Agenda for "2025 International Symposium on Plant Environmental Resilience"

Aug 04-05, 2025

Group Communication and Discussion session will be held on Monday (Aug 4th) morning and Tuesday (Aug 5th) afternoon

Organizers: Guozhi Bi, Yanglin Ding, Liangsheng Wang, Yongliang Zhang, Wenkun Zhou

Meeting Schedule

Lecture Hall, College of Biological Sciences, China Agricultural University, Beijing

Aug 04, Monday Afternoon, 2025

14:00-14:10	**Opening Ceremony** Welcome address by **Shuhua Yang**
14:10-15:50	**Session I** (Chair: **Yanglin Ding**)
14:10-14:40	**Xiaofeng Wang** (Virginia Tech, USA) Protein, lipid, and membrane interactions in positive-strand RNA virus genomic replication
14:40-15:10	**Jian Hua** (Cornell University, USA) Function and regulation of basal calcium ion levels for environmental responses in *Arabidopsis thaliana*
15:10-15:40	**Yiting Shi** (China Agricultural University, China) A natural variant of COOL1 gene enhances cold tolerance for high-latitude adaptation in maize
15:40-15:50	Xuyue (Beijing) Sci.& Tech. Co., Ltd Recent advances in Xuyue NMT for *in vivo* functional analysis of stress-related genes
15:50-16:10	*Group photograph* / *Coffee and Tea Break*

16:10-18:00	**Session II** (Chair: **Liangsheng Wang**)
16:10-16:40	**Chanhong Kim** (Center for Excellence in Molecular Plant Sciences, China) NPR1 and EX1 orchestrate salicylic acid and singlet oxygen signaling to regulate hypocotyl growth in the dark
16:40-17:10	**Changjiang Li** (China Agricultural University, China) ECAP functions as a signaling hub to orchestrate plant development and stress responses
17:10-17:40	**Xiangfeng Wang** (China Agricultural University, China) Specific microtubule-associated proteins facilitate autophagosome formation in plants
17:40-18:00	**Short talk by students** (5 min × 4) Fan Zhang; Xinyan Qin; Tianren Zhang; Tiantian Wang

Aug 05, Tuesday, 2025

8:20-9:50	**Session III** (Chair: **Wenkun Zhou**)
8:20-8:50	**Tonni Grube Andersen** (Max Planck Institute for Plant Breeding Research, Germany) The importance of barriers in a functional relationship
8:50-9:20	**Dae-Jin Yun** (Konkuk University, South Korea) The roles of chromatin-remodeling complex HOS15-PWR-HDA9 in plant development and stress responses
9:20-9:50	**Tae-Wuk Kim** (Hanyang University, South Korea) BZR1-regulated stomatal development and anthocyanin biosynthesis in *Arabidopsis*
9:50-10:10	*Coffee and Tea Break*
10:10-12:00	**Session IV** (Chair: **Guozhi Bi**)
10:10-10:40	**Frank Takken** (University of Amsterdam, Netherlands) SNC1 guards topless family members that encode susceptibility genes for Fusarium wilt in tomato and *Arabidopsis*

10:40-11:10	**Lisha Zhang** (University of Tuebingen, Germany) Leucine-rich repeat receptor proteins-mediated pattern-triggered immunity in *Arabidopsis*
11:10-11:40	**Zhirui Yang** (China Agricultural University, China) The roles and regulatory mechanisms of *Argonautes* in response to biotic and abiotic stressors
11:40-12:00	**Short talk by students** (5 min × 4) Xinyu Zhang; Ruiqi Wang; Gaofeng Lv; Dongyun Jia
12:00-12:10	**Closing Remarks** by **Yan Guo**

NOTES:

Protein, lipid, and membrane interactions in positive-strand RNA virus genomic replication

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Abstract

Positive-strand RNA [(+)RNA] viruses are the largest viral class and include numerous important pathogens infecting humans, animals, and plants. A hallmark of (+)RNA viruses is the formation of membrane-bound viral replication complexes (VRCs) on specific host organelle membranes. The formation of VRCs is driven by viral replication proteins in conjunction with recruited host factors, which modulate lipid compositions and membrane curvatures. We use brome mosaic virus (BMV) as a model to dissect the mechanisms underlying biogenesis and activity maintenance of VRCs. BMV primarily infects monocotyledon plants such as barley and wheat while showing limited infectivity in dicotyledon species except *Nicotiana benthamiana*. BMV replication can be reconstituted in the baker's yeast (*Saccharomyces cerevisiae*), recapitulating key features observed in plant cells. During replication, BMV induces the formation of VRCs on the outer nuclear membrane, a process that can be similarly triggered by expression of the viral replication protein 1a alone. I will highlight features of BMV 1a that enables it to serve as a core organizer of VRCs, including two amphipathic helices that target and insert BMV 1a into the nuclear membranes; and how it interacts and recruits the phosphatidylcholine (PC) synthesis enzyme, Cho2, to stimulate VRC-localized PC synthesis. Additionally, cellular lipid alterations, such as those in yeast deletion mutants *acb*1 and *pah*1, either inhibited or stimulated BMV replication, pointing out the importance of lipid compositions in viral replication and potentially, in virus control. We are currently employing lipidomics approaches to identify and characterize specific lipid species critical for BMV VRC formation and function, and their applicability in other (+) RNA viruses.

Key Words: Positive-strand RNA viruses, viral replication complex, lipid synthesis, viral replication, virus control

Function and regulation of basal calcium ion levels for environmental responses in *Arabidopsis thaliana*

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Abstract

Calcium ion (Ca^{2+}) signaling is essential for growth development and environmental responses in plants. While transient Ca^{2+} signature has long been regarded as a secondary messenger mediating a variety of cellular responses, the basal or resting cytosolic Ca^{2+} concentration ($[Ca^{2+}]_{cyt}$) is emerging as an important determinant of environmental responses as well. In this presentation, I will show that elevated or reduced basal $[Ca^{2+}]_{cyt}$ lead to altered immune responses and temperature stress tolerance in *Arabidopsis*. Basal $[Ca^{2+}]_{cyt}$ is maintained by autoinhibitory Ca^{2+} ATPases (ACAs) in three membrane systems, as indicated by changes of $[Ca^{2+}]_{cyt}$ observed in their loss of function mutants and overexpression transgenic plants. In addition, basal $[Ca^{2+}]_{cyt}$ is regulated by an evolutionarily conserved Ca^{2+} binding protein BON1 that activates ACA proteins independently of calmodulin. Lastly, I will present preliminary data on environment modulation of basal $[Ca^{2+}]_{cyt}$ and discuss its regulatory mechanism.

Key Words: Basal Ca^{2+}, BON1, environment, stress, *Arabidopsis*

A natural variant of COOL1 gene enhances cold tolerance for high-latitude adaptation in maize

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Abstract

Low temperature severely limits the growth, yield, and geographical distribution of maize (Zea mays L.). How maize adapts to cold climates remains largely unclear. Here, we identify a basic helix-loop-helix (bHLH) transcription factor, COLD-RESPONSIVE OPERATION LOCUS 1 (COOL1), as a crucial regulator of maize cold tolerance through genome-wide association studies. Natural variations in the COOL1 promoter affect the binding affinity of ELONGATED HYPOCOTYL5 (HY5), a transcriptional factor repressing COOL1 transcription. COOL1, in turn, negatively regulates downstream cold-responsive genes, thereby modulating cold tolerance. Moreover, calcium-dependent protein kinase CPK17 translocates to the nucleus and stabilizes COOL1 in response to cold stress. Intriguingly, the cold-tolerant allele of COOL1 is predominantly distributed in northern high latitudes with cold climates. This study defines a previously unknown pathway by which the COOL1-centered module regulates cold tolerance for high latitudinal adaptation in maize.

Key Words: COOL1, cold tolerance, natural variation, latitudinal adaptation, maize

NPR1 and EX1 orchestrate salicylic acid and singlet oxygen signaling to regulate hypocotyl growth in the dark

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Abstract

During subterranean growth, germinating seeds must balance growth and defense in microbe-rich soils to transition from heterotrophic to photoautotrophic growth. However, the molecular mechanisms regulating this process in darkness remain poorly understood. Here, we investigate the role of salicylic acid (SA), a key defense hormone, in controlling hypocotyl elongation. SA inhibited hypocotyl growth in a dose-dependent manner, with a stronger effect in the *Arabidopsis npr1* (*nonexpressor of pathogenesis-related genes 1*) mutant, revealing NPR1's role in maintaining growth under SA-accumulating conditions. In *npr1* etiolated seedlings, auxin-responsive genes—including multiple *SMALL AUXIN UP-REGULATED RNA* (*SAUR*) and *EXPANSIN* genes—were downregulated. Overexpression of *SAUR19* or *SAUR63* entirely rescued SA-induced growth inhibition. We also identified EXECUTER1 (EX1), a mediator of singlet oxygen ($^1O_2$) signaling, as a key contributor to SA-induced growth suppression. SA-driven lipid peroxidation increased $^1O_2$ levels in darkness, activating EX1 retrograde signaling to repress auxin-related genes. These findings reveal how NPR1 and EX1 mediate SA and $^1O_2$ signaling to regulate hypocotyl elongation during subterranean growth.

Key Words: Salicylic acid, singlet oxygen, NPR1, EXECUTER1, auxin, subterranean growth

ECAP functions as a signaling hub to orchestrate plant development and stress responses

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Abstract

Due to their sessile nature, plants constantly perceive various developmental and environmental signals and make optimal responses during growth and development. However, the molecular mechanisms underlying how plants balance developmental and stress signals remain largely unclear. Our previous studies identified an EAR motif-Containing Adaptor Protein (ECAP), which forms the JAZs-ECAP-TPR2 complex with JAZ6/8 and the transcriptional corepressor TPR2, epigenetically repressing jasmonate-induced anthocyanin biosynthesis, a key ROS scavenger during environmental stress. Meanwhile, ECAP also participates in early anther development by forming the ECAP-LUG-BEH3 complex with the transcriptional repressor LUG and the transcription factor BEH3, regulating the expression of *SPL* to ensure proper archesporial cell division and microsporocyte formation. In this study, we further demonstrate that ECAP recruits the Polycomb Repressive Complex 2 (PRC2) to facilitate H3K27 trimethylation deposition and spreading at the flowering repressor *FLC* locus, thereby epigenetically regulating flowering time. Interestingly, ECAP directly promotes the interaction between ABA receptors PYR1/PYLs and coreceptors PP2Cs, inhibiting PP2C phosphatase activity to positively regulate ABA signaling-mediated suppression of seed germination. These findings reveal ECAP as a crucial signaling hub that precisely coordinates plant growth/development and stress responses through distinct interactions with core regulators in developmental processes and plant hormone signaling pathways.

Key Words: Transcriptional regulation, ECAP, flowering, ABA signaling

Specific microtubule-associated proteins facilitate autophagosome formation in plants

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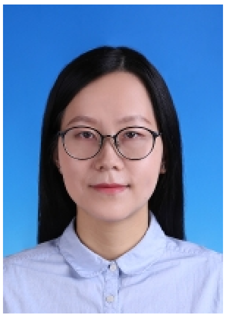

Abstract

Autophagy is a highly conserved degradation pathway in eukaryotes, essential for maintaining intracellular homeostasis. Upon induction, a double-membrane organelle known as the autophagosome is formed to deliver bulky cytoplasmic materials or specific cargoes to the lysosomes/vacuoles for degradation. In plants, autophagy has been reported to play crucial roles in development and in responses to various stresses. However, the precise regulatory mechanisms underlying autophagosome formation remain to be fully elucidated. In this study, we found that specific microtubule-associated proteins participate in the regulation of autophagosome formation through distinct molecular mechanisms. Under autophagy-inducing conditions, the microtubule-associated protein SPR1 re-localizes to the endoplasmic reticulum and interacts with core components of the PI3K complex to positively regulate autophagy. In contrast, the microtubule-severing protein KTN1 interacts with key components of the ubiquitin-like conjugation system and facilitates their dissociation from the autophagosomal membrane, contributing to the regulation of autophagosome closure. These results provide valuable insights into the regulatory mechanisms of autophagosome formation in plant cells.

Key Words: Autophagosome, microtubule-associated protein, SPR1, KTN1

The importance of barriers in a functional relationship

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Abstract

The Casparian strip (CS) is one of the best-known models for root filtering and uptake. However, most of this comes from the model *Arabidopsis thaliana,* and we lack deeper insights into the CS in other species, especially the nodule-forming, nitrogen-fixing legumes, where the initiation of these specialized bacteria-hosting organs occurs in the CS-containing root zone. With basis on this, we focused on the symbiosis model *Lotus japonicus* and identified mutants without CS. Combined, our findings reveal a surprising role for the CS in root-shoot communication of N-status, which is essential for correct nodule establishment. Moreover, in these mutants, the forming nodules are devoid of vascular-associated CS, which creates an intriguing model to study the role of the CS in controlling metabolic exchange between the plant host and the associated bacteria. Through correlative meta-transcript and metabolomic imaging, we were able to study how the homeostasis of nodule-residing bacteriods is affected when the to-and-from flow of photo assimilates, nutrients, and fixed-N is unrestricted. In this talk, I will emphasize how our work establishes a novel toolbox for the study of symbiotic relationships and emphasizes the importance of barriers in spatially restricted plant-microbe associations. Moreover, I will highlight how the so-called endodermal passage cells can be studied in this model, and how they may shed light on overlooked root functions.

Key words: Casparian strip, nitrogen signaling, nodulation, root physiology

The roles of chromatin-remodeling complex HOS15-PWR-HDA9 in plant development and stress responses

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Abstract

Being sessile by nature, plants rely on highly evolved signaling pathways to perceive, integrate, and respond to a wide range of environmental cues. These external stimuli often lead to dynamic epigenetic modifications that are essential for proper plant development as well as for mounting effective responses to biotic and abiotic stresses. Among various epigenetic mechanisms, histone acetylation and methylation play pivotal roles in chromatin remodeling, which in turn governs transcriptional reprogramming by modulating access to DNA. These modifications enable both activation and repression of gene expression in a spatially and temporally regulated manner, often in a tissue-specific context. Recent research has identified multiple classes of chromatin remodelers in plants, with growing attention to their roles in fine-tuning gene expression. One such well-characterized chromatin remodeling complex is the HOS15-PWR-HDA9 multiprotein complex. This complex has been shown to regulate the acetylation status of histone H3 at specific genomic loci, thereby modulating chromatin structure to either promote or suppress the transcription of target genes. Through this regulatory mechanism, the HOS15-PWR-HDA9 complex plays a crucial role in coordinating plant developmental processes and adapting to various environmental challenges. In this report, we explore the biological significance of the HOS15-PWR-HDA9 complex, highlighting its function as an essential epigenetic regulator that integrates developmental signals and environmental stimuli through chromatin remodeling.

Key Words: Chromatin remodeling, plant development, stress response, transcriptional regulation, HDA9/HOS15/PWR

BZR1-regulated stomatal development and anthocyanin biosynthesis in *Arabidopsis*

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Abstract

We show the dual regulatory roles of brassinosteroid (BR) in two distinct biological processes in *Arabidopsis*: stomatal development and anthocyanin biosynthesis. We demonstrate that BR signaling differently regulates stomatal development in the hypocotyls in a concentration-dependent manner. At low to moderate levels, brassinolide (BL) promotes stomatal formation by upregulating SPCH and its downstream targets independently of BIN2. In contrast, both high BL concentrations and BIN2 inhibition by bikinin significantly suppress stomatal development. Genetic analyses reveal that BIN2-mediated inactivation of BZR1 promotes stomatal formation in hypocotyls by repression of SPCH expression. These findings highlight that BR orchestrates stomatal development via both BZR1-dependent and BZR1-independent pathways. In parallel, we explored the role of BR in anthocyanin biosynthesis that is tightly controlled by diverse environmental cues. Anthocyanin production in *Arabidopsis* is regulated by the MBW protein complex composed of PAP1, TT8, and WD40 protein. Here, we show BR promotes anthocyanin production through activation of the MBW complex. BZR1 not only enhances the expression of PAP1 but also physically interacts with PAP1 to cooperatively regulate the expression of PAP1-target genes, such as TT8, DFR, and LDOX. Our findings indicate that BZR1 functions as an integral component of the PAP1-containing transcription complex, contributing to the promotion of anthocyanin biosynthesis.

Key Words: Brassinosteroid, stomatal cell, anthocyanin

SNC1 guards topless family members that encode susceptibility genes for Fusarium wilt in tomato and *Arabidopsis*

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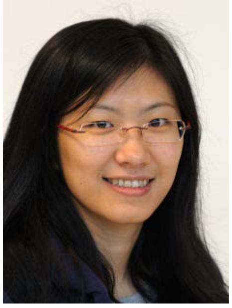
Abstract

Fusarium oxysporum causes Fusarium wilt disease many agricultural important crops. The fungus manipulates its hosts using SIX effectors. We reported that the broadly conserved effector SIX8 targets specific members of the Topless (TPL) family (Aalders *et al*., 2024 *PBJ*; 22, 248). TPLs are transcriptional co-repressors and SIX8-targeted TPL proteins are important for susceptibility to the fungus. Tomato *tpl1/tpl2* mutants and *Arabidopsis thaliana tpr1*/*tpl* double mutants show near complete resistance to Fusarium wilt. Hence, *TPLs* are genuine *S* genes whose inactivation can confer *F. oxysporum* resistance. To study SIX8 function, the effector was expressed in *Arabidopsis* Col-0. The *SIX8* transformants exhibited a temperature-dependent growth phenotype, constitutive *PR1* and *PR2* expression, and local cell death, all indicative for constitutive immune signalling. TPR1 interacts with SNC1, a temperature sensitive NLR-type immune receptor (Zhu *et al.*, 2010 *PNAS*; 107, 13960-13965). To test involvement of *TPL*, *TPR1* and of *SNC1* and SNC1-signalling components (i.e. *eds1*, *pad4*, and NahG) *Arabidopsis* mutants were transformed with *SIX8*. Knockout mutants in *TPL*, *TPR1*, *SNC1* and *EDS1* fully revert the *SIX8* phenotype, while the phenotype was partially reverted in *NahG* plants. These data indicate that SNC1 guards TPL and TPR1 and monitors their perturbation by SIX8, implying that TPLs act upstream of SNC1. Evolution of a guard to monitor Topless proteins provides additional support for an essential role of these proteins in disease resistance and susceptibility. A possible mechanism of how Six8 triggers SNC1-mediated immune signalling and manipulates TPLs will be presented, providing new leads to reduce susceptibility to *F. oxysporum*.

Keywords: Fusarium, NLR immune receptor, immunity, effector protein,
TNL receptor, EDS1

Leucine-rich repeat receptor proteins-mediated pattern-triggered immunity in *Arabidopsis*

Lisha Zhang*



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Abstract

Pattern-triggered immunity (PTI) is plants is a key defense mechanism initiated by the recognition of pathogen-associated molecular patterns (PAMPs) by cell-surface receptors, such as leucine-rich repeat receptor proteins (LRR-RPs). Lipase-like proteins EDS1 and PAD4, along with ADR1 family helper NLRs, are important molecular components of NLR signaling. The small molecule (SM) phosphoribosyl (pRib)-adenosine monophosphate/diphosphate (pRib-AMP/ADP), products of TIR domain NADase activity, serve as second messengers that bind to EDS1-PAD4 dimers, leading to the recruitment of ADR1 and the activation of effector-triggered immunity (ETI). EDS1 and PAD4 are also crucial for PTI activation mediated through LRR-RPs. Here, we show that BAK1 recruitment to LRR-PR complexes is unaffected by the loss of EDS1 or PAD4, but abolished in the sobir1 mutant, highlighting the essential role of SOBIR1 in surface immune receptor complex formation. SM binding to EDS1 and PAD4 is critical for LRR-PR-mediated PTI, as mutations that impair SM binding (EDS1^{R493A} and PAD4^{R314A}) fail to restore PTI responses. We further establish that de novo SM synthesis is required for late PTI responses, including *PR1* gene expression and resistance to *Pseudomonas syringae*, but not for early EDS1-PAD4-required responses, such as ROS production and MAPK activation. The TIR domain containing NLR (TNL) SADR1 is required for late but not early PTI responses, suggesting distinct roles of TIR domain proteins in PTI signaling.

Key Words: LRR-RP receptor, pattern-triggered immunity, EDS1-PAD4,
small molecule, TIR domain protein

The roles and regulatory mechanisms of *Argonautes* in response to biotic and abiotic stressors

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Abstract

RNAs guided RNA silencing or interference (RNAi) play important roles in regulating gene expression and defense against viruses and transposons. Argonaute (AGO) proteins, as core components of RNA interference (RNAi), form RNA-induced silencing complexes (RISCs) through association with small RNAs, including small interfering RNAs (siRNAs) and microRNAs (miRNAs). In our previous studies, we demonstrated that AGO18, a monocot-specific AGO, is upregulated upon viral infection and mediates antiviral immune responses in rice by sequestering specific miRNAs such as miR168 and miR528. Further investigation revealed that the viral infection-induced expression of AGO18 is dependent on JAMYB, a jasmonic acid (JA)-responsive transcription factor. Recently, we identified the RBRL, an RBR-type E3 ubiquitin ligase, perceives viral infection and activates JA signaling to initiate antiviral defense. On the other hand, we found that abiotic stresses like drought also induce the expression of most *AGOs* in maize. Knockout of *ZmAGO4a* enhances the sensitivity of maize plants to drought. Additionally, we characterized the ZmDT10, a key drought-related protein that binds to the promoter region of *ZmAGO4a* and represses its expression. Therefore, the ZmDT10-ZmAGO4a module may play a dual role in maize responses to both biotic and abiotic stresses.

Key Words: Antiviral immunity, RNA silencing, Drought, Epigenetic modifications