

These Community Mini-Symposia at ICAR 2021-Virtual Will Select Short Talks from Abstracts Submitted by 15 April

Active Learning and CUREs in Undergraduate Plant Science Education.

Brit Moss, Whitman College and Thelma Madzima, University of Washington- Bothell, USA

Inspiring and preparing the next generation of plant scientists is imperative to meet the needs of a growing population and a changing climate. Undergraduate education serves as a critical stage during which students explore scientific disciplines and career opportunities. For many students, their first opportunity to dive into the plant biology discipline occurs during introductory or survey biology courses and labs. These experiences serve as a critical opportunity to expose students to the process of research in the plant sciences and to recruit students of diverse backgrounds. Two key pedagogical practices that facilitate these ends and bolster student success in STEM are (i) incorporation of active learning within the classroom setting and (ii) course-based undergraduate research experiences (CUREs). In this symposium, we will bring together plant scientists from diverse campuses and academic ranks who have successfully integrated active learning approaches within their classrooms and are using plant biology-centered CUREs to foster hands-on, authentic research experiences for students at institutions large and small. Due to available genetic resources, small stature and short generation time, *Arabidopsis thaliana* has served as a plant that is highly amenable to undergraduate education. As such, speakers in this session utilize *Arabidopsis* in addition to other model plant systems to achieve these pedagogical goals.

Advancing Quantitative Proteomics in Plant Science.

R. Glen Uhrig, University of Alberta, Canada

To date, our systems-level understanding of plant cell regulation has largely been derived from a combination of genetic and transcriptomic analysis, with comparatively little information available about global protein-level regulation and its impacts on the plant cell environment. Over the past decade extraordinary advancements in quantitative proteomic workflows and technologies now provides exceptional opportunities for characterizing dynamic temporal and spatial changes in the molecular plant cell environment (e.g., post-translational modifications). With proteins representing the outward facing functional elements of the plant cell, they are especially important to advancing our fundamental understanding on plant biology. The goal of this mini-symposium will be to highlight the latest advancements in quantitative plant proteomics and its diverse applications across plant science.

Arabidopsis Informatics.

Nicholas Provart, University of Toronto, Eva Huala and Tanya Berardini (TAIR)

In spite of the *Arabidopsis thaliana* Col-0 genome having been sequenced in 2000, around 50% of its genes still lack a meaningful Gene Ontology Molecular Function or Biological Process annotation. This workshop will cover *Arabidopsis* informatics resources, both established and new, for understanding *Arabidopsis* genomes and for generating quality hypotheses about gene function. TAIR, the BAR, 1001 Genomes, the Ecker Lab, as well as speakers selected from abstract submissions, will present updates and new tools.

Arabidopsis Transposable Element Biology.

R. Keith Slotkin, Danforth Center, USA

Transposable elements (TEs) have traditionally received very little attention in *Arabidopsis* compared other plants with obese genomes. However, there are over 31,000 TEs in the *Arabidopsis* reference genome, and together their high-quality annotation and the traditional molecular strengths of *Arabidopsis* have made *Arabidopsis* a premiere organism to dissect TE function. Today, cutting-edge techniques such as long-read sequencing, single cell approaches, mobilomics and Crispr activation are rapidly revolutionizing the study and appreciation of TEs in *Arabidopsis*. This workshop aims to give *Arabidopsis* TEs the attention that is due.

Cell Polarity: Driving Morphological and Functional Complexity.

Yan Gong, Stanford University, USA, and João Ramalho, Wageningen University, The Netherlands

Plants display an astounding degree of spatial organization essential to their development and function. Underlying this organization is the regulated asymmetric distribution of molecules and structures at the subcellular level, termed cell polarity. The establishment of cell polarity allows cells to spatially organize diverse cellular processes, including orienting cell division planes, assuring directional transport of nutrients and hormones, determining cell morphology and fate, and positioning specialized structures. Guided by the polarity coordinate system, these processes allow plants to precisely execute their developmental programmings and physiological functions at the correct time and place. Given the importance of this fundamental mechanism and the recent noteworthy progress in the field, we believe that a mini-symposium on cell polarity would be a great addition to ICAR 2021 that does not overlap with other parts of the current program. Possible subtopics include the regulation of division asymmetry and cell fate determination in the stomata lineage, control of radial root patterning, regulation of auxin flow during vascular element differentiation, and the existence of a universal coordinate system in land plants. Considering that the topic of this mini-symposium has never been intensively covered by previous ICAR meetings, we believe this mini-symposium would be of particular interest to scientists studying cell polarity, as well as those interested in cell and developmental biology, pattern formation, and morphogenesis.

Circadian Signatures of Fitness.

Xiaodong Xu, Henan University, China

The circadian clocks drive the circadian rhythms and regulate many physiological processes. In recent years, the research progress related to the circadian system is quite abundant, including the response of the circadian clock to the environmental and internal signals, and the critical roles of the circadian oscillators in the output pathways of plant growth, flowering, senescence, and stress resistance.

Encoding Calcium Spikes, Waves, and Oscillations in Arabidopsis.

Sheng Luan, UC Berkeley, USA

Calcium is a second messenger in all eukaryotes ranging from yeast, plants, to human. How does calcium, a simple cation, translate so many signals into distinct cellular responses? How is the specificity of calcium signals encoded and decoded? These are fundamental questions to address in cell biology. For calcium to serve as a signaling agent, the first step is to generate specific calcium signals referred to as “calcium signatures” in response to specific stimuli. This step is to produce a “code” for the specificity and the process thus is referred to as “coding”. The next step is for the cell to interpret the “code” and formulate a specific response, a process named “decoding”. My lab has been working on both coding and decoding processes using Arabidopsis model for the past 25 years. Our earlier work has contributed to the understanding of decoding process through discovery of a calcium sensor-kinase network (the CBL-CIPK network). However, the calcium coding mechanism has been poorly understood in plants. Recent studies in our lab have identified calcium coding mechanisms in pollen tube growth and innate immunity. Recent findings by several labs have greatly enhanced our understanding of mechanisms underlying the “coding/ encoding” of calcium signals in plants. The subtopics of plant biology of impact also include plant cell biology (tip growth), developmental biology (reproduction), plant-microbe interaction, plant-insect interaction, plant abiotic signaling.

Exploring Brassicaceae Diversity.

Kathleen Greenham, University of Minnesota and Patrick Edger, Michigan State University, USA

This mini-symposium aims to highlight exciting discoveries being made in plant biology by leveraging the genetic and phenotypic diversity present across Brassicaceae. We hope to encourage attendees to take advantage of diverse datasets being developed across Brassicaceae that can be used to gain novel insights into processes being studied in Arabidopsis. Topics will include the evolution of noncoding regulatory elements, long noncoding RNA in genome regulation, and developmental biology with a focus on diverse species within Brassicaceae.

Exploring the Single-cell Landscape of Arabidopsis.

Travis Lee and Joseph Swift of the Salk Institute; Rachel Shahan, Duke University; Josh Cuperus and Christine Queitsch of the University of Washington-Seattle, USA

Recently, there has been a dramatic increase in both the breadth and scope of single-cell sequencing methodologies. Utilization of these techniques has permitted the investigation of cell-types, tissues, and whole organisms with unprecedented resolution. Plants present unique challenges for the application of single-cell

methodologies, yet the field of single-cell genomics in Arabidopsis is rapidly emerging. Several published or preprint manuscripts have emerged recently that describe high-throughput single-cell sequencing technologies in several plant species, signaling that efforts toward the generation of single-cell atlases of Arabidopsis is well underway. Currently available manuscripts focused on the Arabidopsis root, and were able to (1) confirm the presence of known cell-type and tissue-type markers in appropriately grouped cells and (2) identify novel cell-type markers with greater specificity and transcript accumulation than well-known marker genes. We believe a mini-symposium focusing on Arabidopsis single-cell applications would allow the research community to showcase these powerful yet nascent technologies. Because of the genetic tools in Arabidopsis, and the anatomical and expression patterns known in Arabidopsis, it will be the first and best opportunity to apply single-cell methods. Several new techniques and technologies are being applied to Arabidopsis and can be explored in this session.

Feeling Stressed? Environmental Adaptation in Extremophyte Relatives of Arabidopsis.

Maheshi Dassanayake, Louisiana State University, USA and Simon Barak, Ben-Gurion University of the Negev, Israel

Plants that naturally inhabit harsh environments, referred to as extremophytes, present novel genetic resources underexplored for their adaptations to multiple environmental stresses. Specially, the extremophytes closely related to Arabidopsis present ideal models that allow the transfer of knowledge gained from this premier model plant to identify functionally significant novel stress responsive mechanisms. Thus, the Brassicaceae extremophytes show great promise for studying genetic mechanisms adapted to multiple environmental stresses that may be missing in Arabidopsis but are crucial to survival in extreme environments, as well as to study how such traits have evolved. These emerging extremophyte models include *Schrenkiella parvula* (adapted to multiple salt and nutrient stresses), *Eutrema salsugineum* (adapted to cold and salt stresses), *Arabidopsis halleri* (adapted to heavy metals), and *Anastatica hierochuntica* (adapted to drought and UV). We plan to include researchers conducting genomic, epigenomic, transcriptomic, metabolomic, and/or physiological studies to highlight the contrasting adaptations of the extremophytes compared to Arabidopsis in this workshop. We expect the Arabidopsis research community interested in using systems biology approaches to understand plant abiotic stress adaptations would be interested and benefit from the proposed workshop. Additionally, our proposed workshop will interest greater plant biology community investigating diverse molecular mechanisms underlying plant adaptations to harsh environments, as well as evolutionary biologists and plant biologists exploring innovative ways to develop new stress-resilient food and bioenergy crops in an age of climate change.

From Molecules to Organs: Quantitative Imaging in Plant Biology.

Marisa Otegui, University of Wisconsin-Madison, USA; Daniel Kierzkowski, University of Montreal, Canada, and Charlotte Kirchhelle, University of Oxford, UK

How do plants robustly and reproducibly generate their organ shapes? Organogenesis is highly complex and involves multiple scales in space and time, posing a significant experimental challenge. Recent technological improvements in fluorescence microscopy and advances in image analysis enable the quantification of cellular growth patterns across entire organs and concomitant sub-cellular events with unprecedented details. During this mini-symposium, we will explore the central role of quantitative live-imaging of plant growth to answer important questions in contemporary developmental biology. Imaging technologies in biology are growing and diversifying at an exponential rate, from being able to capture details of molecules at nearly atomic resolution to imaging whole crop fields in non-invasive manners. New light-based and correlative imaging approaches enable researchers to image cells and tissues in a label-free, multiscale manner to obtain both dynamic and molecular information during cellular processes and cell signaling. Many of these emerging techniques have first been developed for animal models and their application to plant research offers unexplored possibilities and advantages. Our symposium aims to provide an overview of recent growth studies in various plant organs and tissues and to discuss application of emerging imaging modes for both high resolution and highly dynamic processes in plant biology.

Getting More Power From Your Flower: Multi-functional Flowers Improve Plant Fitness.

Diarmuid O'Maoileidigh, University of Liverpool, UK

Flowers are one of the major evolutionary innovations that sculpted the biosphere. The plant community has been largely focused on the important topic of understanding the molecular mechanisms that underlie floral organ formation. However, the mature flowers and fruits perform many functions beyond fertilization, which are less well understood. This mini-symposium aims to provide a partial overview of the innovative work that many groups

are doing to uncover the hidden functions of flowers and how those functions influence plant fitness and may be used to improve crop performance. This mini-symposium has a strong link to core activities in the Arabidopsis community but with a twist that aims to understand the dazzling biological complexity that underlie floral development, floral function, and floral ecology. The research topics that will be presented were originally motivated by Arabidopsis research or provide motivation to perform functional studies using our favorite plant. Early career researchers will benefit most from this mini-symposium as it will provide them with an overview of several fields of research where there are many open questions with possibilities for collaboration. Furthermore, it will provide tangible examples of how ground-breaking science can be done even in very well-studied systems such as flowers by asking the right questions. The subtopics of this mini-symposium are flower and fruit development, biomechanics, metabolism, pollination, bio-optics, plant defense.

How Do Plants Sense and Respond to Elevated Carbon Dioxide, Ozone and Drought?

Maija Sierla, University of Helsinki, Finland and Julian Schroeder, University of California, San Diego, USA
Stomata regulate the diffusion of CO₂ into leaves for photosynthetic carbon fixation and mediate over 90% of plant water loss via transpiration. Stomatal pores are formed by guard cells in the epidermis of leaves and respond to changes in CO₂ concentration. CO₂ regulation of stomatal movements will have profound effects on plants, due to the continuing steep increase in the atmospheric CO₂ concentration. New and substantial advances are being made at isolating new mutants and characterizing the molecular cell signaling mechanisms and network by which CO₂ controls stomatal movements. Furthermore, research is illuminating the effect of CO₂ on water use efficiency and plant growth. Photosynthesis and respiration cause large daily CO₂ concentration (C_i) changes in leaves. Moreover, atmospheric [CO₂] is predicted to double during this century and the ensuing C_i rise reduces stomatal conductance of plants, which will have profound effects on global gas exchange, plant water use efficiency, growth and leaf heat stress. A network of signal transduction mechanisms sense and transduce [CO₂] changes to regulate stomatal movements for optimization of CO₂ influx, water loss and plant growth. However, the underlying CO₂ sensors and communication mechanisms have remained enigmatic. Key genes and mechanisms, including CO₂ sensors, are being identified by several laboratories and a model is emerging for the sequence of events in CO₂ signaling in control of plant gas exchange. Identification of the molecular mechanisms and network principles by which CO₂ modulates stomatal conductance is fundamental to understanding the regulation of gas exchange between plants and the atmosphere, will help predict effects of atmospheric CO₂ elevation on plants and can contribute to future engineering of enhanced water use efficiency in crop plants and plant carbon sinks in the face of the continuing [CO₂] rise and climate change.

Impact and Application of Basic Research to Sustainable Agriculture Improvement.

Sponsored by Bayer Crop Science

Huachun Larue and Xiaoyu Liu, Bayer Crop Science, USA

With growing population size and limited arable land, the world is challenged to make agriculture more productive and sustainable. Arabidopsis thaliana, which serves as the model organism for plant research, has pioneered the foundation of our knowledge about plant development, reproduction, biotic and abiotic responses. Knowledge learnt from Arabidopsis research have proven to be a valuable resource for developing applications in improving crop performance for sustained agricultural practices. During this session, we will highlight Arabidopsis research with potential applications in sustainable agriculture, and industrial applications of research knowledge in commercial crop products. We hope to broaden perspectives and stimulate thinking on how best translate Arabidopsis research knowledge to applied agriculture applications, and ideally inspire more innovative young scientists to leverage their learnings to help shape the sustainable agriculture.

Implications of the non-coding genome on chromatin signaling during plant gene expression.

Soichi Inagaki, The University of Tokyo, Japan, and Sebastian Marquardt, University of Copenhagen, Denmark
A high number of genetic variation underlying key plant traits maps to regions of genomes that do not encode proteins (i.e. the non-coding genome). The question what models are most suitable to interpret how causative genetic variation on the non-coding genome mechanistically affects plant yield and environmental response provides the theme for this mini-symposium. Transcriptional activity in the non-coding genome results in a large number of long non-coding RNAs (lncRNAs). Moreover, lncRNA transcription by RNA polymerase II or V alters the

epigenome through co-transcriptional chromatin signaling. Transcriptional conflicts frequently arise when lncRNA and mRNA expression coincide, for example through overlapping transcription. In Arabidopsis, discovering the extent of overlapping transcriptions through implementation of novel genomics methods represents a key area of breakthrough since the last ICAR meeting. We will focus on molecular mechanisms used in plants to resolve conflicting chromatin signaling and pervasive transcription, and examples where these mechanisms promote plant fitness.

Leveraging Natural Variation to Understand Immune Functions.

Adam Steinbrenner, University of Washington, USA

Natural variation across Arabidopsis thaliana has historically enabled key genetic insights into immune function. Today this variation continues to inform and enable emerging topics in biotic interactions. Such research provides state-of-the-art pipelines for variation-based projects in other species e.g. crop models. Recent exciting findings in Arabidopsis have included 1) species wide screens with various pathogen/beneficial strains, 2) the elucidation of the species-wide intracellular immune receptor repertoire (NLR-ome), 3) important insights from cases of hybrid incompatibility between accessions, and 4) increasing understanding of variation in copy number / domain organization as driving factors in immune function. Subtopics may include variation in plant microbiome, structural variation in immune-related genes, and natural selection. The symposium would be of interest to other ICAR attendees leveraging variation to understand other aspects of plant biology (e.g. GWAS for developmental and abiotic response variation) as well as the traditional plant-pathogen community largely studying Col-0.

Metabolite-mediated Regulation of Plant Growth and Development.

Sponsored by The Plant Journal

Hiroshi A. Maeda, UW-Madison; and Jazz Dickinson University of San Diego, USA

Plants produce a diverse set of secondary metabolites. Some of these are conserved among all land plants while others are lineage-specific. The major plant hormones (auxin, cytokinin, ABA etc.) are all secondary metabolites with very well studied roles in diverse aspects of plant growth, development, and physiology. A growing number of plant genome sequences is facilitating discovery of genes and enzymes involved in specialized metabolism, providing novel tools for plant synthetic biology. Redesigning plant metabolism, however, requires fundamental understanding of biochemical, molecular, and genetic mechanism controlling core (primary) metabolism that support plant growth and development. Model organisms, such as Arabidopsis thaliana, continue to provide powerful tools to provide novel insights into mechanistic basis of plant metabolism and its regulation. This symposium will bring together scientists to discuss novel findings and future prospects in advancing our basic understanding of plant metabolism and potential application in crop improvement and metabolic engineering. In addition, we think that this topic will be particularly attractive and important for attendees because it brings together several research areas in plant biology including biochemistry, physiology, metabolomics, and development.

Molecules on the Move (MOM): Plant-microorganism Communication.

Patricia Baldrich, Danforth Center and Ryan DelPercio, University of Missouri Columbia, USA

The mobility of small molecules between plants and their associated microorganisms, including bacteria, fungi and viruses, is a well-known phenomenon. In the last years, several articles have pointed out evidences of small RNAs, hormones and even protein movement from plant to host and vice versa. However, the mechanism(s) used for this molecular communication between organisms, and the conservation of these mechanisms, remains unknown. In recent years, several hypotheses of extracellular vesicle-mediated transport have been proposed, but it remains unclear how these vesicles would cross the plant cell wall and, in some cases, the microorganism cell wall. This emerging and promising type of molecular communication between species has a broad range of potential applications, from plant protection to nutrient uptake. The use of Arabidopsis as a plant model to study these interactions is helping to expand the basic knowledge, opening new possibilities for crop improvement. This session will be of special interest for early career researchers to present their latest work, help them expand their network connections, and facilitate new international collaborations. The mini-symposium could be divided in several subtopics, such as by the microorganisms (bacterial, fungus or virus) or on the type of moving molecule (small RNAs, RNAs, hormones, proteins, etc.).

Nutrient Signaling Nexus in Control of Plant Architecture.

Franziska Fichtner and Milos Tanurdzic, The University of Queensland, Australia

Nutrient availability is a major factor in determining the patterns of shoot and root development and growth. While macronutrient like nitrate and phosphate have long been known to regulate plant development, sugar signaling is an emerging research area. Recent work in the regulation of axillary bud outgrowth, for example, has identified sugar signalling as a major regulator of shoot branching, in concert with plant hormones. Trehalose-6-phosphate (T6P), a sucrose-specific signaling molecule, has been implicated in this process by genetic and biochemical approaches, showing metabolic shifts in carbon and nitrogen metabolism, and, therefore, linking major nutrient signaling pathways. These findings highlight the existence of a highly complex system of nutrient signal integration that happens across roots and shoots. This session is designed to bring together researchers from the fields of nutrient and sugar signaling, and plant development, utilizing both Arabidopsis and crops model systems. A variety of experimental approaches, from classical plant physiology and molecular genetics, to systems biology and modelling will be featured, to provide a discussion platform for plant biologists interested in the interface of sugar and other nutrient signalling pathways. Possible subtopics include: (i) The regulation of plant development by T6P and its connection to nitrogen metabolism; (ii) The SnRK1 energy signalling pathway; (iii) systemic regulation of carbon and nitrogen responses and their integration; (iv) modelling of nutrient signalling pathways and their impact on plant development. This session will be of interest to scientists of a large variety of research areas such as sugar signalling, macronutrient acquisition and transport, nitrogen fixation, metabolic networks and metabolic modelling and will highlight state-of-art experimental approaches and research questions.

Plant Hormones.

Anna Stepanova, North Carolina State University, USA

Plant hormones are critical growth regulators that control nearly every aspect of the development and interactions of plants with their environment. In the past three decades, Arabidopsis has become an indispensable model in the study of hormone biosynthesis, transport, catabolism, signaling and response, enabling the discovery of key molecular players that orchestrate these processes and implicating plant hormones in the regulation of an ever-expanding list of physiological and environmental responses. With the main hormonal pathways now largely mapped out, research efforts have shifted towards gaining a more in-depth mechanistic understanding, exploring the spatiotemporal control of these hormonal pathways and the responses they trigger, elucidating interactions between growth regulators and other endogenous and exogenous signals, implementing synthetic versions of hormone signaling pathways in heterologous systems, modeling pathway behavior, and developing sensitive genetically-encoded hormone biosensors. Furthermore, foundational discoveries made in Arabidopsis have fueled a large body of translational work in agriculturally-relevant plant species, leveraging our mechanistic knowledge of plant hormones to devise intelligent new approaches to optimizing plant growth, stress tolerance, and productivity and to develop novel environmentally-resilient plant varieties.

Plant Memory: Environmental Information Integration Within and Across Generations.

Gabriela Auge, IIBBA-CONICET, Argentina

Plants integrate information they receive from their environment to align their growth and development to match the seasonal conditions that are best for survival. This adjustment requires fine tuning of responses and integration of environmental information during the whole life cycle. In this way, environments perceived in one developmental stage could influence the response of subsequent developmental transitions, but those effects may be even affecting responses of future generations. This minisymposium gathers researchers investigating how plants integrate information and develop a sort of memory of past environments across scales: from exploring the nature of the memory signal to understanding its ecological and evolutionary consequences. We will show ongoing work on the genetics and epigenetics of transgenerational effects, importance of these effects in ecological and evolutionary contexts and mathematical modeling used to predict responses of future generations. Being a multidisciplinary study area, this minisymposium highlights a topic of growing interest within the plant biology community. We welcome anybody interested in understanding plant responses to a changing climate as an integrative decision process within and across generations.

Quantitative Development in the Digital World.

Margaret Frank, Cornell University and Sam Leiboff, UC Berkeley, USA

From digital profiles of single-cell identities to mathematical reconstructions of 3-dimensional plant morphology, quantitative biology is transforming our fundamental understanding of plant development. The goal of this mini-symposium is to bring together researchers who integrate molecular genetic, mathematical, and/or morphological approaches from diverse experimental systems to discuss emerging quantitative, data-driven models for plant development. Possible topics include: precision profiling of developmental state transitions; role of molecular stochasticity in developmental processes; quantifying morphological plasticity; and integrating biophysics into developmental networks.

RNA Modifications-mechanism and Biology.

Xuemei Chen, University of California, Riverside, USA and Yiji Xia, Hong Kong Baptist University, China

Chemical modifications to RNA are increasingly discovered in eukaryotes and their biological impacts are beginning to be appreciated. RNA modifications occur to noncoding RNAs such as rRNAs, tRNAs, microRNAs, as well as to messenger RNAs. They occur at the 5' end of RNA, such as capping, at the 3' end of RNA, such as polyadenylation and uridylation, and internally. The modifications affect the fate of RNAs, such as their half-life, translatability, and cellular location. The enzymes that deposit (writers), remove (erasers), and bind (effectors) some of the modifications are known or being studied. Through these studies, the biological functions of RNA modifications are emerging. Despite the increasing realization of widespread RNA modifications in plants, this topic has not received much attention at past conferences. There is still a lack of a general awareness for the importance of RNA modifications in plant biology. There are still many RNA modifications that await discovery. As such, we need to increase awareness for RNA modifications as layers of gene expression regulation in response to developmental cues and environmental signals. We need to attract young scientists to delve into related areas of study. This minisymposium on RNA modifications will showcase the importance of the topic.

Sensing the Cell Wall: Mechanical Signals and Downstream Responses.

Lauri Vaahtera, Norwegian University of Science and Technology (NTNU), Norway and Nora Gigli Bisceglia, Wageningen University, The Netherlands

One essential component of all plant cells is the cell wall, a complex and dynamic structure made mostly of polysaccharides and structural proteins. The cell wall forms a barrier between the intracellular and the extracellular environment, consequently protecting plant cells from biotic and abiotic stresses as well as supporting plant growth and development. The properties of the cell wall are actively modified in order to respond to aforementioned challenges. But how are these modifications triggered and adjusted? Optimal response requires information of the mechanical forces at the plasma membrane-cell wall -interphase. This information combined with other stress and developmental signaling cues allows plants to survive and grow maintaining the integrity of their cell walls. With this proposed session we aim to provide an overview of the current state of the research area and facilitate exchange of new ideas on the molecular mechanisms responsible for cell wall integrity sensing and signaling. Scientists interested in plant stress signaling and/or development would benefit from this topic, since the cell wall plays an important role in many aspects of plant's life. Possible subtopics include cell wall integrity signaling a) molecular mechanisms b) role in biotic stress c) role in abiotic stress d) role in development

Social Media and Science Communication.

Javier Brumos, North Carolina State University, USA and Eva Hellmann, Sainsbury at Cambridge University, UK

The growing global internet availability is reshaping the world as we know it. Users of the digital world have one favorite online activity: social media. Around 2.5 billion people, or in other words, one third of the planet, uses social media. We do it for two predominant reasons: to keep in touch with friends and relatives (42% of social media users) and to stay informed on current news, views and events (41% of social media users). Social media has transformed the way we consume news and has democratized the access to information. Today public audiences are turning to social media when looking for information and facts. Social media has become an exceptionally powerful tool, simplifying the path to knowledge but also able to influence the public opinion. There is no quality control when it comes to social media. Nobody needs to be an expert to express their views out to the world. For those reasons, scientists should be at the forefront of social media engagement. We can provide knowledge and data-based facts to an audience eager to find sources of information they can trust. We have an unbeatable

opportunity to take the stage and participate in the education of millions of people. In fact, there has been a significant increase in social media usage by academics in recent years. Social media can help to share science with the public, policy-makers, and other scientists. Science communication reaching the general public makes science more approachable and engaging and, in the end, an educated public can better weigh in with policy-makers and legislators' decisions. Social media provides new venues for disseminating scientific discoveries and keeping up with recent publications. Growing an impactful online footprint is, however, time-consuming and many scientists struggle with becoming active users. It is nonetheless important to define clear goals to be achieved from our digital interactions, to decide which platforms would best suit our purposes, and to enable the right audiences to find us.

Stochasticity and Robustness in Plant Development.

Adrienne Roeder and Batthula Vijaya Lakshmi Vadde, Cornell University, and Jennifer Lachowiec, Montana State University, USA; Arezki Boudaoud, ENS- Lyon, France; and James Locke, Cambridge, UK

A process is stochastic if it has a probabilistic or randomly determined outcome. All processes at the molecular level are stochastic. For example, gene expression in *Arabidopsis* is stochastic, similar to other organisms. On the other hand, a process is robust if it has a reproducible outcome, particularly in the face of various perturbations including stochasticity of molecular or cellular components, environmental variations, pathogen response, and sometimes even genetic mutations. For example, sepals form with the same size and shape despite variability in the growth and division of their constituent cells. The topics of stochasticity and robustness have attracted much attention in single-celled systems and are now expanding to multicellular systems, as exemplified by a series of recent studies in plants, making this an opportune time for a mini-symposium. In this symposium, we hope to generate new ideas by discussing the open questions as well as the current state of research on stochasticity and robustness. For instance, we will examine the variability in gene expression between identical plants as well as discuss the role of network redundancy in generating robustness. We will consider how environmental changes affect robustness. The robustness of a phenotype can be changed in evolution, and we will examine the robustness in seedling emergence across species.

Stress Granules in Plants as Novel Mechanism in Stress Signaling.

Monika Chodasiewicz (Kosmacz), King Abdullah University of Science and Technology, Saudi Arabia

Stress granules are important cellular foci formed under stress conditions to sequester mRNA, proteins but also important metabolites. Mechanism of their assembly and disassembly is well described however still not much is known about mechanism of sequestration for specific proteins and metabolites. Under different stress conditions different mRNA-protein-metabolite complexes might be formed in stress granules with the function to protect or inhibit their function. Recently, there are new functions being associated with Stress granule such inhibition of protein activities, metabolome formation or sequestration to protect important metabolites. Novel mechanisms are important in understanding how stress granules participate in generating stress response and tolerance to stress. Stress granules are liquid-liquid phase non-membranous organelles in all living organism, known to have as main function protection of mRNA stalled at the translation level under stress conditions. Recently many groups in the world started to study those cytosolic foci because it has been shown that aggregates formed under stress conditions between mRNA and proteins are not random. Under stress conditions, protein – mRNA complexes are formed to protect mRNA from degradation but also as recently show, protect proteins from proteasomal degradation or partially inhibit their function in unfavorable stress conditions. Stress granules might be formed in different stresses, suggesting that their composition might differ depending on the stress treatment. What was recently shown is that stress granules are formed under low oxygen stress, salt stress, heat stress but also during autophagy. In addition, there is intense discussion in the plant research community that plastids might have their own stress granules formed, for example, under high light stress. This session on stress granules involvement in stress signaling will be a great opportunity for people from different plant fields to discuss novel discoveries of stress granule functions other than canonical involvement in mRNA protection.

The Arabidopsis Algorithm: Mathematical Modeling in Plant Biology.

Kari Miller, Washington University in St. Louis, USA

Computational and mathematical models are fast becoming indispensable tools for mechanistic studies of complex biological processes, ranging from the molecular to the developmental to the ecological. In addition, some funding

agencies have made modeling an important component of grant applications. As a result, plant biologists have been quick to make use of these approaches, resulting in new insights into many research questions. This series of speakers will demonstrate several diverse applications of mathematical modeling to plant biology, particularly how modeling can be used to predict physiological responses, guide future experiments, and clarify otherwise convoluted biological processes. We anticipate that a symposium on this timely topic would update the audience on new discoveries in plant biology and how mathematical modeling helped with those discoveries. In addition, it will continue to solidify this nascent community of Arabidopsis biologists.

The Cell Cycle in Plant Growth, Development and Stress Responses.

John Larkin, Louisiana State University and Adrienne Roeder, Cornell University, USA

The cell cycle plays a crucial role in plant growth, and recent work has shown that genetic manipulation of the cell cycle can alter organ size and photosynthetic capacity. While the plant cell cycle is closely related to that of other eukaryotes, the plant cell cycle also has unique plant-specific features. For example, plants lack the key regulatory circuit that controls the timing of exit from G2; instead, plants have a unique class of mitosis-specific cyclin-dependent kinases. Furthermore, plants frequently employ an alternate version of the cell cycle, known as endoreplication or endoreduplication, in which DNA is replicated without subsequent mitosis and cytokinesis. Endoreplication frequently accompanies the cell expansion phase of growth, but is also a common response to biotic and abiotic stress, including DNA damage, drought and pathogen infection. Rapid advances in understanding plant cell cycle regulation, and its relationship to plant responses to their environment, have been led by international group Arabidopsis researchers in recent years, making this a topic of broad interest to many. Subtopics could include basic cell cycle mechanisms, the cell cycle in stress responses, and the cell cycle in meiosis.

The Role of Intrinsically Disordered Proteins in Plant Biology.

Heather Meyer, Carnegie Institution, USA, Cesar Cuevas-Velazquez, Universidad Nacional Autónoma de México

In recent years, the field of Intrinsically Disordered Proteins (IDPs) has grown significantly due to an increasing amount of reports showing their ability to phase separate and regulate processes relating to disease, development and stress response. In plant biology, laboratories around the world are starting to report exciting findings showing that IDPs may use their unique biophysical properties to participate in sensing and adapting to biotic and abiotic conditions. In this minisymposium, we aim to gather a diverse group of plant biologists that are exploring the role of IDPs and phase separation under a wide range of physiological conditions such as temperature and light sensing, water deficit, carbon fixation and etc. To the best of our knowledge, this is the very first plant-focused IDP session at a scientific conference. Therefore, we expect this minisymposium will bring recognition to plant IDP research and help establish a new sub-field in plant biology.

Translational Regulation of Gene Expression.

Catharina Merchante, University of Málaga, Spain; Astrid Gadeyne, VIB-UGent, Belgium and Pamela A. Ribone, Sainsbury, University of Cambridge, UK

Traditionally transcription was considered as the central step for the response to stimuli and regulation in plants. For decades, translational regulation has gotten much less attention although it is clear that, among post-transcriptional and post-translational modification and degradation, translational regulation of gene products plays a major role in all organisms. Translational regulation enables a fast response to rapid changes in environmental conditions. By fine-tuning translation, protein synthesis can be precisely adjusted to the actual demand, which is important since protein synthesis is one of the most energy-consuming cellular processes. Still, translational regulation is often disregarded and, despite the large number of examples illustrating that transcriptional profiles not always match protein levels in cells, researchers still rely on transcript levels to draw conclusions on protein expression. The emergence of various new technologies that allow in-depth study of translation resulted in a resurgence in the plant translation field. New plant-specific translation mechanisms are being unveiled, and translationally-regulated mRNAs have been found to be key in the plant's adaptational responses. Recent examples have exquisitely demonstrated the biological significance of translational regulation in plants, and its potential in the generation of new, powerful biotechnological tools. Today it is clear that the regulation of translation is a rather complex process, involving numerous steps and diverse actors, that we would like to discuss as the subtopics of this symposium.

Using Evolutionary Novelty to Understand General Principles of Plant Biology.

Daniel Kliebenstein, University of California, Davis, USA

A broad range of plant traits are controlled by evolutionarily novel mechanisms like non-host resistance, microbiome composition and development that contributes to environmental adaptation. Yet there is a common misperception that only conserved mechanisms provide general principles. And this translates into the broader research community under-estimating the power of studying evolutionary novelty in developing a deeper understanding of general evolutionary principles that shape molecular mechanisms. The session aims to feature speakers that are utilizing evolutionarily novelty within Arabidopsis to address fundamental principles of the microbiome, development and gene regulatory networks. This mini-symposium will highlight how evolutionarily novel mechanisms contribute to our understanding of general principles underlying interactions with a particular focus on plant-environment interactions. A further goal of this mini-symposium is to generate a speaker list that maximized the potential for unexpected integrative connections that occur by having people listening to seminars outside of their area of specialization. For example, how does leaf morphology influence specialized metabolite regulation and ensuing phyllosphere microbiome. These are the potential connections that would not occur in a mini-symposium more focused on specific processes or mechanisms.

When Development Meets Stress- Integration of Plant Growth and Defense.

Cris Argueso, Colorado State University, USA

Strong activation of plant immune responses often results in reduced plant growth. Uncoupling of resistance from yield penalties can lead to increased crop productivity. This session will focus on research that explores the molecular mechanisms by which plants integrate plant growth and defense activation.