bristol)*
PO-294	**The function of thylakoid membrane fusion by FZL protein in sustaining optimized photosynthetic electron transfer** *Yu Ogawa (Okayama University, Japan)*
PO-295	**The molecular mechanisms underlying floral organ photosynthesis** *Roisin Fattorini (University of Liverpool)*
PO-296 Online-only	**Chloroplast functions in photoautotrophically cultured green cells of Arabidopsis** *Satomi Takeda (Graduate School of Science, Osaka Prefecture University)*

11 Metabolism/Metabolome

PO-297	**BrMYBR1, an R2R3 MYB transcription factor, directly inhibits anthocyanin biosynthesis in Chinese cabbage** *DaHye Kim (1Division of Horticultural Biotechnology, School of Biotechnology, Hankyong National University)*
PO-298	**Multi-omics approach to elucidate the biosynthesis of diterpene alkaloids in Aconitum japonicum** *Megha Rai (Graduate School of Pharmaceutical Sciences, Chiba University)*
PO-299	**MHP1 and MHL generate odd-chain fatty acids from 2-hydroxy fatty acids in sphingolipids and are related to immunity in Arabidopsis thaliana** *Minoru Nagano (Ritsumeikan University, Japan)*
PO-300	**LIPID RICH 1 regulates the metabolic balance between triacylglycerols and starch in plastids of Arabidopsis thaliana** *Takashi L. Shimada (Graduate School of Horticulture, Chiba University)*
PO-301	**A pair of differentially localized lipid phosphate phosphatases mediate endoplasmic reticulum glycerolipid metabolism in Arabidopsis.** *Van Cam Nguyen (Plant lipid research team, RIKEN Center for Sustainable Resource Science (CSRS), RIKEN Yokohama)*

12 Hormone synthesis

PO-302	**Towards resolving the contribution of the IAOx pathway to auxin biosynthesis in Arabidopsis thaliana** *Mario Fenech-Torres (North Carolina State University)*
PO-303	**Isolation of interactors of Agrobacterium cytokinin synthase Tmr by Proximity Labeling method (PL method)** *Shuhei Komori (Nagoya University, Nagoya, Japan)*
PO-304	**Uncovering Regulatory Mechanisms of Salicylic Acid Biosynthesis and plant systemic immunity in Brassicaceae species** *Heejin Yoo (Department of Plant Biology, Ecology, and Evolution, Oklahoma State University, Stillwater, OK 74078 USA)*
PO-305	**D27-like isomerases in Arabidopsis: at the crossroads of strigolactone and ABA biosynthesis?** *Vilmos Soos (Centre for Agricultural Research, Martonvásár, Hungary)*
PO-306	**Steps catalyzed by unknown enzymes in brassinosteroid biosynthesis.** *Rikuto Hamada (Utsunomiya Univ., Japan)*
PO-307	**Survey the tissue localization of brassinosteroid biosynthesis enzymes by using fluorescent labeled specific inhibitors combined with mutants of CYP90s** *Keimei Oh (Department of Biotechnology, Akita Prefectural University)*
PO-308	**Initiation of root Jasmonate biosynthesis** *Yunjing Ma (Martin Luther University Halle-Wittenberg)*
PO-309	**Genetic analysis of β-carotene isomerase genes in Arabidopsis** *Hitomi Kobuna (Utsunomiya Univ., Japan)*
PO-310	**Strigolactone biosynthesis in Arabidopsis and bryophytes** *Kozue Hiugano (Utsunomiya Univ., Japan)*
PO-311	**Genetic mutant analysis of Arabidopsis CYP707As, which encode key enzymes for ABA catabolism.** *Masanori Okamoto (Utsunomiya Univ., Japan)*
PO-312 Online-only	**Knockout of an ER-localized HSP90 family protein impairs seedling development and cellular auxin homeostasis in Arabidopsis** *Rongmin Zhao (University of Toronto)*

13 Hormone signaling

PO-313	**An activity of phytoene desaturase negatively regulates auxin biosynthesis and signaling** *KANG XU (Grad. Sch. Life., Univ. Hokkaido)*
PO-314	**PIN-Interacting Protein 1 (PIP1), a phospho-lipid modifier, modulates PINs' intracellular trafficking in Arabidopsis** *KWANG HO MAENG MAENG (Department of Biological Sciences, Seoul National University)*
PO-315	**Genetic analysis of the TGN-localized membrane trafficking factor Sec1/Munc18 protein BEN2/VPS45 in Arabidopsis development** *Kosuke Ogita (Life Sciences Program, Graduated School of Agriculture, Meiji University)*
PO-316	**SYP4 Qa-SNARE proteins redundantly regulate auxin distribution and root development in Arabidopsis** *Hirokazu Tanaka (Life Sciences Program, Graduate School of Agriculture, Meiji University)*
PO-317	**Physiological studies on the auxinic regulation of hydrotropism in Arabidopsis thaliana** *Kotaro Akita (Yamagata University, Japan)*
PO-318	**An intronic enhancer directs stomatal lineage and epidermal-specific expression of PIN-FORMED 3 (PIN3) in Arabidopsis** *ZIMIN ZHOU (National University of Singapore)*

PO-319	**Auxin-sensitive autonomous bioluminescence to visualize auxin in near-to-nature conditions** *Michael Karampelias (Laboratory of Plant Hormonal Regulations in Plants, Institute of Experimental Botany, Prague, Czech Republic)*
PO-320	**ABP1-likes and TMKs are co-receptors for extracellular auxin in plants** *Tongda Xu (Fujian Agriculture and Forestry University, Fuzhou, Fujian, China)*
PO-321 CC26	**A phosphoinositide hub connects CLE peptide signaling and polar auxin efflux regulation** *Qian Wang (Department of Plant Molecular Biology, University of Lausanne, CH-1015 Lausanne, Switzerland)*
PO-322	**MAJOR LATEX PROTEINs affect auxin signaling** *Michael Liebthal (Chair of Botany, TUM School of Life Sciences Weihenstephan, Technical University Munich, Freising, Germany)*
PO-323	**Characterization of the BIMP family in Arabidopsis thaliana as a link between brassinosteroid signaling and cortical microtubules in plant growth** *Charlotte Delesalle (Laboratoire de Recherche en Sciences Végétales, University of Toulouse, France)*
PO-324	**A signaling circuit maintains cell integrity during hormone induced cell expansion** *Ajeet Chaudhary (Department of Plant biology, Carnegie Science Stanford)*
PO-325 CC32	**Brassinosteroid receptor BRI1 deubiquitination by UBP12/UBP13 fine-tunes plant growth** *Yongming Luo (Department of Plant Biotechnology and Bioinformatics, Ghent University, Belgium)*
PO-326	**Ectopic expression of a corepressor OsTPR1 in Arabidopsis to dissect the crosstalk between GA and JA signaling pathways** *Shing Lon Ho (Department of Agronomy, National Chiayi University, Taiwan)*
PO-327 CC27	**Chemical biology study of jasmonate signaling by development of a biased agonist derived from stereoisomers of coronatine** *Kengo Hayashi (Graduate School of Science, Tohoku University, Japan)*
PO-328	**Mode of action of a novel putative plant defense activator that induces the accumulation of both jasmonic acid and salicylic acid in Arabidopsis** *Kazuyuki Kuchitsu (Tokyo University of Science, Japan)*
PO-329	**Transcriptome landscape under combinations of Salicylic Acid and Jasmonic Acid in various concentrations** *Atsuki Tomita (Dept. Environment & Info. Studies., Keio Univ.)*
PO-330	**The carboxy terminal transmembrane domain of SPL7 mediates interaction with RAN1 at the endoplasmic reticulum to regulate ethylene signalling in Arabidopsis** *Yanzhi YANG (Peking University)*
PO-331	**Significance of EIN2 Phosphorylation Status to EIN2 Stability and CTR1-independent Ethylene Signaling** *HangWei Zhao (CAS Center for Excellence in Molecular Plant Sciences)*
PO-332	**The miRNA156/SPL9 module controls apical hook development via auxin responses** *Flaviani Gabriela Pierdona (University of Sao Paulo)*
PO-333	**Dissecting apical hook development with small molecules** *Kai Jiang (Southern University of Science and Technology)*
PO-334	**More than just ABA receptors: Ligand spectrum of RCARs from Arabidopsis and Marchantia** *Isabel Doch (Chair of Botany, TUM School of Life Sciences Weihenstephan, Technical University Munich, Freising, Germany)*
PO-335	**Isolation of an Arabidopsis mutant involved in abscisic acid-independent stomatal closure** *Satoko Nakae (Dept. Biol., Fac. Sci., Univ. Kyushu)*
PO-336	**Guard-cell expression of abscisic acid receptors for engineering water efficient-productive plants** *Zhenyu Yang (Department of Botany, Technical University of Munich, Germany)*
PO-337	**bHLH transcription factor AKSs mediate ABA-dependent down regulation of gene expression in guard cells and seedlings** *Yuki Hayashi (Division of Biological Science, Graduate School of Science, Nagoya University)*
PO-338	**Structure-guided engineering of a receptor-agonist pair for inducible activation of the ABA adaptive response to drought** *Jorge Lozano-Juste (Instituto de Biologia Molecular y Celular de Plantas (IBMCP-UPV-CSIC))*
PO-339	**Integrating multi-omics data reveals energy and stress signaling activated by abscisic acid in Arabidopsis** *Takuya Yoshida (Lehrstuhl für Botanik, Technische Universität München, Germany)*
PO-340	**Functional analysis of DOG1-dependent ABA signaling cascade** *Noriyuki Nishimura (National Agriculture and Food Research Organization, Japan)*
PO-341	**The evolution of ABA receptors: Transition to hormone-regulated signaling.** *Assaf Mosquna (the Hebrew University of Jerusalem)*
PO-342	**Phosphoproteomic analysis of Arabidopsis guard cells for screening of SnRK2 substrates** *Kota Yamashita (BASE, Tokyo Univ. Agric. Tech.)*
PO-343	**Abscisic acid and G-protein regulated redox proteome of Arabidopsis** *Sona Pandey (Donald Danforth Plant Science Center, St. Louis, MO USA 63132)*
PO-344	**Characterization of the PEAPOD Jas domain to understand their interaction partner specificity** *Michele Schneider (Department of Plant Biotechnology and Bioinformatics, Ghent University, 9052 Ghent, Belgium)*

14 Organelles/Membranes

PO-345	**Analysis of a nuclear lamina protein CRWN and its interacting proteins** *Sachihiro Matsunaga (Graduate School of Frontier Sciences, The University of Tokyo, Japan)*
PO-346	**The nuclear pore complex is involved in the two-step regulation of centromere arrangement in Arabidopsis thaliana** *Nanami Ito (Dept. of Integr. Biosci., Grad. Sch. of Front. Sci., Univ. of Tokyo, Japan)*
PO-347	**Light-dependent nuclear relocation in land plants: differences and similarities between Arabidopsis thaliana and the liverwort Marchantia polymorpha** *Ikuko Hara-Nishimura (Konan Univ.)*
PO-348	**A pair of phosphoinositide-binding proteins act downstream of the IRE1-bZIP60 pathway and function redundantly in the unfolded protein response** *Chao-Yuan Yu (RIKEN Center for Sustainable Resource Science, Yokohama, Japan)*
PO-349	**Localization dynamics of BGLU18, a β-glucosidase that releases ABA from its glucose conjugates, in Arabidopsis leaf cells under dehydration stress** *Yutong Song (Graduate School of Integrated Sciences for Life, Hiroshima University, Japan)*
PO-350	**Endoplasmic reticulum body in the lateral root cap: Visualization of direct transport of β-glucosidase to the vacuole by correlative light and electron microscopy** *Kiminori Toyooka (RIKEN Center for Sustainable Resource Science)*
PO-351	**MAIGO3-dependent mechanism underlying dynamic capture-and-release process of ER exit sites by Golgi stacks in Arabidopsis** *Junpei Takagi (Fac. Sci. and Grad. Sch. Life Sci., Hokkaido Univ., Japan)*
PO-352	**Nanobody-epitope interaction-based intracellular in vivo immunotracing reveals the bidirectional trafficking of vacuolar sorting receptors** *Peter Pimpl (Southern University of Science and Technology (SUSTech))*
PO-353	**Elucidating the final stages of plant Clathrin-Mediated Endocytosis in vivo and in vitro** *Nataliia Gnyliukh (Institute of Science and Technology Austria (ISTA))*
PO-354	**Subcellular localization of NPR1 shifts between chloroplast and nucleus in accordance with the circadian rhythm** *So Yeon Seo (Sunchon national university)*
PO-355 CC03	**Location, location, location: a system-wide assesment of subcellular protein localization in Arabidopsis roots by mass-spectrometry** *Monique van Schie (Wageningen University, the Netherlands)*
PO-356 CC18	**The role of DGK1 and DGK2 in Membrane Contact Sites and Stress Tolerance** *Selene Garcia-Hernandez (Instituto de Hortofruticultura Subtropical y Mediterránea, Universidad de Málaga-Consejo Superior de Investigaciones Científicas (IHSM-UMA-CSIC))*
PO-357 CC05	**Fuctional characterization of Arabidopsis thaliana Synaptotagmin1 domains using Tricalbin3 chimeras in Saccharomyces cerevisiae.** *Francisco Benitez-Fuente (Departamento de Biologia Molecular y Bioquimica, Instituto de Hortofruticultura Subtropical y Mediterranea "La Mayora", Universidad de Malaga-CSIC, Malaga 29071, Spain)*
PO-358 CC05	**405nm Photostimulation of the Endoplasmic Reticulum-Chloroplast Contact Site in Arabidopsis Hypocotyls Causes Rapid Cytoskeletal Depolymerization, Elevated Cytoplasmic Calcium, and Elevated Organellar ROS** *Sara Maynard (Texas A&M University)*
PO-359 CC18	**SEED LIPID DROPLET PROTEIN 1 and 2 and LD-PLASMA MEMBRANE ADAPTOR form a lipid droplet-plasma membrane contact site that might play a role under stress** *Janis Dabisch (Uni Münster)*
PO-360	**Balanced activities of chloroplasts and mitochondria is crucial for optimal plant growth** *Boon Leong Lim (The University of Hong Kong)*
PO-361	**Defining and dissecting mitochondrial specific stress signalling pathways in Arabidopsis thaliana** *Cunman He (College of Life Science, Zhejiang University, Hangzhou, Zhejiang 310058, P.R. China.)*
PO-362	**The ANAC017 transcription factor links transcriptional and post-translational regulation of mitochondrial biogenesis and signalling.** *James Whelan Whelan (Zhejiang University, China)*
PO-363	**Overexpression of the transcription factor ANAC017 results in a genomes uncoupled phenotype under lincomycin** *Yanqiao Zhu (College of Life Science, Zhejiang University, Hangzhou, Zhejiang 310058, P.R. China)*
PO-364	**An isoform of the plastid RNA polymerase-associated protein FSD3 affects chloroplast development** *Geupil Jang (The National Academy of Sciences, Republic of Korea)*
PO-365	**Analysis for the molecular mechanism of chloroplast development via BPGs, novel brasinosteroid signaling factors** *Ryo Tachibana (Kyoto University, Japan)*
PO-366 CC02	**Sensory plastids in growth- and defense-related epigenetic phenotype adjustment** *Ha Eun Jeh (Pennsylvania State University, PA, USA)*
PO-367	**Comparative transcriptomic analysis to characterize Stromule Regulatory Genes** *Jongchan Woo (University of Wyoming)*
PO-368 CC05	**Light-induced chloroplast biogenesis: photobodies control alternative promoter selection as a mechanism of nucleus-chloroplast communication** *Chan Yul Yoo (School of Biological Sciences, University of Utah, Salt Lake City, UT, 84112, USA)*

PO-369	**Nanotechnology research in Arabidopsis for developing precision agriculture and plant biomanufacturing tools** *Juan Pablo Giraldo (University of California, Riverside)*
PO-370	**Fluorescent staining of the chloroplast outer envelope membrane in living plant cells** *Shintaro Ichikawa (Utsunomiya University, Japan)*
PO-371	**Linkage between ADP-ribosylation and chloroplast stress response under thylakoid proteostasis perturbation** *Kenji Nishimura (Kwansei Gakuin University, Japan)*
PO-372 CC06	**Molecular mechanism for peroxisomal protein transport via the ubiquitin system** *Shoji Mano (National Institute for Basic Biology, Japan)*
PO-373	**A tonoplast-localized magnesium transporter is crucial for stomatal opening in Arabidopsis under high Mg2+condition** *Shin-ichiro Inoue (Nagoya University, Japan)*
PO-374	**IntEResting: RHD3 and RTN3/4 Oppose in ER network connectivity but cooperate in ER-phagy in response to environmental stresses** *Huanquan Zheng (McGill University)*
PO-375	**An Arabidopsis Rab GTPase regulates ER association of ATG18a to promote ER-phagy in response to carbon starvation** *Jiaqi Sun (Shandong University, China)*
PO-376	**KNO1-mediated autophagic degradation of the Bloom syndrome complex component RMI1 promotes homologous recombination** *Poyu Chen (Kanazawa University, School of Biological Science and Technology)*
PO-377	**Dissecting the plant ATG9 vesicle trafficking in autophagy pathway** *KA KIT CHUNG (Centre for Cell & Developmental Biology and State Key Laboratory of Agrobiotechnology, School of Life Sciences, The Chinese University of Hong Kong, Hong Kong, China)*
PO-378	**A novel reciprocal regulation mechanism for SH3P2 in crosstalk between endocytosis and autophagy** *Kai Ching Law (The Chinese University of Hong Kong, Hong Kong China)*
PO-379 Online-only	**Chloroplast chaperone HSP90C C-terminal extension regulates client binding and plant stress resilience** *Bona Mu (University of Toronto, Scarborough)*

15 Cytoskeleton/Cell polarity

PO-380	**Arabidopsis MPK6 Phosphorylates MAP18 to Mediate Root Growth Control in Response to Salt Stress** *Ying Fu (China Agricultural University, China)*
PO-381	**Microtubule-dependent phase separation tunes cell wall spacing in xylem vessels** *Yoshihisa Oda (The University of Tokyo, Japan)*
PO-382	**NIMA-related protein kinases regulate microtubule response to tensile stress in Arabidopsis thaliana** *Yumeko Nomura (Department of Biological Science, Faculty of Science, Okayama University, Japan)*
PO-383	**Elucidating molecular mechanisms of anchoring complexes that stabilize the association of daughter microtubule minus end to their nucleation sites** *Masayoshi Nakamura (Nagoya University, Japan)*
PO-384	**Enzymatic activities and tissue-specific expression of Arabidopsis thaliana class XI and VIII myosins** *Shizuha Ito (Department of Biology, Graduate School of Science, Chiba University, Japan)*
PO-385	**GraFT - Robust spatiotemporal filament disentanglement using a network theoretic framework** *Isabella Østerlund (Department of Plant and Environmental Sciences, University of Copenhagen, 1871 Frederiksberg C, Denmark)*
PO-386	**Structure and regulation of Arabidopsis Myosin XI, MYA2** *Takeshi Haraguchi (Department of Biology, Graduate School of Science, Chiba University, Japan)*
PO-387	**Functional Differentiation among the lipid signaling producing Genes PIP5K1, PIP5K2, and PIP5K3 in Arabidopsis** *Machiko Watari (Institute for Chemical Research, Kyoto university, Japan)*
PO-388	**Molecular mechanisms underlying rapid cell growth in the root epidermis** *Hirotomo Takatsuka (Kanazawa University, Japan)*
PO-389	**Evolution of RHO cell polarity signalling in plants** *Hugh Mulvey (Gregor Mendel Institute (GMI), Austria)*
PO-390 CC32	**Mechanisms underlying polar membrane targeting of SOSEKI protein** *Andriy Volkov (Laboratory of Biochemistry, Wageningen University, Netherlands)*

16 Cell walls

PO-391	**Mutations in Golgi-localised proton pyrophosphatase, AVP2;1 enhances root growth under limited boron supply by changes in cell wall stability** *Amarachukwu Faith ONUH (Hokkaido University, Japan)*
PO-392	**Analysis of regulatory mechanisms of cell wall construction during fruit morphological changes under calcium deficiency conditions in Tomato (Solanum lycopersicum) cv. 'Micro Tom'** *Kiei Soyama (Graduate School of Science and Technology, University of Tsukuba, Japan)*

PO-393	**Hormone-regulated expansins localization and their putative role in cell wall biomechanics controlling the Arabidopsis root growth** *Marketa Samalova (Masaryk University, Czech Republic)*
PO-394	**TMK-based cell-surface auxin signalling activates cell-wall acidification** *Wenwei Lin (Fujian Agriculture and Forestry University)*
PO-395	**Contribution of Epidermis and Vasculature to the Mechanical Integrity of Arabidopsis Inflorescence Stem** *Mariko Asaoka (Tokyo Gakugei University, Tokyo, Japan)*
PO-396	**Transcriptional Control of Hypocotyl Cell Elongation by SHORT-ROOT** *Jun Lim (Dept. of Systems Biotechnology, Konkuk University, Seoul 05029, Korea)*
PO-397	**CALCIUM-DEPENDENT PROTEIN KINASE32 regulates cellulose biosynthesis through post-translational modification of cellulose synthase** *Ying Gu (Pennsylvania State University)*
PO-398 CC14	**A cell wall-modifying gene-dependent CLE peptide transport in conferring drought resistance** *Satoshi Endo (Kyoto Univ. Adv. Sci., Japan)*
PO-399	**Periodicity and disorder in protoxylem secondary cell wall of Arabidopsis is orchestrated by an ABA-ROP11 toggle switch** *Shaul Yalovsky (School of Plant Sciences and Food Security, Tel Aviv University)*
PO-400	**Proper synthesis of Secondary Cell Wall in Arabidopsis requires regulation by copper-miRNAs and the miRNA-processing protein Dicer-like 1** *Alessandro Giannetti (University of Copenhagen)*
PO-401	**Cloning and Functional Analyses of SET Gene Whose Loss-of-Function Suppresses de-etiolatedt3-1 Inflorescence Stem Dwarfism** *Shizuka Gunji (Department of Biology, Tokyo Gakugei University)*
PO-402 CC14	**An Evolutionarily Conserved Long-distance Migrating Peptide Regulates Lignin Biosynthesis Pathway and Plant Immunity** *Ying-Lan Chen (Department of Biotechnology and Bioindustry Sciences, College of Bioscience and Biotechnology, National Cheng Kung University, Tainan, Taiwan)*
PO-403	**Elucidating the role of lignification during silique development in Arabidopsis thaliana** *Justin Nichol (University of Calgary)*
PO-404 Online-only	**Redox partner preference of monolignol cytochrome P450 monooxygenases C4H and F5H** *Xianhai Zhao (Brookhaven National Laboratory)*

17 Symplasmic signaling/Plasmodesmata

PO-405	**Changes in plasmodesmal stress responses across development** *Emma C. Raven (John Innes Centre, Norwich, United Kingdom)*
PO-406	**Reaction Without Diffusion: Role Of Plasmodesmata in Floral Pigmentation Patterning** *Steven Harmon-Jarsen (University of Connecticut)*
PO-407	**The primary PD density is reduced in brood cells of the moss Physcomitrium patens** *Chiyo Jinno (Hokkaido University, Japan)*
PO-408 CC20	**A novel mechanism for plasmodesmata mediated cell-cell communication in plants** *Marija Smokvarska (Laboratoire de Biogenèse Membranaire, UMR5200, CNRS, Université de Bordeaux, Villenave d'Ornon, France)*
PO-409	**AGP polysaccharide chains are required for normal biogenesis of plasmodesmata** *Mari Ohnishi Ogawa (Nagoya university)*
PO-410	**Exploring the intercellular plasmodesmal protein transport in Marchantia polymorpha** *Kuan-Ju Lu (Graduate Institute of Biochemistry, National Chung Hsing University)*
PO-411 CC31	**Investigating the role of the Arabidopsis ROTAMASE CYCLOPHILIN gene family in organelle-mediated mobile mRNAs transport** *Yu-Hsien Chang (Institute of Plant and Microbial Biology, Academia Sinica, Taiwan)*
PO-412 CC31	**A cell wall-modifying enzyme controls symplastic movement of RNA silencing in aerial Arabidopsis tissues** *Florence Brioudes (Swiss Federal Institute of Technology (ETH-Zürich), Switzerland)*
PO-413	**Arabidopsis cyclophilins direct intracellular transport of mobile mRNA via organelle hitchhiking** *Tien-Shin Yu (Institute of Plant and Microbial Biology, Academia Sinica, Taipei, Taiwan)*

18 Circadian & biotic rhythms

PO-414	**Weather-dependent flower movement: the functions and mechanisms for downward-facing of flowers during rain** *Akari Shibata (Kyoto university, Japan)*
PO-415 CC29	**Microfocus X-ray CT Analysis of Arabidopsis Petioles for Leaf Movement** *Maika Hayashi (NAIST, Japan)*
PO-416 CC21	**CIRCADIAN CLOCK-ASSOCIATED1 (CCA1) controls resistance to aphid by altering indole glucosinolate production** *Keyan Zhu Salzman (Texas A&M University)*
PO-417	**Association of NPR1 with ROS and ethylene signaling pathways in relation to the circadian rhythm** *Yumi Kim (Sunchon national university)*

PO-418	**Circadian-period variation underlies the local adaptation of photoperiodism** *Tomoaki Muranaka (Nagoya University, Japan)*
PO-419	**Identifying E3 ubiquitin ligases interacting with Arabidopsis circadian clock regulators** *Chen-An Chen (Institute of Plant Biology, National Taiwan University, Taipei, Taiwan)*
PO-420	**The essential role of TOC1 phosphorylation in selective circadian clock gene regulation** *David Somers (Ohio State University, USA)*
PO-421 CC08	**Quantity regulation of TOC1 and PRR5 for temperature compensation in the Arabidopsis circadian clock** *Akari Maeda (Nagoya university, Japan)*
PO-422	**Circadian rhythms under controlling light irradiation in accordance with lunar rhythm.** *Naoki Seki (Toyota Boshoku Corporation)*
PO-423 CC29	**Long-distance circadian coordination via a phloem-delivered mobile transcript** *András Székely (Max Planck Institute of Molecular Plant Physiology)*
PO-424	**Imaging and functional analysis of 24-h rhythmic interactions of circadian core oscillators in Arabidopsis** *Xiaodong Xu (Henan University, China)*
PO-425	**BIG regulates the circadian clock and development** *Dora Luz Cano Ramirez (Sainsbury Laboratory, University of Cambridge, Bateman Street, Cambridge CB2 1LR, UK)*
PO-426 CC07	**Role of the Arabidopsis AtbZIP63 transcription factor stability in energy management** *Pamela Carlson (University of Campinas)*
PO-427 CC23	**Assessing the impacts of genetic defects on starch metabolism in Arabidopsis plants using the carbon homeostasis model** *Shuichi Kudo (Kyushu Univ., Japan)*
PO-428	**ROS around the clock: Superoxide as a metabolic signal affecting circadian rhythms and growth** *Mike Haydon (University of Melbourne)*
PO-429	**Comparing circadian activity of CAM plant Kalanchoë laxiflora promoters in their native environment and in the C3 Arabidopsis thaliana** *Jessica Harding Pritchard (University of Liverpool)*
PO-430	**Multiple uORFs-mediated Light-dependent Translational Repression in the Arabidopsis Clock Gene** *Haruka Aoyama (Graduate School of Life Science, Hokkaido University,Japan)*
PO-431 CC29	**Identification of LWD1-interacting proteins reveals novel regulators for Arabidopsis circadian clock** *Chun-Kai Huang (Institute of Plant and Microbial Biology, Academia Sinica, Taiwan, ROC)*
PO-432 Online-only	**Investigating the circadian regulation of TAG biosynthesis in nitrogen-starved Arabidopsis seedlings** *Kristen Edgeworth Edgeworth (Washington University in St. Louis)*

19 Light signaling

PO-433	**Light-induced SUMOylation of NF-YC3 regulates stepwise histone modification switch for inhibition of hypocotyl elongation** *Jun Xiao (Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, P.R.China)*
PO-434	**Dynamic H3K27me3 regulatory mechanism mediated by histone demethylase REF6 responding to red light** *Yan Yan (Institute of Genetics and Developmental Biology, Chinese Academy of Sciences)*
PO-435	**Understanding the role of DNA-DNA interactions in regulating de-etiolation in Arabidopsis** *Laila Dabab Nahas (Durham University)*
PO-436	**Complex genetic interactions among MYC transcription factors underlie seedling photomorphogenesis in Arabidopsis** *Vikas Garhwal (Department of Biological Sciences, Indian Institute of Science Education and Research Kolkata, Mohanpur 741246 West Bengal, India)*
PO-437	**Investigation of PCH1 in promoting liquid-liquid phase separation of photoreceptor photobodies in Arabidopsis thaliana** *Sarah Pardi (Donald Danforth Plant Science Center)*
PO-438	**Phenotypic analysis in suppressors of phototropin double mutant** *Taku Sakakibara (Nagoya University, Japan)*
PO-439	**Phosphorylation of two Thr residues in the C-terminal auto-inhibitory domain of plasma membrane H+-ATPase is crucial for light-induced stomatal opening** *Saashia Fuji (Department of Biology, Graduate School of Sciences and Technology for Innovation, Yamaguchi University, Japan)*
PO-440	**Characterization of blue light-induced phosphorylation and dephosphorylation in guard cells.** *Kohei Fukatsu (Devision of Biological Science, Nagoya University, Japan)*
PO-441 CC09	**Phosphorylation of WD-repeat protein WDR by phototropins is essential for starch degradation to promote stomatal opening** *Shota Yamauchi (Department of Biology, Graduate School of Sciences and Technology for Innovation, Yamaguchi University, Yamaguchi, Japan)*
PO-442	**Functional analysis of novel compounds that inhibit stomatal opening** *Kwang Chul Shin (Graduate School of Science, Nagoya, University, Japan)*
PO-443	**Characterization of a protein kinase inhibitor for stomatal opening and H+-ATPase phosphorylation inhibition.** *Shogo Kuwayama (Grad. Sch. Sci., Nagoya University, Japan)*

20 Flowering/Growth phase transition

PO-444	**Changes in daily temperature control the expression patterns of FT to optimize flowering time in nature** *Akane Kubota (Nara Institute of Science and Technology)*
PO-445	**The role of AtDRIFs in the promotion of flowering under long days** *Ana Cunha (University of Minho)*
PO-446	**A cryptic role of BASIC PENTACYSTEINEs in the temporal development of Arabidopsis** *Huang-Lung Tsai (Institute of Molecular and Cellular Biology, National Taiwan University, Taiwan)*
PO-447 CC07	**A B-Box protein suppresses flowering in Arabidopsis through multi-level regulation of the photoperiod pathway** *Rahul Puthan Valappil (Plant Cell and Developmental Biology Laboratory, Indian Institute of Science Education and Research (IISER) Bhopal, Madhya Pradesh - 462066, India)*
PO-448	**Arabidopsis MAC3A and MAC3B integrates environmental signals in modulating flowering time** *Yu-Wen Huang (Institute of Plant Biology, National Taiwan University, Taiwan)*
PO-449	**A study on the florigen transport mechanisms around the shoot apical meristem in Arabidopsis** *Yusuke Murata (Graduate School of Arts and Sciences, The University of Tokyo)*
PO-450	**Multilevel interactions of drought signals with the floral genes network** *Lucio Conti (University of Milan, Italy)*
PO-451	**Beyond FD: the bZIP AREB3 mediates FT signalling and floral transition at the Arabidopsis shoot apical meristem** *Damiano Martignago (University of Milan)*
PO-452	**For identification of factors on early flowering in ddm1 mutant of C24 accession in Arabidopsis thaliana** *KOHEI KUNITA (Kobe University, Japan)*
PO-453	**Arabidopsis EAF6 is part of the NuA4 Histone Acetyl Transferase complex and participates in plant developmental control** *Manuel Piñeiro (Centro de Biotecnología y Genómica de Plantas (CBGP; UPM-INIA/CSIC))*
PO-454	**Unraveling the role of INHIBITOR OF GROWTH FACTOR (ING) proteins in the regulation of flowering time in Arabidopsis** *Jose Antonio Jarillo (Centro de Biotecnología y Genómica de Plantas, Universidad Politécnica de Madrid (UPM) – Centro Nacional Instituto de Investigación y Tecnología Agraria y Alimentaria (INIA-CSIC), Madrid*
PO-455	**WRKY63 transcriptional activation of COOLAIR and COLDAIR regulates vernalization-induced flowering** *Keqiang Wu (Institute of Plant Biology, National Taiwan University)*
PO-456 CC16	**Erasure of Epigenetic Memory in Arabidopsis Flowering Control** *Toshiro Ito (Nara Institute of Science and Technology)*
PO-457	**CBFs have a function to directly activate the expression of COOLAIR, an antisense RNA of FLC, during vernalization** *Ilha Lee (Seoul National University)*
PO-458	**Retrotransposon-induced epigenetic regulation of FLC accelerates Arabidopsis life cycling in response to herbicide** *Leandro Quadrana Quadrana (Institute of Plant Sciences Paris-Saclay, CNRS)*
PO-459	**An Arabidopsis nucleoporin acts as a regulator for photoperiodic flowering** *Jae-Hyeok Park (Division of Life Sciences, Jeonbuk National University, 567 Baekje-daero, Deokjin-gu, Jeonju, Jeollabuk-do 54896, Republic of Korea)*
PO-460	**Mutual repression of AP2 and SOC1 couples changes in shoot apical meristem morphology with floral transition in Arabidopsis** *Enric Bertran Garcia de Olalla (Max Planck Institute for Plant Breeding Research, Germany)*
PO-461	**The size of the Arabidopsis inflorescence meristem and stem is regulated in response to photoperiod by the bZIP transcription factor bZIP13** *Vitor da Silveira Falavigna (Max Planck Institute for Plant Breeding Research)*
PO-462	**TWAS coupled with eQTL analysis reveals the genetic connection between gene expression and flowering time in Arabidopsis** *Tzyy-Jen Chiou (Academia Sinica, Taiwan)*
PO-463	**Insights into polycarpic plant development through natural variation in longevity phenotypes in Arabidopsis thaliana** *Thalia Luden (Universiteit Leiden, the Netherlands)*
PO-464	**CRISPR/Cas9-mediated genomic editing of crucial gene regulating flowering time in lettuce (Lactuca sativa L.)** *Young jae YUN (Jeonbuk national university)*
PO-465	**TERMINAL FLOWER 1, a FT homolog interacts with FD in shoot apical meristem during floral transition** *Momoka Maeno (The University of Tokyo)*
PO-466	**Transcriptional repression of FLOWERING LOCUS C by LUMINIDEPENDENS involved in the autonomous pathway for flowering** *Daesong Jeong (Seoul National University)*

PO-467	**Degradation of SHORT VEGETATIVE PHASE (SVP) at high temperature is mediated by the CUL3A–LFH1–UBC15 ubiquitin ligase complex in Arabidopsis** *Geummin Youn (Korea university, Republic of Korea)*
PO-468	**C-TERMINAL DOMAIN PHOSPHATASE-LIKE 1 protein interacts with TAF15b and together promote the repression of FLOWERING LOCUS C.** *Jinseul Kyung (Seoul National University, Republic of Korea)*

21 Flower development

PO-469	**To ventral or not to ventral, it may depend on SISTER-OF-PIN1** *Ya Min (Department of Ecology and Evolutionary Biology, University of Connecticut)*
PO-470	**Organ-specific transcriptome analysis reveals candidate genes involved in floral organogenesis in wild barley** *Gang Chen (Institute of Crop Science, National Agriculture and Food Research Organization, Tsukuba, JAPAN)*
PO-471	**Molecular dissection of floral proximal-distal patterning in Torenia fournieri** *Shihao Su (Sun Yat-sen University, China)*
PO-472	**Molecular mechanisms patterning the petal of Hibiscus trionum** *Elena Salvi (Sainsbury Laboratory - University of Cambridge)*
PO-473	**Effects of mechanical forces on the floral development in Arabidopsis thaliana using a novel experimental system** *Akitoshi Iwamoto (Kanagawa University)*
PO-474	**Histone Demethylases ELF6 and JMJ13 Antagonistically Regulate Self-Fertility in Arabidopsis** *Charlie Keyzor (Imperial College London)*
PO-475	**SPATULA's role in radial symmetry establishment via cell-cycle coordination.** *Samuel Wee Han Koh (John Innes Centre, UK)*
PO-476	**Investigating the role of CYCLIN-P3s in Arabidopsis style development** *Iqra Jamil (John Innes Centre)*
PO-477	**Comparing the fruit development between Arabidopsis thaliana and other Brassicaceae species** *Binghan Wang (Institut de Recherche en Biologie Végétale, Département de Sciences Biologiques, Université de Montréal, Canada)*
PO-478	**Competing developmental gradients coordinate gynoecium morphogenesis in Arabidopsis thaliana** *Andrea Gomez Felipe (Institut de Recherche en Biologie Végétale, Département des Sciences Biologiques, Université de Montréal, Canada)*
PO-479	**The molecular origin of sensitive stigmas: using Torenia fournieri as a model** *Xuan Zhou (Sun Yat-sen University, China)*
PO-480	**Sugars on SPATULA: The Bitter and Sweet of Symmetry Establishment During Plant Organogenesis** *Seamus Curran (John Innes Centre)*
PO-481	**Auxin and gibberellic acid coordinate gene expression networks during receptacle growth** *Chizuko Yamamuro (College of life science, Fujian Agriculture and Forestry University, Fuzhou 350002, Fujian, China)*
PO-482	**Jasmonate biosynthesis gene SIDAD1 regulates reproductive development in tomato** *Yukako Nomura (Graduate School of Life and Environmental Sciences, University of Tsukuba, Japan)*
PO-483	**A ZINC FINGER PROTEIN plays a role in mediating silique development through integration of phytohormone signaling** *Wei Ma (School of Biological Sciences, Nanyang Technological University, Singapore 637551, Singapore.)*
PO-484	**Fruit indehiscence mutation increases seed size in Arabidopsis** *Somin Song (Department of Agriculture, Forestry and Bioresources, Seoul National University, 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea)*
PO-485	**Characteristics of a Radish Mutant with Longer Siliques** *shisheng li (Huanggang Normal University, China)*

22 Meiosis/Gamete/Fertilization

PO-486	**DGK2 and DGK4 are the essential kinase for gametogenesis and eukaryotic phospholipid metabolism** *Artik Elisa Angkawijaya (Center for Sustainable Resource Science, RIKEN, Yokohama, 230-0045 Japan)*
PO-487	**The Plant Pontin and Reptin Homologues, RUVBL1 and RUVBL2A, are involved in plant gametophyte development** *Petra Prochazkova Schrumpfova (Masaryk University, Czech Rep.)*
PO-488	**Deciphering the evolutionary conservation of SPOROCYTELESS** *Heecheol Yu (Seoul National University, South Korea)*
PO-489	**Cell-cycle synchronized organelles clustering in meiocytes** *Yuki Hamamura (University of Hamburg, Germany)*
PO-490	**Molecular dynamics of rice MEL2 as a component of cytoplasmic RNP granules regulating proper meiosis initiation** *Kenichi Nonomura (Plant Cytogenetics, Dept. Gene Function & Phenomics, National Institute of Genetics)*
PO-491	**A cytological framework of female meiosis in Arabidopsis by live-cell imaging** *Bingyan Hu (University of Hamburg, Germany)*

PO-492	**DNA methylation profiling in Arabidopsis egg cells** *Hiroki Tsutsui (Department of Plant and Microbial Biology & Zurich-Basel Plant Science Center, University of Zurich, Zurich, Switzerland)*
PO-493	**Identification of a novel U-chromosomal gene required for egg cell differentiation in Marchantia polymorpha** *Yen-Ting Lu (Graduate School of Biological Science, Nara Institute of Science and Technology (NAIST), Ikoma 630-0192 Japan)*
PO-494 CC16	**Distinct chromatin signatures in the Arabidopsis male gametophyte** *Zhe Wu (School of Life Sciences, Southern University of Science and Technology, China)*
PO-495	**Functions of serine from the phosphorylated pathway on growth, male gametogenesis, and metabolism in Marchantia polymorpha** *Mengyao Wang (RIKEN Center for Sustainable Resource Science, Japan)*
PO-496	**Extensive N4 Cytosine Methylation is Essential for Marchantia Transcriptional Programming and Sperm Function** *James M Walker (Salk Institute)*
PO-497	**Live imaging of chromosome behavior in pollen mother cells of Arabidopsis meiotic mutant** *Yoshitaka Azumi (Faculty of Science, Kanagawa University)*
PO-498 CC11	**Control of meiosis under heat stress** *Arp Schnittger (University of Hamburg, Germany)*
PO-499	**Effect of callose on symplast and apoplast related events in controlling proper meiosis initiation in rice anther locules** *Harsha Somashekar (Plant Cytogenetics Laboratory, National Institute of Genetics, Mishima, Japan)*
PO-500	**Arabidopsis novel proteins required for the construction of pollen exine reticulate structure** *Sumie Ishiguro (Nagoya University, Japan)*
PO-501	**KNOLLE/SYP111 and SYP112 cooperate in cytokinesis during gametogenesis in Arabidopsis thaliana** *Kazuo Ebine (NIBB, Japan)*
PO-502 CC32	**Ca2+-induced removal of inner vegetative plasma membrane in Arabidopsis sperm cells** *Naoya Sugi (KIBR, Yokohama City Univ.)*
PO-503	**Cytosolic phosphoglucose isomerase is essential for microsporogenesis and embryogenesis in Arabidopsis** *Hung-Chi Liu (Agricultural Biotechnology Research Center, Academia Sinica, Taipei, Taiwan)*
PO-504	**Gene expression dynamics in developing pollen of Arabidopsis thaliana addressed by multi-omics approaches** *Božena Klodová (Institute of Experimental Botany of the Czech Academy of Sciences, Laboratory of Pollen Biology, Czech Republic)*
PO-505	**DNA demethylases act together to regulate reproductive development in Arabidopsis** *Joo Young Lim (Department of Agriculture, Forestry and Bioresources, College of Agriculture and Life Science, Seoul National University, Seoul 08826, South Korea)*
PO-506	**Requirement of Non-specific Phospholipase C (NPC) in Plant Viability** *Anh Hai Ngo (RIKEN Center for Sustainable Resource Science (CSRS))*
PO-507	**A novel Arabidopsis thaliana protein, POTI, plays an important role in maintaining pollen tubes' integrity** *Natalia Julia Rzepecka (Graduate School of Humanities and Sciences, Ochanomizu University, Japan)*
PO-508	**Analysis of a Rab GTPase in pollen tube guidance** *Kumi Matsuura-Tokita (The University of Tokyo, Japan)*
PO-509	**Proposed molecular mechanism for persistent growth capability in physiologically anuclear pollen tubes** *Kazuki Motomura (Ritsumeikan Univ., Japan)*
PO-510	**The Regulation of Arabidopsis MALE STERILITY1 (MS1) in Pollen Development** *Helen White (University of Nottingham)*
PO-511	**Investigation of genes involved in species-specific pollen tube guidance and gametophyte development.** *Masahiro Kanaoka (Prefectural University of Hiroshima)*
PO-512	**Tip-localized receptor modules orchestrate pollen tube behavior in angiosperms** *Hidenori Takeuchi (Nagoya University, Japan)*
PO-513	**Quantification of species-preferential pollen tube guidance by the ovule in Arabidopsis species** *Takuya T Nagae (Graduate School of Agricultural and Life Sciences, The University of Tokyo)*
PO-514	**Novel function of cuticles as a reproductive barrier in Brassicaceae** *Yoshinobu Kato (Grad. Sch. Agric. Lif. Sci., The University of Tokyo)*
PO-515	**Roles of cytoskeleton in Arabidopsis synergid cells** *Daichi Susaki (Yokohama City University, Japan)*
PO-516	**Type II arabinogalactans play important roles in pollen - pistil interactions** *Sílvia Coimbra (LAQV/REQUIMTE, Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, Rua Campo Alegre s/n, 4169-007 Porto, Portugal)*
PO-517	**Analysis of a key factor regulating cell fusion between early endosperm and persistent synergid.** *Daisuke Maruyama (Kihara Institute for Biological Research, Yokohama City University)*
PO-518	**Cytological Analysis of Cell Invasion during Gametophyte Interactions in Arabidopsis** *Nicholas James Desnoyer (University of Zurich)*

PO-519	**Molecular control of dominance/recessivity interactions between self-incompatibility alleles in Arabidopsis** *Vincent Castric (CNRS - University of Lille)*
PO-520	**Molecular basis of multi-phased pistil defense mechanism against foreign pollen** *Sota Fujii (The University of Tokyo)*
PO-521	**Studies toward unveiling the molecular scenario of double fertilization in Arabidopsis thaliana** *Tomoko Igawa (Chiba University, Japan)*
PO-522	**Identification and analysis of the putative GCS1-interacting proteins in Arabidopsis** *Ari Yoshimura (Chiba University, Japan)*
PO-523	**Sperm nuclear fusion is not required for the onset of embryogenesis** *Shuh-ichi Nishikawa (Faculty of Science, Niigata University)*
PO-524	**The female gametes expressed protein FOG3 is required for gamete fusion in Arabidopsis thaliana** *Yuan Wang (State Key Laboratory of Protein and Plant Gene Research, Peking-Tsinghua Center for Life Sciences at College of Life Sciences, Peking University, China)*

23 Embryogenesis/Seed development

PO-525	**Approach to elucidate the molecular mechanism regulating the basal meristem of hornwort sporophytes** *Kazune Ezaki (Rikkyo university)*
PO-526	**Delayed embryo-proper development triggers suspensor derived polyembryony in Arabidopsis** *Honglei Wang (Wageningen University & Research, Netherland)*
PO-527	**Quantification of zygote polarization dynamics for body axis formation in Arabidopsis** *Minako Ueda (Tohoku University, Japan)*
PO-528	**Elucidation of elongation mechanism of Arabidopsis zygote using image analysis methods based on live-cell imaging** *Hikari Matsumoto (Tohoku University, Japan)*
PO-529	**Antagonistic effects on Arabidopsis hybrids exhibiting endosperm based post-zygotic hybridization barriers** *Renate Marie Alling (University of Oslo)*
PO-530	**Endosperm cellularization is initiated by a family of auxin related factors** *Nicolas Butel (Max Planck Institute of Molecular Plant Physiology, Potsdam-Golm, Germany)*
PO-531	**The identification of type I MADS box genes as the upstream activators of an endosperm-specific invertase inhibitor in Arabidopsis** *Dongfang Wang (Spelman College)*
PO-532	**Natural variation in WHITE-CORE RATE 1 regulates redox homeostasis in rice endosperm to affect grain quality** *Bian Wu (Food Crops Institute, Hubei Academy of Agricultural Sciences, Wuhan, China)*
PO-533	**Identification and functional investigation of diversifying seed genes at the maternal-offspring interface in Arabidopsis thaliana** *Caroline Anne Martin (MIT, USA)*
PO-534	**The plant hormone ABA alleviates the interploidy barrier** *Hikaru Sato (Swedish University of Agricultrual Sciences, Sweden)*
PO-535	**Impact of LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE 2 (LPAT2) in de novo glycerolipid metabolism and developmental control: Two sides of the same coin?** *Niña Alyssa Barroga (Center for Sustainable Resource Science, RIKEN, Yokohama 230-0045, Japan)*
PO-536	**Comparative Omics of Arabidopsis Developing Seed with Enhanced Fatty Acid Synthesis** *Brian P Mooney (University of Missouri)*
PO-537	**Molecular basis of the key regulator WRINKLED1 in plant oil biosynthesis** *Que Kong (School of Biological Sciences, Nanyang Technological University, Singapore 637551, Singapore.)*
PO-538	**A MYB transcription factor regulates the biosynthesis of very-long-chain fatty acids in Arabidopsis** *Yuzhou Yang (School of Biological Sciences, Nanyang Technological University)*
PO-539	**Direct balancing of lipid mobilization and ROS production by the epoxidation of fatty acid catalyzed by a cytochrome P450 protein during seed germination** *chun-peng song (State Key Laboratory of Crop Stress Adaptation and Improvement, Henan University, Kaifeng, 475004, China)*
PO-540	**Exploring RRT1 function in the synthesis of Arabidopsis seed mucilage RG1** *Yuki Aoi (INRAE, Institut Jean-Pierre Bourgin, Université Paris-Saclay, AgroParisTech, 78000, Versailles, France)*
PO-541	**Apetala 2 regulates seed longevity through lipid polyester accumulation** *Eduardo Bueso Rodenas (Instituto de Biología Molecular y Celular de Plantas, Universitat Politecnica de València, 46022 Valencia, Spain)*
PO-542 CC19	**Rational approaches to synchronizing germination in seed populations** *Liam Walker (School of Life Sciences, University of Warwick)*
PO-543	**AtC3H59/ZFWD3, an Arabidopsis nuclear protein, interacts with Desi1 and is involved in seed germination, seedling development, and seed development** *Hye-Yeon Seok (Pusan National University, Republic of Korea)*

PO-544	**AtC3H12, an Arabidopsis non-TZF transcriptional activator, negatively affects seed germination and seedling development** *Yong-Hwan Moon (Pusan National University)*
PO-545	**Constructing and testing a genetic network for controlling seed germination in Arabidopsis** *Ming Yang (Department of Plant Biology, Ecology, and Evolution, Oklahoma State University, Stillwater, OK 74078, USA)*
PO-546	**Arabidopsis INDETERMINATE DOMAIN 4 is involved in the control of seed germination by light** *Akiko Kozaki (Shizuoka University, Japan)*
PO-547	**AtC3H12, an Arabidopsis non-TZF transcriptional activator, negatively affects seed germination and seedling development** *Mairaj Bibi (PUSAN NATIONAL UNIVERSITY)*
PO-548	**Structure-function analysis of TMB-RESISTANT1, a B2 Raf-like kinase in Arabidopsis thaliana** *Eunsun Kim (Sejong University, Republic of Korea)*
PO-549	**Heterosis in Intraspecific Hybrid of Arabidopsis thaliana during Early Development** *Putri Wijayanti (Division of Biological Science, Graduate School of Science and Technology, Nara Institute of Science and Technology, Japan)*
PO-550	**Identification and characterization of soybean KIX genes by comparative analysis with Arabidopsis thaliana** *MI-SUK SEO (National institute of crop science, Republic of Korea)*
PO-551	**Analysis of a blue light receptor CRY1 during plant regeneration** *Min Li (University of Tokyo, Japan)*

24 Stem cell/Regeneration

PO-552	**Molecular Mechanisms of Light-Mediated Regulation of Plant Regeneration** *Yetkin Caka Ince (RIKEN)*
PO-553	**HY5-mediated light signals determine the new meristem fate during plant regeneration** *Yu Chen (Department of Biological Sciences, The University of Tokyo, Japan)*
PO-554	**ASHH2 regulates plant regeneration through regulation of photosynthesis and glucose metabolic pathways** *Kana Yoshida (University of Tokyo, Japan)*
PO-555	**Hyperosmotic stress-induced somatic embryogenesis and its continuous culture in Japanese honewort (Cryptotaenia japonica; Apiaciae)** *Sana Takahashi (Yokohama City University, Japan)*
PO-556	**Molecular identities of wounding signals that promote plant regeneration and their perception mechanisms** *Yosuke Sasai (The University of Tokyo, Japan)*
PO-557	**Roles of At2-MMP during tissue reunion in incised Arabidopsis inflorescence stem** *Afiifah Machfuudzoh (Graduate School of Science and Technology, University of Tsukuba, Japan)*
PO-558	**Exposure to long-term cold enhances callus formation in Arabidopsis** *Fu-Yu Hung (RIKEN, CSRS)*
PO-559	**Mechanistic analysis of the improvement of shoot regeneration ability by gamma irradiation** *Ryuhei Hashimasa (The University of Tokyo, Japan)*
PO-560	**Brassinosteroid receptor-mediated regulation of tissue regeneration in Arabidopsis** *Ye Zhang (Nara Institute of Science and Technology, Japan)*
PO-561	**Utilization of Arabidopsis thaliana developmental regulator genes for differentiation control of transgenic plant cells** *Shohei Koyama (Chiba University, Japan)*
PO-562	**Transcriptome and metabolome profiles during cellular differentiation of tobacco transgenic cells expressing Arabidopsis developmental regulator genes** *Yuka Sato (Chiba University, Japan)*
PO-563	**Genetics and Multi-Omics Integration Analyses Identified Cell Differentiation State Maintenance Mechanisms in hope-1 Mutant Hypocotyls** *Ali Ferjani (Department of Biology, Tokyo Gakugei University)*
PO-564 CC04	**It's All in the Timing: Enhancing Regeneration Efficiency Using Morphogenic Factors** *Bastiaan Bargmann (Virginia Tech)*
PO-565	**Finding the sweet spot – How brassinosteroids interfere with shoot regeneration processes** *Luiselotte Rausch (RIKEN Center for Sustainable Resource Science, Tsurumi, Yokohama, Kanagawa 230-0045, Japan)*
PO-566	**Submergence promotes auxin-induced callus formation through ethylene-mediated post-transcriptional control of auxin receptors** *Seung Yong Shin (Plant Systems Engineering Research Center, Korea Research Institute of Bioscience and Biotechnology, Korea)*
PO-567	**Functional analysis of histone methyltransferase required for shoot regeneration** *Masako Migihashi (The University of Tokyo, Japan)*
PO-568	**Checkpoints in cellular programming during root regeneration** *Bruno Guillotin (New York University, Center for Genomics and Systems Biology)*
PO-569	**Functional analysis of a chromatin remodeling factor involved in the process of plant regeneration** *Ayaka Horie (University of Tokyo, Japan)*

PO-570	**WIND1 controls site-specific histone acetylation/deacetylation and promotes somatic embryogenesis in Arabidopsis** *Akira Iwase (RIKEN CSRS, Japan)*
PO-571	**Molecular mechanisms underlying local histone modification changes during stem cell formation in the moss Physcomitrium patens** *Masaki Ishikawa (National Institute for Basic Biology, Japan)*
PO-572	**Single-nuclei transcriptome and chromatin accessibility analyses reveal gene regulatory networks underlying stem cell formation in the moss Physcomitrium patens** *Ruan Morne De Villiers (National Institute for Basic Biology, Japan)*
PO-573	**Cytokinin-dependent regulation of plant cell dedifferentiation via pre-mRNA splicing in Arabidopsis** *Ami Takeuchi (The University of Tokyo, Japan)*
PO-574	**Single-nucleus RNA-seq revealed transcriptomic landscapes of epidermal reprogramming** *Hatsune Morinaka (CSRS, RIKEN, Kanagawa, Japan)*
PO-575 CC04	**Transcriptional Regulation of Cell-cell Movement During Root Tip Regeneration** *Itay Cohen (Hebrew University of jerusalem)*
PO-576	**Plant Regeneration: To Cell and Back** *Kelsey Reed (Virginia Tech, USA)*
PO-577	**An induced pluripotent stem cell (iPS) tool to overcome regenerative recalcitrance in plants** *Jana Wittmer (Wageningen University and Research)*
PO-578	**Uncovering the transcriptional regulatory network involved in boosting wheat regeneration and transformation** *Xuemei Liu (Institute of Genetics and Developmental Biology, Chinese Academy of Sciences)*
PO-579	**Confocal microscopy-enabled morphometric reverse tracking of Arabidopsis callus development from leaf mesophyll protoplasts** *Patience Chatukuta (Max Planck Institute for Biology Tübingen, Germany)*
PO-580	**Molecular genetic analysis of the role of BTAF1, a TBP-associated factor, in shoot regeneration** *Takaaki Yonekura (University of Tokyo, Japan)*
PO-581	**CLE peptides modulate shoot development through WUS regulation** *Nadiatul A. Mohd-Radzman (Sainsbury Laboratory Cambridge University (SLCU), Bateman Street, CB2 1LR, Cambridge, United Kingdom.)*
PO-582 CC10	**Analysis of stem cell-promoting CLE peptide signaling in the shoot apical meristems of land plants** *Yuki Hirakawa (Gakushuin University, Japan)*
PO-583	**Functional analysis of JINGASA transcription factor in stem cell dynamics in Marchantia polymorpha** *Go Takahashi (Gakushuin University, Japan)*
PO-584	**Conserved expression of a core plant stem cell regulator despite extreme divergence in cis-regulatory sequence and organization** *Danielle Ciren (Cold Spring Harbor Laboratory)*
PO-585 Online-only	**Budding Heads: Activation and Competition of Arabidopsis Axillary Buds** *Zoe Nahas (Sainsbury Laboratory, University of Cambridge)*

25 Leaf development

PO-586	**Competition for resources during semi-sequential growth of developmental units drive allometric patterns in the grass Setaria** *Renée Dale (Donald Danforth Plant Science Center, USA)*
PO-587	**Spiralling out of Control: Regulation of Phyllotactic Stability** *Merijn Kerstens (Plant Developmental Biology, Wageningen University and Research)*
PO-588 CC16	**Temporal expression of BLADE-ON-PETIOLE 1 and 2 in successive leaves define the shape of their lamina** *Mingli Xu (University of South Carolina, USA)*
PO-589	**Multi-platform Metabolomics Identified Key Metabolites that Coordinate Cell Number and Size During Leaf Morphogenesis** *Hiromitsu TABETA (RIKEN Center for Sustainable Resource Science)*
PO-590	**Molecular functions of AS2, a plant-specific AS2/LOB domain protein essential for leaf development and differentiation** *Sayuri Ando (Chubu University, Japan)*
PO-591	**TCP transcription factors regulate cell expansion in leaf development** *Tomotsugu Koyama (Suntory Foundation for Life Sciences)*
PO-592	**ORESARA15 and ANGUSTIFOLIA3: Key Regulators of Cell Proliferation during Arabidopsis Leaf Growth** *Sang Eun Jun (Dong-A University, Republic of Korea)*
PO-593	**Analysis of gene expression patterns in specific meristems of one-leaf plant Monophyllaea glabra by whole-mount in situ hybridization** *Shunji Nakamura (Grad. Sch. Sci., Univ. Tokyo, Japan)*
PO-594 CC07	**What did the grasses gain by losing PEAPOD? Evolution and conserved functionality of organ size and shape regulator PEAPOD** *Ruth Cookson (Plant Biotechnology, Grasslands Research Centre, AgResearch Ltd., Palmerston North, New Zealand)*

PO-595 CC06	**Identification of interacting factors of the TARANI/ Ubiquitin-specific protease 14 (UBP14) in Arabidopsis thaliana** *Anjana S Hegde (Department of Microbiology and Cell Biology, Indian Institute of Science, Bengaluru, India)*
PO-596	**Genetic interaction of Arabidopsis ELP4 and DRL1 in the regulation of cell proliferation and establishment of leaf dorsoventral polarity** *Gyung-Tae Kim (Dong-A University, Republic of Korea)*
PO-597	**A quantitative study of pavement cell shape in the upper leaf epidermis** *Jacqueline Nowak (University of Potsdam, Germany)*
PO-598	**Puzzle-shaped plant cells are developmental constraints driven by mechanical stress** *Nicola Trozzi (John Innes Centre, United Kingdom)*
PO-599	**Fluorescence imaging analysis of the structure and development of hydathodes in Arabidopsis** *Hiroki Yagi (Konan Univ.)*
PO-600	**Thallus development controlled with Marchantia-specific peptide hormone-receptor pair** *Hidefumi Shinohara (Fukui Prefectural University, Japan)*

26 Root development

PO-601	**A group of C2H2 Zinc Finger proteins coordinates the developmental reprogramming mediated by danger signals in the Arabidopsis root meristem** *Souvik Dhar (School of Biological Sciences, Seoul National University, Korea)*
PO-602	**Roles of XAL2, SOC1 and AGL24 MADS-box genes in Arabidopsis thaliana root development and osmotic stress responses** *Claudio Augusto Castañón-Suárez (Laboratorio de Genética Molecular, Epigenética y Desarrollo de Plantas, Instituto de Ecología, Universidad Nacional Autónoma de México, Ciudad de México, México)*
PO-603	**Does LHP1 act independently of Polycomb in roots?** *Gabriela Guzmán-Favila (Laboratorio de Genética Molecular, Epigenética, Desarrollo y Evolución de plantas. Instituto de Ecología, Universidad Nacional Autónoma de México, México)*
PO-604	**As above so below? ULTRAPETALA1 regulation in Arabidopsis root development** *Carlos Emiliano Cortés-Quiñones (Laboratorio de Genética Molecular, Epigenética, Desarrollo y Evolución de Plantas, Instituto de Ecología, Universidad Nacional Autónoma de México (UNAM), México)*
PO-605	**SCFFBS1 Regulates Root Quiescent Center Cell Division via Protein Degradation of APC/CCCS52A2** *Kyoung Rok Geem (Chungbuk National University, Korea)*
PO-606	**Combined Approach of GWAS and Phylogenetic Analyses to Identify New Candidate Genes That Participate in Arabidopsis thaliana Primary Root Development Using Cellular Measurements and** *Brenda Anabel Lopez-Ruiz (Laboratorio de Genética Molecular, Desarrollo y Evolución de Plantas, Departamento de Ecología Funcional, Instituto de Ecología, UNAM)*
PO-607	**Uncovering the hidden aspects of cell division and elongation dynamics at the tip of growing Arabidopsis roots using 4D-microscopy, AI-assisted image processing, and data sonification** *Tatsuaki Goh (Div. Biol. Sci., NAIST, Japan)*
PO-608	**Dissecting the role of miR160-dependent regulation of ARF gene expression in root cap** *Keita Tanaka (Nara Institute of Science and Technology, Graduate School of Science and Technology, Division of Biological Science)*
PO-609	**A comprehensive developmental atlas of suberized tissues at the single cell level** *Charlotte Noelle Miller (The Salk Institute of Biological studies)*
PO-610	**Single-cell profiling of suberizing cells identifies a novel periderm regulator** *Manisha V. Haag (Salk Institute for Biological Studies)*
PO-611	**An inquiry into the origin of radial patterning of root-hair-cell distribution** *Kyeonghoon Lee (Department of Biological Sciences, Seoul National University)*
PO-612	**SUPERROOT2-dependent Fine-tuning of Local Auxin Distribution for Arabidopsis Lateral Root Formation** *Chieko Goto (Grad. Sch. of Sci., Kobe Univ.)*
PO-613	**Auxin biosynthesis inhibitors impair auxin-induced directional nuclear migration in lateral root founder cells in Arabidopsis thaliana** *Sanae Kaneta (Osaka University, Japan)*
PO-614	**Dimorphism of LR growth regulated by auxin and cytokinin** *Feiyang Lin (Grad. Sch. Life Sci., Hokkaido Univ., Japan)*
PO-615	**Functional Analysis of RLF, a Cytochrome b5-Like Heme Binding Protein, in Plant Organ Development** *Kentaro Iwata (Grad. Sch. of Sci., Kobe Univ., Japan)*
PO-616	**Two-step regulation of lateral root spacing in Arabidopsis thaliana** *Shohei Oshiro (Div. Bio. Sci., NAIST)*
PO-617 CC26	**Coordinating root system architecture: the intersection of CEP and Cytokinin hormone pathways in Arabidopsis** *Michael Taleski (ANU, Australia)*

PO-618	**Transcriptional network to synchronize alteration in the developing lateral root primordium (LRP) and LRP-overlay cells** *Kosuke Mase (Faculty of Agriculture, Meijo University)*
PO-619	**MYB93-mediated Very Long-Chain Fatty Acid Signaling networks in lateral root primordium development** *Yuta Uemura (Meijo University, Japan)*

27 Cell division/Cell cycle

PO-620	**Two Arabidopsis cyclins are sensitive targets to intracellular acidification acting as a hub between perception and stress response** *gaetano bissoli (Universitat Politecnica Valencia, Spain)*
PO-621	**Cell proliferation control mediated by ANAC082 in response to nucleolar stress in Arabidopsis thaliana** *Tai-yin Hsu (National Cheng Kung University, Taiwan)*
PO-622	**Control of DNA replication by histone methyltransferases ATXR5 and ATXR6 in Arabidopsis thaliana** *Kar Yee Moo (Graduate School of Science and technology, Nara Institute of Science and Technology, Japan)*
PO-623	**A GRAS family transcription factor, SCARECROW-LIKE28, regulates cell size by inhibiting G2 progression in Arabidopsis** *Masaki Ito (Sch. Biol. Sci. Tech., Col. Sci. Eng., Kanazawa Univ., Japan)*
PO-624	**CRISPR/Cas9-mediated mutagenesis of SAMBA gene alters growth and development in plants.** *Nubia Eloy (Universidade de São Paulo, Department of Biological Sciences, Escola Superior de Agricultura 'Luiz de Queiroz')*
PO-625	**Functional analyses of HPY2/NSE2 and SMC5/6 complex.** *Takashi Ishida (Kumamoto University, Japan)*
PO-626	**Analysis of the effect of autopolyploidization on root growth in Arabidopsis thaliana with spatial reference to "high-ploidy syndrome"** *Suzuka Kikuchi (Fac. Adv. Sci. and Tech., Kumamoto Univ., Japan)*
PO-627	**CDKG2 and SKIP act downstream of UBP14 to control endoreduplication and cell growth in Arabidopsis** *Shan Jiang (Institute of Genetics and Developmental Biology, Chinese Acadamy of Sciences, China)*
PO-628	**Expanding the kinetochore universe in flowing plants** *Shinichiro Komaki (Nara Institute of Science and Technology, Graduate School of Biological Sciences, Japan)*
PO-629	**Keeping it together: The role of scaffold proteins during division plane control** *Jonas Buhl (Leibniz-Institute of Plant Biochemistry, Halle (Saale), Germany)*
PO-630	**Novel plant cell division inhibitors identified by chemical screening using Arabidopsis zygote** *Yusuke Kimata (Tohoku University, Japan)*
PO-631	**Plant-specific mitotic microtubule structures and cell division modes** *Takema Sasaki (Graduate School of Science, Nagoya University, Japan)*
PO-632	**GRAS Family Transcription Factor Is A New Regulator Of Asymmetric Cell Division And Polarity In Moss Physcomitrium Patens** *Alisa Vyacheslavova (Hokkaido University, Graduate School of Life Science)*
PO-633	**Shaping root architecture** *V Willemsen (Cluster Plant Developmental Biology, Wageningen University & Research, Droevendaalsesteeg 1, Wageningen, The Netherlands)*

28 Cell & tissue differentiation

PO-634	**PBLs and their role in defining root endodermis signaling specificity** *Irene Guzmán-Benito (University of Lausanne, Switzerland)*
PO-635	**CRISPR activation (CRISPRa) as a powerful tool for engineering gene regulatory networks in plants** *Anaxi Houbaert (UNIL - DBMV)*
PO-636	**Patterning in 3D: imaging three-dimensional anatomy and epidermal cell fate in Arabidopsis roots** *George Janes (University of Nottingham, School of Biosciences, UK)*
PO-637	**Light regulates xylem cell differentiation via PIF in Arabidopsis** *Miguel de Lucas (Durham University - UK)*
PO-638	**Visualization of spatiotemporal dynamics of cytokinin responses and its role in secondary growth initiation in Arabidopsis roots** *Shunji Shimadzu (University of Tokyo, Japan)*
PO-639	**A zinc-finger transcription factor, LGA1, negatively regulates lateral growth in Arabidopsis and trees** *Wiktoria Fatz (Organismal and Evolutionary Biology Research Programme, Faculty of Biological and Environmental Sciences, Viikki Plant Science Centre (ViPS), University of Helsinki, 00790, Helsinki, Finland)*
PO-640	**Towards elucidation of the molecular mechanisms of tuberous root development in cassava** *Yoshinori Utsumi (RIKEN CSRS)*
PO-641	**Ubiquitination-mediated xylem vessel element formation in response to pathogen in plants** *Ya MA (Grad Sch Front Sci, Univ Tokyo)*

PO-642	**FLY Ubiquitin E3 Ligases Are Transcriptionally Regulated by VND7 during Xylem Vessel Cell** *Tadashi Kunieda (NAIST, Japan)*
PO-643	**Investigation of the function of Clade B AT-hook motif nuclear-localized proteins in the root xylem development** *Hee-Ji Shin (Seoul national university)*
PO-644 CC20	**A long-distance top-down movement of a transcription factor regulating the root phloem development** *Ji-Young Lee (Seoul National University)*
PO-645	**Characterization of NAC-REGULATED SEED MORPHOLOGY1 transcription factor for regulating the root phloem development** *Jongsung Park (School of Biological Sciences, College of Natural Science, Seoul National University, 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Korea)*
PO-646 CC20	**Cellular adaptations for long-distance transport through the phloem sieve tube** *Lothar Kalmbach (University of Lausanne, Department of Plant Molecular Biology)*
PO-647 CC19	**Phloem cells - from single cell transcriptomics to development and function** *Jiyun Kim (Institute for Molecular Physiology, Heinrich-Heine-University Düsseldorf, Düsseldorf 40225, Germany)*
PO-648	**Regulatory Functions of NAC domain Transcription Factors for Root Phloem Development in Arabidopsis thaliana** *Heewon Shin (School of Biological Sciences, College of Natural Science, Seoul National University, Seoul 08826, Republic of Korea)*
PO-649	**Revealing autolytic mechanisms of sieve elements by an improved induction system** *Yuki Sugiyama (Institute for Advanced Research, Nagoya University)*
PO-650	**Specification of epidermal cell fate in plant shoots** *Shinobu Takada (Osaka University, Japan)*
PO-651 CC04	**Leaf epidermal patterning and fate determination** *Chin-Min Kimmy Ho (Institute of plant and microbial biology, Academia Sinica)*
PO-652	**Identification and expression analysis of six CsCPC genes in tea leaves (Camellia sinensis).** *Juri WAKAMATSU (Hiroshima University, Japan)*
PO-653	**Cell type-specific attenuation of brassinosteroid signaling precedes stomatal asymmetric cell division** *Boyu Guo (Ghent University, Belgium)*
PO-654	**Abscisic acid regulates stomatal production by imprinting a SnRK2 kinase–mediated phosphocode on the master regulator SPEECHLESS** *XIN YANG (National University of Singapore, Singapore)*
PO-655	**The epigenetic regulation of the master stomatal regulator SPEECHLESS by the Arabidopsis VAL family of transcriptional repressors** *Li Cong Chua (National University of Singapore)*
PO-656	**A roadmap to guard cell: how the cis-trans regulome drives fate transitions** *Ao Liu (Stanford University)*
PO-657	**HOMEODOMAIN-LIKE protein (HDL) mediated chromatin organization modulates leaf epidermal** *Ansar Ali (Institute of Plant and Microbial Biology, Academia Sinica)*
PO-658	**Turn over a new leaf: A single cell view of leaf epidermis in Arabidopsis** *Chi Kuan (Institute of Plant and Microbial Biology, Academia Sinica, Taiwan)*
PO-659	**Experimental Validation of the Mechanism of Stomatal Development Diversification** *Yuki Doll (NAIST, Japan)*
PO-660 CC26	**Stomata-derived intercellular signaling that directs mesophyll air space formation** *Yuki Yoshida (Kumamoto University, Japan)*
PO-661	**Comparative analysis of airspace formation process between Arabidopsis and Duckweed** *Kyungyoon Kim (Research Institute of Basic Sciences, Seoul National University, Seoul 08826, Republic of Korea)*
PO-662	**Co-option of the conserved and reduced stomatal transcriptional network FAMA-WASABI MAKER for the myrosinase-glucosinolate defense system** *Makoto Shirakawa (Nara Institute of Science and Technology, Japan)*
PO-663	**De novo specification of epidermal cells in Arabidopsis abscission zone** *Xiaohong Wen (Department of New Biology, DGIST, Daegu 42988, Republic of Korea)*
PO-664	**Conserved (Epi)Genetic Mechanisms of Aging in Plants: Insights from Laminopathies in Arabidopsis thaliana** *Oscar Juez (Okinawa Institute of Science and Technology)*
PO-665	**MnSOD fine-tunes the root growth and floral organ abscission by modulating ROS metabolism in Arabidopsis** *Jinsu Lee (Seoul national university, Republic of Korea)*

29 Cell death/Senescence

PO-666	**PLTs and VNDs oppositely regulate ZAT transcription factors to control cell death in the Arabidopsis root** *Ming Feng (Swedish university of agricultural sciences)*
PO-667	**MBD10 is involved in ABA-inducible leaf senescence in Arabidopsis** *Yangdan Li (Tokyo University of Agriculture and Technology)*
PO-668	**Multiple N-conjugated forms of Cytokinins are Involved in Delaying Natural and Abiotic Stress Senescence** *Aaron M Rashotte (Auburn University)*
PO-669	**Uncovering the possible link between cytosolic and apoplastic glutathione degradation** *Takehiro Ito (Tokyo University of Agriculture and Technology, Japan)*
PO-670	**Comprehensive transcriptomic analysis of age-, dark-, and salt-induced senescence reveals underlying mechanisms and key regulators of leaf senescence in Zoysia japonica** *Lanshuo Wang (Interdisciplinary Graduate Program in Advanced Convergence Technology & Science, Jeju National University, Jeju, South Korea)*
PO-671	**Genetic Variants Driving Distinct Senescence Programs in Arabidopsis Accessions from the Kyrgyz-Tajik Mountainous Region** *PHAN PHUONG THAO DOAN (Interdisciplinary Graduate Program in Advanced Convergence Technology & Science, Jeju National University, Jeju 63243, Republic of Korea)*
PO-672	**Genetic variants of Accelerated Cell Death 6 drive natural diversity of age-induced leaf senescence through accession-dependent cell death process in Arabidopsis** *Jin Hee Kim (Subtropical Horticulture Research Institute, Jeju National University, Republic of Korea)*

30 Genetic variation/Population

PO-673 CC30	**Altitudinal genetic differentiation in the leaf wax-mediated flowering bud protection against frost in an early-spring flowering herb, Arabidopsis halleri** *Hiroshi Kudoh (Kyoto University, Japan)*
PO-674	**Altitudinal divergence of cold tolerance in Arabidopsis halleri and their genetic background: investigation of the key leaf traits and genome in F2 population** *Naofumi Yoshida (Tohoku University)*
PO-675	**Genetic basis of semi-dwarfism and increased branching phenotypes in Tibetan Arabidopsis thaliana** *Jixuan Yang (State Key Laboratory of Protein and Plant Gene Research, School of Life Sciences, Peking University, China)*
PO-676	**Larger genomes evolve under temperature-stable environments in allohexaploid Rorippa indica (Brassicaceae)** *Ting-Shen Han (Xishuangbanna Tropical Botanical Garden, the Chinese Academy of Sciences)*
PO-677 CC30	**Seasonal dynamics of epigenome in a natural population of Arabidopsis halleri** *Haruki Nishio (Shiga Univ., Japan)*
PO-678	**Seasonally distinct controls of leaf senescence in response to self-shading and sink demand in Arabidopsis helleri** *Genki Yumoto (Kyoto university, Japan)*
PO-679 CC01	**The genetic diversity provided by natural Arabidopsis accessions to identify potentially adaptive differences in root morphology and soil resource capture** *Christian RM Hermans (University of Florida, USA)*
PO-680	**Field transcriptome dynamics of barley during winter cultivation** *June-Sik Kim (RIKEN Center for Sustainable Resource Science, Japan)*
PO-681	**Remote-sensing-combined haplotype analysis using MAGIC population reveals the characters of phenology QTLs for canopy height in rice** *Daisuke Ogawa (Institute of Crop Science, National Agriculture and Food Research Organization)*
PO-682 CC15	**Rapid evolution in Arabidopsis thaliana in global field experiments in the pan-genomic era** *Xing Wu (Carnegie Institution for Science, USA)*
PO-683	**Staying alive: resistant evaluation to acetolactate synthesis-inhibitors herbicides in Amaranthus palmeri recombinant proteins.** *Alfredo Manicardi (Department of Forestry and Agricultural Science and Engineering, Agrotecnio-CERCA Center, University of Lleida, Lleida, Spain)*
PO-684	**1001 Phenomes: a community resource** *Almudena Mollá Morales (Gregor Mendel Institute of Molecular Plant Biology, Austrian Academy of Sciences, Vienna BioCenter, Austria)*

31 Genomics/Bioinfomatics

PO-685	**Construction of Genetic Engineering System for Robust and Versatile Inter-species Gene Function Analysis in Viola** *Donghyeon Kim (Seoul National University, Korea)*
PO-686	**Col-CC: An Updated Reference Genome of Arabidopsis thaliana** *Xiao Dong (Max Planck Institute for Plant Breeding Research)*
PO-687	**Functional annotation of proteins for signaling network inference in non-model species** *Lisa Van den Broeck (North Carolina State University, US)*
PO-688 CC23	**New elements of cis-regulatory code of plant genes revealed by deep learning models** *Jedrzej Szymanski Szymanski (Forschungszentrum Juelich, CEPLAS, BioSC, Institute of Bio- and Geosciences, IBG4 Bioinformatic, 52428 Juelich, Germany)*
PO-689	**Controlling transcription from within transcribed regions in plants** *Yoav Voichek (Gregor Mendel Institute (GMI), Vienna)*
PO-690	**Improve the coverage of Arabidopsis proteome by alternative proteases and mass spectrometry data independent acquisition mode** *Runxuan Zhang Zhang (The James Hutton Institute)*
PO-691	**Development of a unified theory for molecular biology** *Ryoichi Sato (RIKEN Center for Sustainable Resource Science)*
PO-692	**Inference of developmental trajectories from single-cell sequencing data** *Philip Shushkov (Indiana University)*
PO-693 CC03	**A single-nucleus transcriptome atlas of seed-to-seed development in Arabidopsis** *Travis Lee (Plant Biology Laboratory, Salk Institute for Biological Studies, La Jolla, CA 92037)*
PO-694	**Implementation of the single-nucleus atlas of Arabidopsis thaliana to the entire plant research** *Jaewook Kim (Department of Biological Sciences, Chungnam National University, Daejeon 34134, Republic of Korea)*
PO-695	**Phylogenetic profiling in Arabidopsis thaliana as a new annotation platform for revealing gene functions in plants** *Elad Sharon (The Robert H. Smith Institute of Plant Sciences and Genetics in Agriculture, The Hebrew University of Jerusalem, Israel)*
PO-696	**Updated phylogeny and protein structure predictions revise the hypothesis on the origin of MADS-box transcription factors in land plants** *Yichun Qiu (Max Planck Institute of Molecular Plant Physiology, Germany)*
PO-697	**Application of a method detecting functionally diversified duplicate pairs from Arabidopsis duplicate genes to wheat homoeologous genes** *Akihiro Ezoe (Riken)*
PO-698	**Single-plant omics : profiling individual plants in a field to identify processes affecting yield** *Steven Maere (Department of Plant Biotechnology and Bioinformatics, Ghent University, Technologiepark 71, 9052 Ghent, Belgium)*
PO-699	**Optimization of sampling conditions for predicting gene expression in rice** *Dan Eiju (Keio University Faculty of Environment and Information Studies)*
PO-700	**Cellular Clarity: A Logistic Regression Approach to Identify Root Epidermal Regulators of Iron Deficiency Response** *Selene R Schmittling (Department of Electrical & Computer Engineering, NC State University)*

32 Gene transfer/Gene editing

PO-701	**The simple and useful Agrobacterium-mediated infiltration method for transient expression assays and single-cell genome editing in Arabidopsis thaliana** *Miho Ikeda (Fukui Prefectural University, Japan)*
PO-702	**Layered double hydroxide (LDH) nanosheets as an efficient nanotransporter of biomolecules enable the advancement of genome engineering in intact plant cells** *Wenlong Bao (Hainan University)*
PO-703 CC33	**Single-cell targeted chemical or genetic boosting of genome editing in maize** *Ling Meng (KWS Group)*
PO-704	**Generating minimum set of gRNA to cover multiple targets in multiple genomes with MINORg** *Rachelle R. Q. Lee (National University of Singapore)*
PO-705	**Pooled CRISPR/Cas9-induced perturbations followed by single-cell RNA-sequencing in Arabidopsis thaliana protoplasts** *Graeme Oliver Vissers (New York University)*
PO-706	**Allelic Variations in GA20ox1 via CRISPR-Mediated Base Editing Lead Quantitative Clines of Growth in Arabidopsis** *Jun-Hyuk Kim (The Catholic University of Korea, Republic of Korea)*
PO-707	**Insights into the molecular mechanisms of CRISPR/Cas9-mediated gene targeting at multiple loci in Arabidopsis** *Daisuke Miki (Shanghai Center for Plant Stress Biology, CAS Center for Excellence in Molecular Plant Sciences, Chinese Academy of Science)*

PO-708	**Developing tools for targeted C-to-T base editing in the plastid and mitochondrial genome of Arabidopsis thaliana** *Issei Nakazato (Graduate School of Agricultural and Life Sciences, The University of Tokyo)*
PO-709	**Targeted A-to-G base editing in chloroplast and mitochondrial genomes in Arabidopsis thaliana** *Chang Zhou (Tokyo University, Japan)*
PO-710	**PRIMA: PRobe-Induced heteroduplex Mobility Assay, a reliable method to detect single-nucleotide variations time- and cost-effectively** *Misako YAMAZAKI (Department of Evolutionary Biology and Environmental Studies, University of Zurich, Switzerland)*
PO-711	**The development of a new gene editing technology based on Brassica rapa microspore regeneration system and carbon nanotube** *Jinhee Kim Kim (Institute of horticultural and herbal science, Korea)*
PO-712	**Establishing transformation protocols for efficient genome editing and transgene expression across the Brassicaceae family** *Evelyn Cassandra Alferez (Faculty/Staff)*

33 Imaging/Quantification

PO-713	**Plant Accessible Tissue Clearing Solvent System for 3-D Imaging of Whole Plant** *Hantao Zhang (China Agricultural University)*
PO-714	**Whole-mount smFISH allows combining RNA and protein quantification at cellular and subcellular resolution** *Lihua Zhao (Swedish University of Agricultural Sciences)*
PO-715	**A live imaging system to analyze spatiotemporal dynamics of transcription activity.** *Mio K. Shibuta (Yamagata University, Japan)*
PO-716	**Deep Learning-based Recognition of Arabidopsis Accessions using Time-Series RGB High-Throughput Measurements** *Rijad Saric (La Trobe Institute for Sustainable Agriculture & Food (LISAF), Department of Animal, Plant and Soil Sciences, La Trobe University, VIC 3086, Australia.)*
PO-717 CC15	**Time-series field phenotyping system PlantServation using machine learning revealed seasonal pigment fluctuation trends in diploid and polyploid Arabidopsis** *Toshiaki Tameshige (Yokohama City University, Japan)*
PO-718	**An automated robotic system on the RIPPS for chemical stimulation to plants** *Miki Fujita (RIKEN, Japan)*

Appendix: List of short talk speakers

Name	Regist-ration number	Poster ID	Talk title	Session number	Date	Session start time	Talk duration incl. Q/A (min)
Akari Maeda	C000653	PO-421	Quantity regulation of TOC1 and PRR5 for temperature compensation in the Arabidopsis circadian clock	Concurrent 08	Day 2: Tue. Jun. 6	16:30	10
András Székely	C000473	PO-423	Long-distance circadian coordination via a phloem-delivered mobile transcript	Concurrent 29	Day 4: Thu. Jun. 8	10:30	6
Andrea Ramirez Ramirez	C000050	PO-008	A Comparative Study of Adaptive Stress Tolerance in the Brassicaceae Family	Concurrent 19	Day 3: Wed. Jun. 7	11:00	9
Andriy Volkov	C000541	PO-390	Mechanisms underlying polar membrane targeting of SOSEKI protein	Concurrent 32	Day 4: Thu. Jun. 8	14:00	9
Anjana S Hegde	C000514	PO-595	Identification of interacting factors of the TARANI/ Ubiquitin-specific protease 14 (UBP14) in Arabidopsis thaliana	Concurrent 06	Day 2: Tue. Jun. 6	14:30	9
Arp Schnittger	C000047	PO-498	Control of meiosis under heat stress	Concurrent 11	Day 2: Tue. Jun. 6	16:30	13
Bastiaan Bargmann	C000351	PO-564	It’s All in the Timing: Enhancing Regeneration Efficiency Using Morphogenic Factors	Concurrent 04	Day 2: Tue. Jun. 6	14:30	11
Chan Yul Yoo	C000611	PO-368	Light-induced chloroplast biogenesis: photobodies control alternative promoter selection as a mechanism of nucleus-chloroplast communication	Concurrent 05	Day 2: Tue. Jun. 6	14:30	10
Chen Xiao	C000342	PO-234	Arabidopsis DXO1, a decapping enzyme for NAD-capped RNAs, activates RNMT1 to methylate the mRNA guanosine cap	Concurrent 17	Day 3: Wed. Jun. 7	9:00	7
Chih-Pin Chiang	C000656	PO-239	Dose-dependent long-distance movement of microRNA399 duplex regulates phosphate homeostasis in Arabidopsis	Concurrent 31	Day 4: Thu. Jun. 8	14:00	8
Chi-Hsin Chang	C000016	PO-152	The phytocytokine AtCAPE9 and its receptor AtCAPER1 functions on plant systemic stomatal immunity	Concurrent 14	Day 3: Wed. Jun. 7	9:00	9
Chin-Min Kimmy Ho	C000022	PO-651	Leaf epidermal patterning and fate determination	Concurrent 04	Day 2: Tue. Jun. 6	14:30	11
Christian RM Hermans	C000545	PO-679	The genetic diversity provided by natural Arabidopsis accessions to identify potentially adaptive differences in root morphology and soil resource capture	Concurrent 01	Day 2: Tue. Jun. 6	14:30	7
Chun-Kai Huang	C000200	PO-431	Identification of LWD1-interacting proteins reveals novel regulators for Arabidopsis circadian clock	Concurrent 29	Day 4: Thu. Jun. 8	10:30	12
Daniel Slane	C000307	PO-056	Epidermal Cell Type-Specific Chromatin Dynamics Underlying Arabidopsis Heat Stress Memory	Concurrent 02	Day 2: Tue. Jun. 6	14:30	9
Eleftheria Saplaoura	C000497	PO-242	Insights into tRNA-like structures (TLS) as motifs facilitating long-distance transport of mRNAs	Concurrent 33	Day 4: Thu. Jun. 8	14:00	8
Florence Brioudes	C000315	PO-412	A cell wall-modifying enzyme controls symplastic movement of RNA silencing in aerial Arabidopsis tissues	Concurrent 31	Day 4: Thu. Jun. 8	14:00	8
Francisco Benitez-Fuente	C000471	PO-357	Fuctional characterization of Arabidopsis thaliana Synaptotagmin1 domains using Tricalbin3 chimeras in Saccharomyces cerevisiae.	Concurrent 05	Day 2: Tue. Jun. 6	14:30	10
Ha Eun Jeh	C000030	PO-366	Sensory plastids in growth- and defense-related epigenetic phenotype adjustment	Concurrent 02	Day 2: Tue. Jun. 6	14:30	9
Haruki Nishio	C000529	PO-677	Seasonal dynamics of epigenome in a natural population of Arabidopsis halleri	Concurrent 30	Day 4: Thu. Jun. 8	14:00	9
Hiroshi Kudoh	C000599	PO-673	Altitudinal genetic differentiation in the leaf wax-mediated flowering bud protection against frost in an early-spring flowering herb, Arabidopsis halleri	Concurrent 30	Day 4: Thu. Jun. 8	14:00	9
Ho-Ming Chen	C000247	PO-215	Plant miRNA-target 3′-end pairing affects miRNA-mediated translational repression	Concurrent 12	Day 2: Tue. Jun. 6	16:30	11
HUAN-CHI TIEN	C000211	PO-243	The role of plant extracellular vesicles in mRNA intercellular trafficking	Concurrent 28	Day 4: Thu. Jun. 8	10:30	10
Itay Cohen	C000493	PO-575	Transcriptional Regulation of Cell-cell Movement During Root Tip Regeneration	Concurrent 04	Day 2: Tue. Jun. 6	14:30	11
Janis Dabisch	C000486	PO-359	SEED LIPID DROPLET PROTEIN 1 and 2 and LD-PLASMA MEMBRANE ADAPTOR form a lipid droplet-plasma membrane contact site that might play a role under stress	Concurrent 18	Day 3: Wed. Jun. 7	9:00	5
Jedrzej Szymanski Szymanski	C000456	PO-688	New elements of cis-regulatory code of plant genes revealed by deep learning models	Concurrent 23	Day 3: Wed. Jun. 7	11:00	10

Name	Regist-ration number	Poster ID	Talk title	Session number	Date	Session start time	Talk duration incl. Q/A (min)
Jeremy Berthelier	C000474	PO-191	Gene-transposon transcripts can be epigenetically regulated and impact gene response to stress conditions in Arabidopsis thaliana	Concurrent 24	Day 3: Wed. Jun. 7	11:00	5
Jie Linnan	C000670	PO-263	Histone chaperone NAP1 proteins are involved in plant growth under nitrogen deficient conditions in Arabidopsis thaliana	Concurrent 01	Day 2: Tue. Jun. 6	14:30	7
Ji-Young Lee	C000204	PO-644	A long-distance top-down movement of a transcription factor regulating the root phloem development	Concurrent 20	Day 3: Wed. Jun. 7	11:00	9
Jiyun Kim	C000504	PO-647	Phloem cells - from single cell transcriptomics to development and function	Concurrent 19	Day 3: Wed. Jun. 7	11:00	9
Jose Antonio Duarte-Conde	C000512	PO-254	Deciphering the role of specialized ribosomes in plants´ translation efficiency	Concurrent 12	Day 2: Tue. Jun. 6	16:30	11
Jose M Alvarez	C000520	PO-259	NLP7 is a central integrator of transcription networks in nitrogen signaling and drought stress	Concurrent 07	Day 2: Tue. Jun. 6	16:30	9
Jose R Dinneny	C000591	PO-160	Studying the genetic basis for plant-microbe associations using a synthetic biology approach	Concurrent 13	Day 3: Wed. Jun. 7	9:00	14
Kengo Hayashi	C000261	PO-327	Chemical biology study of jasmonate signaling by development of a biased agonist derived from stereoisomers of coronatine	Concurrent 27	Day 4: Thu. Jun. 8	10:30	8
Kenji Matsui	C000489	PO-148	Is Ca2+-induced activation of Arabidopsis lipoxygenase 2 involved in green leaf volatile burst?	Concurrent 21	Day 3: Wed. Jun. 7	11:00	9
Keyan Zhu Salzman	C000237	PO-416	CIRCADIAN CLOCK-ASSOCIATED1 (CCA1) controls resistance to aphid by altering indole glucosinolate production	Concurrent 21	Day 3: Wed. Jun. 7	11:00	9
Liam Walker	C000453	PO-542	Rational approaches to synchronizing germination in seed populations	Concurrent 19	Day 3: Wed. Jun. 7	11:00	9
Ling Meng	C000079	PO-703	Single-cell targeted chemical or genetic boosting of genome editing in maize	Concurrent 33	Day 4: Thu. Jun. 8	14:00	7
Ling Wang	C000092	PO-194	RNA deadenylation pathway suppresses transposable elements in Arabidopsis	Concurrent 24	Day 3: Wed. Jun. 7	11:00	5
Lothar Kalmbach	C000519	PO-646	Cellular adaptations for long-distance transport through the phloem sieve tube	Concurrent 20	Day 3: Wed. Jun. 7	11:00	9
Lucia Piro	C000435	PO-153	Investigating the Role of Carbohydrate Metabolism in Bacterial-Triggered Stomatal Movements Using the Model System Arabidopsis thaliana and Pseudomonas syringe pv tomato	Concurrent 09	Day 2: Tue. Jun. 6	16:30	8
Maika Hayashi	C000577	PO-415	Microfocus X-ray CT Analysis of Arabidopsis Petioles for Leaf Movement	Concurrent 29	Day 4: Thu. Jun. 8	10:30	12
María del Rosario González Bermúdez	C000218	PO-029	Identification of new targets for improving abiotic stress tolerance in plants	Concurrent 27	Day 4: Thu. Jun. 8	10:30	8
Marija Smokvarska	C000028	PO-408	A novel mechanism for plasmodesmata mediated cell-cell communication in plants	Concurrent 20	Day 3: Wed. Jun. 7	11:00	9
Michael Taleski	C000696	PO-617	Coordinating root system architecture: the intersection of CEP and Cytokinin hormone pathways in Arabidopsis	Concurrent 26	Day 4: Thu. Jun. 8	10:30	9
Miho Sanagi	C000021	PO-260	Nitrogen-responsive SnRK1-FBH4 module affects flowering time and metabolism in Arabidopsis	Concurrent 19	Day 3: Wed. Jun. 7	11:00	9
Mingli Xu	C000099	PO-588	Temporal expression of BLADE-ON-PETIOLE 1 and 2 in successive leaves define the shape of their lamina	Concurrent 16	Day 3: Wed. Jun. 7	9:00	9
Monique van Schie	C000334	PO-355	Location, location, location: a system-wide assesment of subcellular protein localization in Arabidopsis roots by mass-spectrometry	Concurrent 03	Day 2: Tue. Jun. 6	14:30	12
Moriaki Saito	C000690	PO-133	AGO2 condensates behavior after bacterial inoculation	Concurrent 22	Day 3: Wed. Jun. 7	11:00	7
Naoya Sugi	C000382	PO-502	Ca2+-induced removal of inner vegetative plasma membrane in Arabidopsis sperm cells	Concurrent 32	Day 4: Thu. Jun. 8	14:00	9
Natanella Illouz-Eliaz	C000252	PO-043	Drought Recovery Induced Immunity Confers Pathogen Resistance	Concurrent 13	Day 3: Wed. Jun. 7	9:00	11
Nicolas Figueroa Fuentealba	C000249	PO-060	Characterization of Arabidopsis ECT family in stress tolerance and stress granules assembly	Concurrent 11	Day 2: Tue. Jun. 6	16:30	13

Name	Regist- ration number	Poster ID	Talk title	Session number	Date	Session start time	Talk duration incl. Q/A (min)
NoA Bae	C000579	PO-002	Enhanced Salt Tolerance by an Antarctic moss gene	Concurrent 30	Day 4: Thu. Jun. 8	14:00	9
Nobuhiro Suzuki	C000596	PO-041	Response of Arabidopsis thaliana to flooding with physical flow	Concurrent 25	Day 4: Thu. Jun. 8	10:30	10
Nobutoshi Yamaguchi	C000226	PO-053	Transcription factor and chromatin-based heat memory in plants	Concurrent 25	Day 4: Thu. Jun. 8	10:30	10
Pamela Carlson	C000141	PO-426	Role of the Arabidopsis AtbZIP63 transcription factor stability in energy management	Concurrent 07	Day 2: Tue. Jun. 6	16:30	9
Qian Wang	C000096	PO-321	A phosphoinositide hub connects CLE peptide signaling and polar auxin efflux regulation	Concurrent 26	Day 4: Thu. Jun. 8	10:30	9
Rahul Puthan Valappil	C000350	PO-447	A B-Box protein suppresses flowering in Arabidopsis through multi-level regulation of the photoperiod pathway	Concurrent 07	Day 2: Tue. Jun. 6	16:30	9
Ruth Cookson	C000277	PO-594	What did the grasses gain by losing PEAPOD? Evolution and conserved functionality of organ size and shape regulator PEAPOD	Concurrent 07	Day 2: Tue. Jun. 6	16:30	9
Sara Maynard	C000764	PO-358	405nm Photostimulation of the Endoplasmic Reticulum-Chloroplast Contact Site in Arabidopsis Hypocotyls Causes Rapid Cytoskeletal Depolymerization, Elevated Cytoplasmic Calcium, and Elevated Organellar ROS	Concurrent 05	Day 2: Tue. Jun. 6	14:30	10
Satoshi Endo	C000077	PO-398	A cell wall-modifying gene-dependent CLE peptide transport in conferring drought resistance	Concurrent 14	Day 3: Wed. Jun. 7	9:00	9
Selene Garcia-Hernandez	C000522	PO-356	The role of DGK1 and DGK2 in Membrane Contact Sites and Stress Tolerance	Concurrent 18	Day 3: Wed. Jun. 7	9:00	5
Shao-Li Yang	C000046	PO-065	Heat-regulated phosphorylation of TOT43 is a switch for stress granule association to contribute to heat tolerance in Arabidopsis	Concurrent 11	Day 2: Tue. Jun. 6	16:30	13
Shoji Mano	C000280	PO-372	Molecular mechanism for peroxisomal protein transport via the ubiquitin system	Concurrent 06	Day 2: Tue. Jun. 6	14:30	9
Shota Yamauchi	C000214	PO-441	Phosphorylation of WD-repeat protein WDR by phototropins is essential for starch degradation to promote stomatal opening	Concurrent 09	Day 2: Tue. Jun. 6	16:30	8
Shuichi Kudo	C000223	PO-427	Assessing the impacts of genetic defects on starch metabolism in Arabidopsis plants using the carbon homeostasis model	Concurrent 23	Day 3: Wed. Jun. 7	11:00	10
Timo Schlemmer	C000757	PO-210	Proof of concept: circular antisense RNAs (caRNAs) as a new mode of action for RNA-based plant protection	Concurrent 28	Day 4: Thu. Jun. 8	10:30	10
Toshiaki Tameshige	C000567	PO-717	Time-series field phenotyping system PlantServation using machine learning revealed seasonal pigment fluctuation trends in diploid and polyploid Arabidopsis	Concurrent 15	Day 3: Wed. Jun. 7	9:00	11
Toshiro Ito	C000580	PO-456	Erasure of Epigenetic Memory in Arabidopsis Flowering Control	Concurrent 16	Day 3: Wed. Jun. 7	9:00	9
Travis Lee	C000090	PO-693	A single-nucleus transcriptome atlas of seed-to-seed development in Arabidopsis	Concurrent 03	Day 2: Tue. Jun. 6	14:30	12
Xing Wu	C000635	PO-682	Rapid evolution in Arabidopsis thaliana in global field experiments in the pan-genomic era	Concurrent 15	Day 3: Wed. Jun. 7	9:00	11
Yan Yan	C000171	PO-211	siRNAs derived from nitrate reductases, NIA1 and NIA2, play vital roles in growth and stress adaptation	Concurrent 17	Day 3: Wed. Jun. 7	9:00	7
Ying-Lan Chen	C000701	PO-402	An Evolutionarily Conserved Long-distance Migrating Peptide Regulates Lignin Biosynthesis Pathway and Plant Immunity	Concurrent 14	Day 3: Wed. Jun. 7	9:00	9
Yohei Takahashi	C000543	PO-075	Stomatal CO2/bicarbonate Sensor Consists of Two Interacting Protein Kinases HT1 and MPK4/12 in Arabidopsis	Concurrent 09	Day 2: Tue. Jun. 6	16:30	8
Yongming Luo	C000098	PO-325	Brassinosteroid receptor BRI1 deubiquitination by UBP12/UBP13 fine-tunes plant growth	Concurrent 32	Day 4: Thu. Jun. 8	14:00	9
Yu-Hsien Chang	C000167	PO-411	Investigating the role of the Arabidopsis ROTAMASE CYCLOPHILIN gene family in organelle-mediated mobile mRNAs transport	Concurrent 31	Day 4: Thu. Jun. 8	14:00	8
Yuki Hirakawa	C000664	PO-582	Analysis of stem cell-promoting CLE peptide signaling in the shoot apical meristems of land plants	Concurrent 10	Day 2: Tue. Jun. 6	16:30	12
Yuki Yoshida	C000712	PO-660	Stomata-derived intercellular signaling that directs mesophyll air space formation	Concurrent 26	Day 4: Thu. Jun. 8	10:30	9

Name	Regist-ration number	Poster ID	Talk title	Session number	Date	Session start time	Talk duration incl. Q/A (min)
Yukio Kurihara	C000390	PO-236	NMD and translation of intergenic splicing-mediated polycistronic transcripts	Concurrent 12	Day 2: Tue. Jun. 6	16:30	11
Zhe Wu	C000336	PO-494	Distinct chromatin signatures in the Arabidopsis male gametophyte	Concurrent 16	Day 3: Wed. Jun. 7	9:00	9
Zhen Lei	C000064	PO-193	Translation-coupled Epigenetic Regulation of Transposable Elements in Plants	Concurrent 12	Day 2: Tue. Jun. 6	16:30	11