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SYMPOSIUM ABSTRACT BOOK

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Plenary Speakers

A Unified Mechanism of NLR-mediated Immune Signaling in Plants

Ji-jie Chai
Westlake University, Hangzhou, China

Plant nucleotide-binding, leucine-rich repeat (NLR) receptors are central components of immunity, recognizing specific pathogen effectors to trigger defense responses. These immune receptors consist of two primary classes: coiled-coil NLRs (CNLs) and toll-interleukin 1 receptor NLRs (TNLs). Recent discoveries reveal that upon pathogen detection, both NLR types assemble into higher-order oligomeric complexes called resistosomes, though with distinct biochemical functions. CNL resistosomes directly form evolutionarily conserved calcium-permeable channels essential for immune signaling. In contrast, TNL resistosomes function as NADase holoenzymes, producing nucleotide-derived small molecules that act as second messengers. These messengers activate the CNL-type helper NLRs, which subsequently form their own calcium-channel resistosomes. Despite their different activation mechanisms, both CNL and TNL pathways ultimately converge on calcium signaling as the common currency of plant immunity. This mechanistic understanding bridges pathogen recognition to downstream immune responses and offers promising targets for engineering enhanced disease resistance in crops. In this presentation, I will provide evidence for this unified model of NLR resistosome assembly and calcium signaling in plant immunity.

Temperature and Movement Regulate Plant Condensates

Lucia Strader
Salk Institute for Biological Studies, USA

Multiple factors drive biomolecular condensate formation. In plants, condensation of the transcription factors AUXIN RESPONSE FACTOR7 and 19 (ARF7 and 19) attenuates response to the plant hormone auxin. Here, we report that actin-mediated movement of cytoplasmic ARF condensates enhances condensation. Coarse-grained molecular simulations of active polymers reveal that applied forces drive the associations of macromolecules to enhance phase separation while giving rise to dense phases that preferentially accumulate motile molecules. Our study highlights how molecular motility can drive phase separation, with implications for motile condensates while offering insights into cellular mechanisms that can regulate condensate dynamics.

Keynote Speakers

Life at the Interface: How Membrane Nanodomains Protect Plant Cells from Stress

José R. Dinneny
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Howard Hughes Medical Institute, Stanford University, Stanford, USA

The interface between the plant cell wall and plasma membrane is a critical site for sensing and responding to environmental stress, yet the molecular basis of their attachment has remained unclear. We identify two nanodomain-dependent mechanisms that govern wall–membrane adhesion: one mediated by the Cellulose Synthase Complex (CSC), whose membrane density correlates with resistance to hyperosmotic shock, and a second mediated by REMORIN proteins, which act in opposition to CSC function. Proximity-labeling proteomics further reveals SHOU4/4L as REM-associated factors that enable this antagonism. These findings demonstrate how membrane nanodomains organize wall–membrane attachments to enhance plant cell resilience under water stress.

5' Capping of RNA by Cellular Metabolites

Xuemei Chen
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In eukaryotes, messenger RNAs (mRNAs) harbor a 5’ methylguanosine (m7G) cap, which stabilizes mRNAs and assists with their processing, nuclear export and translation. In recent years, it has come to be realized that cellular metabolites, such as NAD+, dpCoA, FAD, UDP-glucose and UDP-GlcNAc, etc., can serve as noncanonical RNA caps in prokaryotes and eukaryotes. These metabolites are thought to be incorporated into RNA as the initiating nucleotide during transcription. The caps can also be removed by decapping enzymes, some acting on many noncanonical caps while others are highly specific. To begin to understand the molecular and biological functions of the noncanonical caps, we are developing various technologies to detect and quantify these noncanonical RNA caps and methods to profile RNAs with these metabolite caps, and identify decapping enzymes that specifically target one type of RNA cap. I will mainly discuss progress made towards characterizing RNAs with the dpCoA cap and hope to initiate collaborations with colleagues to explore the functions of dpCoA-RNA in various biological contexts.

New Roles for Second Messengers in Plant Signalling

Jiří Friml
Institute of Science and Technology Austria (ISTA), Klosterneuburg, Austria

The plant hormone auxin is a versatile endogenous signal influencing virtually all aspects of plant life. Nuclear, transcriptional auxin signalling involves the TIR1/AFB auxin receptors, Aux/IAA transcriptional repressors, and ARF transcription factors. TIR1/AFBs are part of the ubiquitin ligase complex, mediating the ubiquitination and degradation of Aux/IAAs and thereby releasing ARFs from their inhibition. The unexpected identification of adenylate cyclase enzymatic activity in TIR1/AFB receptors (Qi et al., 2022) and the crucial importance of its product, cAMP, for the downstream regulation of transcription (Chen et al., 2025) revise this canonical model, which has withstood the test of time for 20 years. The major open questions relate to the target and roles of the cAMP within auxin signalling mechanism and whether similar cAMP roles can be found in context of other signalling mechanisms. I will present novel insights into these questions and provide other mechanistic updates on cAMP-mediated signalling and show how these insights may serve as a blueprint for gaining a new understanding of other signalling pathways in plants.

Deciphering the Role of a Transcriptional Machinery Condensate in Temperature-dependent Plant Immunity

Sheng-Yang He
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Howards Hughes Medical Institute, USA

As climate change accelerates and extreme weather events become more frequent, plants are increasingly vulnerable to infectious diseases. Salicylic acid (SA), a key phytohormone in plant immunity, is notably suppressed at elevated temperatures, weakening plant defense responses. To understand how high temperatures influence SA-related gene regulation, we focus on CBP60g, a key transcription factor involved in temperature-dependent immune responses, in Arabidopsis thaliana. Previous research showed that GBPL3 defense-activated biomolecular condensates (GDACs) facilitate transcriptional condensate formation at the CBP60g genomic locus. We hypothesize that GDACs are part of temperature-sensitive regulatory hubs, recruiting specific genes and regulatory elements to modulate the transcription of immune-related genes such as CBP60g. To test the hypothesis, we employed CBP60g promoter-specific proximity labeling, GDAC proximity labeling, and chromatin capture sequencing. These approaches allowed us to identify potential transcriptional regulators of CBP60g, characterize temperature-dependent compositional changes in GDAC formation, and uncover alterations in chromatin architecture under heat stress. Our findings provide new insights into the transcriptional regulation of SA-mediated immunity under combined thermal and immune stress, shedding light on how biomolecular condensates might shape plant immune responses under changing climate conditions.

How RNA Can Encode Physical Information for Biomolecular Condensates

Amy Gladfelter
Cell Biology, Duke University, 308 Research Drive, Durham, USA

Biomolecular condensates are vessels to spatially and temporally control biochemistry in cells for a variety of processes. Despite their ubiquitous roles in the entire lifecycle of RNA, how RNA impacts the composition, properties and functions of condensates remains poorly understood. The chemical properties and sequence of RNAs are generally considered in light of housing or regulating the genetic code. However, most amino acids are encoded by multiple codons, making the genetic code degenerate. Synonymous mutations in RNA sequences affect protein translation and folding, but their impact on RNA itself is often neglected. We developed a genetic algorithm that introduces synonymous mutations to control the conformational heterogeneity of structures sampled by an mRNA. The behavior of the designed mRNAs reveals physical information layered in the genetic code. We find that mRNA conformational heterogeneity impacts the physical properties and functional outputs of RNA-protein complexes and biomolecular condensates. The role of structure and disorder of proteins in biomolecular condensates is well appreciated, but we find that RNA conformational heterogeneity is a major contributor to condensate properties. This feature of RNA enables both evolution and engineers to build cellular structures with specific material and responsive properties.

Dynamic Ca2+ Signals Drive Autophagosome Formation

Hong Zhang
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Autophagy, an evolutionarily conserved lysosomal degradation pathway, sustains cellular homeostasis by recycling cytoplasmic material and eliminating cytotoxic threats. The core of this process is the biogenesis of the autophagosome, a double-membraned vesicle that forms through the initiation, expansion, and closure of an isolation membrane. In metazoans, autophagosomes assemble on the endoplasmic reticulum (ER). Pioneering genetic studies in model organisms identified a core autophagy machinery (ATG and EPG genes), and subsequent work revealed that the FIP200 complex—the functional equivalent of the yeast Atg1 complex—translocates to the ER to recruit downstream factors upon autophagy induction. Despite these advances, the fundamental mechanism that initiates the formation of the autophagosome on the ER membrane has remained a central unanswered question in the field. Our previous research revealed that diverse autophagy stimuli trigger localized Ca2+ transients on the outer ER membrane, a process regulated by the metazoan-specific autophagy protein EPG4/EI24. We discovered that these ER-localized Ca^{2+} signals trigger the liquid-liquid phase separation of the FIP200 complex. This generates liquid-like condensates on the ER, which then mature into functional autophagosome formation sites. In my talk, I will present our recent progress in understanding how these ER Ca^{2+} transients are sustained during autophagy induction and how they are decoded to trigger the assembly of ER-associated FIP200 condensates.

Mixing Water, Transducing Energy, Shaping Membranes: Osmotically Induced Molecular Organization

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School of Materials Science & Engineering, Singapore Centre for Environmental Life Sciences & Engineering, and Institute for the Digital Molecular Analytics & Science, Nanyang Technological University, Singapore

The physical properties of membranes are now largely well-understood at thermodynamic equilibrium. But generic descriptions of far-from-equilibrium behaviors of membranes – which allow living cells to sense, respond, and adapt to environmental perturbations while displaying extraordinary stability – are conspicuously lacking. Here, non-equilibrium activities of membrane-proteins, underlying cytoskeleton, and osmotic activities of water bathing the membrane, all couple with membrane's physical, chemical, and mechanical degrees of freedom producing long-lived out-of-equilibrium structures with emergent reconfigurable morphologies and cooperative behaviors. Drawing from recent experiments in our labs employing giant vesicles, this talk considers how the osmotic activity of water is transduced across cell-like compartments. It highlights how water activity and accompanying dissipation of osmotic energy can (1) induce intravesicular liquid-liquid phase separation; (2) couple with the compartmental boundary, mechanically remodeling the membrane shape and redistributing membrane domains; and (3) facilitate solute uptake through mechanical folding and scission reminiscent of endocytosis.

Invited Speakers

Decoding RNA Language in Plants

Yiliang Ding
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RNA structure plays an important role in the post-transcriptional regulations of gene expression. Using in vivo RNA structure profiling methods, we have determined the functional roles of RNA structure in diverse biological processes such as mRNA processing (splicing and polyadenylation), translation and RNA degradation in plants. We also developed a new method to reveal the existence of tertiary RNA G-quadruplex structures in eukaryotes and uncovered that RNA G-quadruplex structure serves as a molecular marker to facilitate plant adaptation to the cold during evolution. Additionally, we have developed the single-molecule RNA structure profiling method and revealed the functional importance of RNA structure in long noncoding RNAs. Recently, we established a powerful RNA foundation model, PlantRNA-FM, that facilitates the explorations of functional RNA structure motifs across transcriptomes.

Phase Separation of RNA-binding Proteins in Plant Development and Stress Responses

Lisha Shen
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Department of Biological Sciences, National University of Singapore, Singapore

RNA-binding proteins (RBPs) accompany RNA from synthesis to decay, mediating every aspect of RNA metabolism and impacting diverse cellular and developmental processes in eukaryotes. Many RBPs undergo phase separation along with their bound RNA to form and function in dynamic membraneless biomolecular condensates for spatiotemporal coordination or regulation of RNA metabolism. Increasing evidence suggests that phase-separating RBPs with RNA-binding domains and intrinsically disordered regions play important roles in plant development and stress adaptation. Here, we discuss how phase separation of RBPs contributes to plant development and stress responses, using hnRNP R-LIKE PROTEIN (HRLP) and the N6-methyladenosine (m6A) reader EVOLUTIONARILY CONSERVED C-TERMINAL REGION 8 (ECT8) as examples. HRLP, together with the splicing factor ARGININE/SERINE-RICH 45 (SR45), forms phase-separated nuclear condensates, which are essential for HRLP function in regulating FLOWERING LOCUS C (FLC) splicing during flowering time control. Moreover, phase separation of ECT8 preferentially sequesters a subset of m6A-modified mRNAs, including that of the ABA receptor PYRABACTIN RESISTANCE 1-LIKE 7 (PYL7), into stress granules for temporary storage, thereby ensuring a normal response to abscisic acid.

Unravelling the Cellular Biochemistry of the Pyrenoid in a Marine Diatom

Oliver Mueller-Cajar
School of Biological Sciences, Nanyang Technological University, Singapore

The slow and non-specific kinetics of the photosynthetic CO2-fixing enzyme Rubisco are compensated by CO2-concentrating mechanisms in the majority of unicellular algae. This strategy involves compartmentalization of all cellular Rubisco in a phase-separated compartment of the chloroplast, the pyrenoid. In our studies of the Phaeodactylum tricornutum pyrenoid we have recently described the Rubisco linker protein PYCO1, which contains both Rubisco large and small subunit binding motifs. We have identified seven additional proteins harbouring either Rubisco binding motif and find all localize to the pyrenoid. Combinatorial expression of fluorescently tagged versions of four proteins localizing to the pyrenoid shell revealed specific banding patterns. We also identified four additional putative Rubisco linker proteins that possess highly divergent mobility in vivo. Systematic affinity purification-mass spectrometry analyses using these fluorescent baits suggest functional specialization, such as strategic positioning of Calvin cycle enzymes at the pyrenoid tips. Bottom-up biochemical reconstitution is ongoing in an attempt to recapitulate the in vivo observations and generate in vitro assays to dissect the relevant molecular mechanisms. As a consequence of their size, their biochemical diversity and tractability pyrenoids are well positioned to serve as models for functional phase separation in biology.

Membrane-anchored Condensates Use Molecular Gradients to Sort RNAs and Amplify Cellular Responses

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While membrane-bound organelles like mitochondria and plastids are well-established, a new paradigm has emerged: biomolecular condensates. These "membrane-less" assemblies, formed through phase separation, concentrate molecules and control reactions in time and space. My lab is exploring a distinct class of "membrane-rich" condensates (Dobranszki et al., 2025; Hatzianestis et al., 2023; Mountourakis et al., 2023; Solis-Miranda et al., 2023). These structures directly interact with or engulf membranes, fundamentally altering their properties and functions (Liu et al., 2024a; Liu et al., 2024b). I will present our findings demonstrating how membrane-rich condensate interactions mediate trans-organellar communication and how these local events translate into broader organismal responses, including unique adaptive strategies (Di Fino et al., 2025; Liu et al., 2023a; Liu et al., 2023b). Furthermore, I will introduce a novel molecular code, dependent on the physical properties of both condensates and membranes, that governs protein-nucleic acid interactions (Guarino et al., 2022). Beyond fundamental insights, our research holds potential for applications, informing also our understanding of life's origins.

Fast and Furious: Plant Hypersensitive Cell Death in Action!

Chih-Hang Wu
Institute of Plant and Microbial Biology, Academia Sinica, Taiwan

Plant nucleotide-binding domain leucine-rich repeat (NLR) proteins function as immune receptors that recognize pathogens and confer resistance. Upon activation, many NLRs assemble into membrane-associated resistosomes that trigger immune signaling and lead to hypersensitive cell death. However, the sequential subcellular events that connect resistosome activation to cell death remain unclear. In this study, we explored the spatiotemporal dynamics of organelles upon activation of NLR required for cell death 4 (NRC4) resistosome. Using a copper-inducible system, we performed time-lapse imaging upon triggering NRC4-mediated hypersensitive cell death. By employing various subcellular markers, we observed that cytoplasmic streaming and organelle movement were disrupted upon visible resistosome puncta appeared. Coinciding with the emergence of resistosome puncta, both actin and microtubules were depolymerized. This was followed by a loss of plasma membrane (PM) integrity, fragmentation of the endoplasmic reticulum into vesicle-like structures, and nuclear envelope breakdown. Eventually, the cells collapsed, with the PM and tonoplast shrinking toward the cell center. These findings define the temporal order of subcellular changes during plant hypersensitive cell death and lay the foundation for future research on the molecular mechanisms underlying subcellular processes following immune activation.

Zinc as a Novel Second Messenger Mediates Control of Nitrogen Fixation via Transcription Factor Filamentation and Condensation

Jieshun Lin
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Nitrogen fixation in legume nodules is tightly regulated to adapt to changing environmental conditions. However, the mechanisms by which nodules perceive and respond to environmental signals remain largely unknown. Here, using nitrate as an example, we investigate how nodules sense external cues. We demonstrate that zinc, an essential plant micronutrient, acts as an intracellular second messenger that connects environmental changes to the regulation of nitrogen fixation in root nodules. We identify a transcriptional factor, FIXATION UNDER NITRATE (FUN), which acts as a novel zinc sensor. Under zinc-replete nodules when soil nitrate level is low, FUN assembles into filaments and condensates that maintain it in an inactive state. When soil nitrate increases, nodule zinc levels decline, triggering FUN to dissociate from filaments/condensates and become transcriptionally active. FUN then directly targets multiple pathways to initiate breakdown of the nodule. This zinc-dependent filamentation and condensate mechanism provides a quantitative readout of environmental nitrogen availability, enabling nodules to adjust their function accordingly. More broadly, these findings offer insights into the role of metal ions in integrating environmental signals with plant developmental processes and have potential implications for improving nitrogen delivery efficiency in legume crops.

Chloroplast Tethering at the Pathogen Interface Underpins Plant Focal Immunity

Tolga O Bozkurt
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Pathogens remodel host cell architecture to secure nutrients and evade defence, yet how plants spatially organise immunity at the exact site of attack remains unclear. I will present evidence for a defence-related membrane contact site (MCS) that tethers chloroplasts to the extrahaustorial membrane (EHM) during infection by the oomycete pathogen Phytophthora infestans. Our work have revealed how a dedicated tethering complex assembles into puncta precisely at chloroplast–EHM contacts, positioning chloroplast-derived defences where they are needed most. Disrupting this tether abolishes plant focal immunity: chloroplast–EHM attachment fails, callose deposition around haustoria declines, and susceptibility to Phytophthora infestans increases—despite intact broader immune signalling. These findings reframe chloroplasts as mobilised front-line defenders actively anchored to pathogen interfaces, with MCSs serving as positional hubs for immune output.

Membrane-based Regulation and Evolution of Cell Surface Signaling

Julien Gronnier
TUM School of Life Sciences, Technical University of Munich, Germany

The plasma membrane is a dynamic molecular patchwork composed of billions of individual molecules and serves as a central hub integrating endogenous and environmental signals. We question how, in space and time, signaling events are regulated within the plasma membrane during plant development and immunity. Comparative phylogenomic analyses identify structural components of the plasma membrane as key evolutionary innovations of the green lineage. We demonstrate they function as inhibitors of the plasma membrane H+-ATPases thereby promoting apoplastic alkalinization, modulating receptor kinases signaling, and pacing Arabidopsis root developmental transitions —a function we found conserved in the liverwort Marchantia polymorpha and which such predate the emergence of the root system itself. Leveraging a minimal cell surface receptor network, we uncovered a nanoscale spatial and temporal logic underlying ligand-induced receptor complex formation and identified key operational principles. We identified a structural determinant that defines receptors diffusion within the plasma membrane and conditions their activity. Our studies highlight the roles of the plasma membrane in the regulation and evolution of cell surface signaling.

Unlocking Cell Type Specific-Phase Separation via Arabidopsis Crowding Atlas

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While biophysical signatures offer the fundamental molecular grammar for molecular condensation, cellular physiological factors govern the reactive window for effective combinations of associative signatures. It is critical to understand cell-type-specific phase separation within each cell type's environment, enabling differential yet continuous phase-separation-based reactions across tissues and thereby regulating plant development and responses to biotic and abiotic stresses differently. Here, we present the first comprehensive atlas of living Arabidopsis viscoelasticity at single-cell resolution. Through quantitative in vitro and in vivo calibration of crowding, effective viscosity, protein homeostasis, cytoskeleton organization, and condensate dimensionality within individual living cells, our comprehensive viscoelastic atlas reveals the basal effectiveness range of the regulatory framework in modulating phase separation in a cell-type-differentiated manner. Under environmental stress conditions, it demonstrates how each parameter shifts into or away from effective ranges to control plant phase separation behaviors and function. Our living plant atlas establishes a reference-based approach to studying spatially and temporally regulated phase separation, enabling insights into differential degrees of condensation across cell types under varying or evolving biotic and abiotic stress conditions.

Understanding Plant-environment Interactions via Biomolecular Condensation

Xiaofeng Fang
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Abstract: Plants, unable to move on their own, have evolved more rapid and complex mechanisms to perceive and respond to environmental changes. The condensation or decondensation of biomacromolecules within cells exhibits sensitivity to the surrounding physicochemical environment. In my talk, I will explore the possibility of biomolecular condensation as a mechanism for plants to sense and respond to abiotic stress. My laboratory has developed methods and techniques to discover stress-responsive condensates and dissect their function in stress adaptation. Our recent work has showcased that biomolecular condensation can be both sensors and executors of hyperosmotic stress and heat stress. Biomolecular condensation is expected to become a new direction in the study of plant-environment interactions.

Stress Granules: From Signaling to Tolerance

Monika Chodasiewicz
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Plants are sessile organisms that had to develop molecular mechanisms to deal with changes in their environment. One of such mechanism is formation of stress-induced condensates called Stress Granules (SGs). SGs are liquid-liquid phase separation (LLPS) biomolecular condensates composed of proteins, mRNA and metabolites. The main function of the SGs is protective sequestration of their components. When analyzed the composition of SGs in plants we realized high similarity to SGs described in mammalian and yeast cells suggesting that there is conservation of SGs across different species. Therefore, research on SGs in plants might be beneficial for understanding the response of whole organism into stressful conditions. With the use of cell biology, biochemistry, molecular biology and omic approaches, our group is interested to uncover the mechanism of SGs formation/disassembly but also the true role of SGs in stress signaling and tolerance. Recent research in our lab shows that by manipulation of key SG proteins or their biophysical properties we can affect the overall SG dynamics leading to improved stress tolerance. During my talk, I will focus on few projects to highlight this interesting direction of research.

Decoding Stress Granules Through the Lens of RNA Structure

Anthony Khong
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Department of Physiology, National University of Singapore

Efficient adaptation to environmental stress is essential for cellular survival, and stress granules (SGs)—cytosolic mRNP condensates formed upon acute translational repression—play a central role in this process. While SG assembly has long been attributed to multivalent interactions mediated by proteins such as G3BP1/2 and RNA-driven phase separation, the mechanistic contribution of RNA structure and RNA–RNA interactions has remained unresolved. To address this gap, we performed the first comprehensive cell-wide and granule-resolved analysis of the RNA structurome under sodium arsenite stress. Our data reveal a striking divergence in RNA structural behaviour: although global RNA structure becomes more double-stranded during stress, SG-enriched RNAs remain predominantly single-stranded. Both intra- and intermolecular RNA–RNA interactions are markedly reduced within SG-localized transcripts, indicating active unwinding rather than aggregation. We identify specific RNA-binding proteins, including DDX3X, that recruit and remodel RNAs within SGs, and show that DDX3X activity is required for timely SG dissolution during recovery. Together, these findings uncover an unanticipated principle of SG biology: stress granules selectively maintain single-stranded RNA environments through RBP-mediated remodeling, enabling reversible condensation and controlled gene regulation. Our work provides a structural framework for understanding how SGs assemble, function, and disassemble—and how their dysregulation may contribute to disease.

Short Talk Speakers

* denotes presenting speaker

Stress Granules as Regulatory Hubs for MAPK Signaling During Plant Stress Response

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Stress Granules (SGs) are a type of biomolecular condensates formed through liquid-liquid phase separation (LLPS) and composed of RNAs and proteins that arise in the cytoplasm in response to both environmental and internal signals. The formation of SGs minimizes stress-related damage and promotes cell survival, although the molecular mechanisms underlying pro-survival effects of SGs remain to be established 2. The last past few years, SGs are emerging as an important concept in signalling. In fact, our recent results suggest that SGs might act as a key signalling hub in the plant stress response. In this line, we have recently found that in the model plant Arabidopsis thaliana, Tudor staphylococcal nuclease (TSN) is an intrinsically disordered protein acting as a scaffold for a large pool of signalling proteins, including a well-conserved mitogen-activated protein kinase (MAPKs) module constituted by MEKK1-MKK2-MPK4 proteins (hereafter the MEK4 module). In this way, we found that sequestration of the MEK4 module into stress granules, which was specifically induced under high growth temperatures, promoted its inhibition. The MEK4 module is known to be activated by flagellin, a plant pathogen-associated molecular pattern (PAMP), promoting a specific gene response. How high temperature and plant immune signalling are linked remains unclear. In this scenario, we found that condensation of heat-induced MEK4 into SGs promoted the suppression of the PTIinduced response in plants. Our recent findings indicate that SGs may serve as platform for integrating phosphoregulatory signalling events to control specific biological processes.

Duet Between Stress Granule and Glutathionylation Establishes Cytosolic Heterogeneity of Redox Potential to Maintain Proteostasis in Plants

Wei Wang
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Buried under the soil, the emerging seedlings suffer from severe energy deprivation prior to emergence. How plant cells economize energy to ensure successful emergence remains poorly understood. Here, we identify dark-induced stress granules (DISGs) as cytoplasmic hubs of energy conservation that implement a genome-encoded, Pareto-efficient strategy. DISG formation is both light- and energy-sensitive. Integrated proteomic and transcriptomic analyses reveal that DISGs coordinate energy conservation across multiple layers during etiolation, spanning mRNA splicing, ribosome biogenesis, and translation. Notably, we find that a small subset of genes (~0.5%) disproportionately accounts for the majority of energy expenditure upon light exposure, manifesting a Pareto-like distribution of energy investment. These energy-intensive genes are selectively localized and repressed in DISGs in dark. Collectively, our findings uncover a multi-level energy conservation role of stress granule during seedling etiolation, and reveal an intrinsic, Pareto-efficient cytoplasmic energy-saving mechanism orchestrated by DISGs.

Full-length FUS Protein Condensates Exhibit Domain-Specific Architecture

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The formation mechanisms of biomolecular condensates have recently become a pivotal research focus due to their critical roles in physiological functions and neurodegenerative diseases and cancer pathogenesis. In this work we took the paradigmatic protein FUS as an example and decoded how single-protein sequences dictate condensate architecture and the relationship between condensate architecture and condensate functionality, using coarse-grained molecular dynamic simulation method on our self-developed software IPAMD. Specially, we found that the low-complexity domain (LCD) — key driver of condensate formation — tends to be localized in the inner core of the condensate while the RNA recognition motif (RRM) is preferentially localized to the outer shell, a spatial arrangement that optimizes RNA-recognition accessibility and facilitates direct engagement with RNA recognition. We therefore propose a sequence-structure-function paradigm within the context of biomolecular condensates: through the cooperation emerging from multiple stickers, individual domains function as integrated units in shaping the structure and functionality of biomolecular condensates, which may also represent a paradigm of protein-protein interaction (PPI) in biomolecular condensate research. Our findings may unravel the evolutionary significance of protein sequence in shaping liquid-liquid phase separation (LLPS) behavior.

The Snap Hypothesis: Cooperative Transitions in Centriole Assembly

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How do cells build precise nanostructures in the face of tight temporal constraints? The centriole, a microtubule-organizing organelle defined by 9-fold symmetry, assembles during the ~10-minute embryonic divisions of Drosophila. Construction requires the ordered incorporation of several hundred Sas-6 molecules into stacked cartwheel rings, yet how such accuracy and speed are achieved has remained unclear. By developing a quantitative in vivo assay to track centriole biogenesis in real time, I found that assembly occurs significantly faster than expected. These kinetics point to a highly cooperative, switch-like mechanism, which I propose as the “Snap hypothesis” of centriole assembly. This work highlights the centriole as a tractable model for studying self-organization, cooperative transitions, and robustness in organelle biogenesis, providing a conceptual bridge between molecular mechanisms and systems-level principles of cellular architecture.

Synthetic Non-canonical Resistosome Confer Multipathogen Resistance Independent of NLRs

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Effector-triggered immunity of plants is mediated by nucleotide-binding leucine-rich repeat receptors (NLRs). When recognizing cognate pathogen effectors, NLRs are activated and form transmembrane pores in their functioning. Animal gasdermins are autoinhibitory non-NLR immune proteins. When cleaved, the N-terminus of gasdermin proteins oligomerizes into transmembrane pores, inducing cell death. Whether pore-forming proteins like gasdermins can trigger immune responses in plants is worthy of investigation. Here, we engineered gasdermins in plants and observed that the N-terminus formed transmembrane Ca2+-permeable pores that induced cell death. By replacing the cleavage site of gasdermins with proteases from multiple plant pathogens, engineered gasdermins were cleaved and conferred resistance to viral, bacterial and fungal pathogens in plants as noncanonical resistosomes. Finally, using protein design we redesigned gasdermin, which functioned specifically in plants with high programmability but low protein sequence identity (66.4%). This study provides direct evidence that unifies the functioning mechanism, transmembrane pore formation, in animal and plant innate immunity. The study also presents a strategy for engineering multipathogen resistance by clustering protease effector cleavage sites in gasdermins. Moreover, the cross-species immunity engineering shows how protein design can enable specific function in another species.

Biomolecular Condensation of ERC Protein Family in Plant Autophagosome Formation

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Biomolecular condensation is emerging as a crucial process for cellular stress responses. Upon stress conditions, macroautophagy serves as a fundamental metabolic pathway by forming a double-membrane autophagosome. However, the initiation mechanisms via biomolecular condensation remain largely unexplored. Here, we have identified an uncharacterized but conserved plant ERC protein family as novel ATG8-interacting scaffolds in plant autophagy. We unveil an ER-associated condensate mediated by ERC1 for autophagosome initiation in plant cells. Further analysis of the ERC1 interactome and functional analysis reveal an undescribed role of ERC1 in NBR1 turnover and heat stress recovery via direction interaction with NBR1. This work unveils a biomolecular condensation-driven mechanism for plant autophagosome formation and has implications for plant adaptation to heat stress.nism for plant autophagosome formation and has implications for plant adaptation to heat stress.

Poster Abstracts

Poster #1

Decoding Conformational Interfaces within RIN4-XopR Immune Condensates via HDX-MS

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Plants experience continual assaults from phytopathogens in their antagonistic encounters. Throughout co-evolution, phytobacteria deliver effectors into hosts to subvert immune signaling cascades. While extensive work emphasizes effector domain mimicry, relatively little attention addresses intrinsically disordered regions (IDRs) beyond their contribution to secretion. We recently examined how XopR, a representative IDR-rich effector, engages host plasma-membrane–associated immune assemblies. By targeting the guardee RIN4, XopR fluidized RIN4 condensates and prevented activation of RPM1-mediated defense. Yet, the precise binding mode and structural alterations within RIN4 immune condensates under XopR influence remained unclear. To investigate this, we employed hydrogen–deuterium exchange mass spectrometry (HDX-MS) to interrogate the internal dynamics of guardee nanocondensates. Our analyses revealed that RIN4 adopts an exposed configuration involving residues P149 and T166 during condensate formation, highlighting potential accessibility for kinase activation. Incorporation of XopR further distorted RIN4 conformation, unveiling a crucial segment encompassing a proline isomerization site. Collectively, these findings uncover intricate structural rearrangements underlying guardee activation and effector-driven perturbation, establishing a paradigm for mechanistic exploration of IDR-mediated virulence.

Poster #2

Spatiotemporal Formation of Glands in Plants is Modulated by MYB-like Transcription Factors

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About one third of vascular plants develop glandular trichomes, which produce defensive compounds that repel herbivores and act as a natural biofactory for important pharmaceuticals such as artemisinin and cannabinoids. However, only a few regulators of glandular structures have been characterized so far. Here we have identified two closely-related MYB-like genes that redundantly inhibit the formation of glandular cells in tomatoes, and they are named as GLAND CELL REPRESSOR (GCR) 1 and 2. The GCR genes highly express in the apical cells of tomato trichomes, with expression gradually diminishing as the cells transition into glands. The spatiotemporal expression of GCR genes is coordinated by a two-step inhibition process mediated by SlTOE1B and GCRs. Furthermore, we demonstrate that the GCR genes act by suppressing Leafless (LFS), a gene that promotes gland formation. Intriguingly, homologous GCR genes from tobacco and petunia also inhibit gland formation, suggesting that the GCR-mediated repression mechanism likely represents a conserved regulatory pathway for glands across different plant species.

Poster #3

Synergistic Interaction Between Arbuscular mycorrhizal Fungi and Falciphora oryzae Enhances Rhizosphere Microbiota, Plant growth, and Nitrogen Uptake in Pepper

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Arbuscular mycorrhizal fungi (AMF) and dark septate endophytic fungi (DSE) are pivotal root-associated fungi that promote plant growth and nutrient acquisition. Our study investigated the individual and combined effects of AMF (Rhizophagus irregularis) and Falciphora oryzae (FO, a DSE strain) on pepper (Capsicum annuum) growth, nutrient accumulation, and microbial communities across rhizosphere compartments. FO alone enriched soil mineral nutrients, but was less efficient than AMF in facilitating plant nutrient uptake. Notably, the AMF+FO combination significantly increased N uptake in both roots and leaves compared to single inoculations. Microbiome analysis revealed a significant decline in microbial diversity and abundance closer to the internal root tissues. The AMF+FO combination specifically enriched microbial communities with N-fixing taxa. FO inoculation alone enriched beneficial bacteria and soil nutrients, but also led to the monogenus dominance of Fusarium in the fungal community,while AMF inoculation promoted fungi with reported disease-suppressive traits and reduced the relative abundance of Fusarium. Collectively, our study suggests that the dual inoculation of AMF and FO establishes a balanced underground microbial community in the rhizosphere that enhances the plant's N absorption and utilization efficiency to promote plant growth, while also providing a potential ecological fitness boost with its diversity.

Poster #4

Arbuscular mycorrhizal Fungi Enhance Insect Resistance in Lettuce Through Modulation of Phytohormone Signaling and Defense Metabolism

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Arbuscular mycorrhizal fungi (AMF) are important symbionts that enhance plant nutrient uptake and induce systemic resistance against herbivores. In this study, we evaluated the role of AMF in improving insect resistance in soil-grown lettuce (Lactuca sativa) challenged by the generalist pest Spodoptera litura. AMF inoculation significantly reduced larval weight and feeding damage compared to non-inoculated controls. Targeted metabolomic profiling revealed AMF-induced activation of defense-related metabolic pathways, including tryptophan-derived secondary metabolites, auxin signaling, and jasmonic acid (JA) biosynthesis. Chemical inhibition of auxin transport further enhanced resistance, suggesting that auxin homeostasis plays a role in AMF-mediated priming. Expression analysis of key defense genes, such as OPR3, AOC, and PAL, confirmed transcriptional activation of JA and phenylpropanoid pathways. These results demonstrate that AMF colonization can enhance lettuce resistance to chewing insects by modulating phytohormone signaling and activating multiple layers of defense metabolism, offering new perspectives for sustainable pest control in leafy vegetables.

Poster #5

Molecular Mechanism of ERC1-mediated Biomolecular Condensate in Plant Autophagy

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Autophagy, a conserved degradation pathway in eukaryotes, plays a crucial role in maintaining cellular homeostasis. During this process, double membrane vesicles called autophagosomes are formed which sequester and engulf the cellular contents in a selective or non-selective way under stress condition. Different types of biomolecular condensates have been suggested to actively participate in autophagy, such as autophagosome initiation and cargo sequestration. A number of unique molecular scaffolds have been identified to drive biomolecular condensation in mammals and yeasts, how biomolecular condensation functions in plant autophagy remains largely unknown. Recently, we have identified ERC protein family as a novel ATG8-ineracting partner in Arabidopsis, which forms membrane-less condensates together with ATG8 and NBR1. Moreover, ERC1 dysfunction suppresses the turnover of ubiquitinated substrates and plant tolerance to heat stress. In this project, I will focus on characterizing the composition of ERC1 condensates and the underlying assembly mechanism using a combination of biochemical, cellular and genetic approaches. This work might provide new insights into how biomolecular condensation contribute to plant autophagy and stress adaptation.

Poster #6

Bacterial XopR Subverts RIN4 Complex-mediated Plant Immunity via Plasma Membrane-associated Percolation

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Bacterial XopR Subverts RIN4 Complex-mediated Plant Immunity via Plasma Membrane-associated Percolation Phytobacteria release Type III effectors (T3Es) abundant in intrinsically disordered regions (IDRs) to undermine plant defenses. How flexible IDRs contribute to T3Es' function in subverting plant immunity remains unclear. Here, we unveil a plant plasma membrane (PM)-associated macromolecular condensation mechanism that governs the sophisticated interplays between T3E XopR and the plant's RIN4 immune complex. Upon deployment into plants, XopR undergoes PM-association, percolation clustering, and spanning networking on the PM, ranging from subnanomolar to tens of nanomolar. This spatiotemporal building of the XopR network enables an efficient manipulation of plant surface immune regulators, including a Coiled-coil Nucleotide-binding Leucine-rich repeat receptors (CNL)-guardee complex with highly disordered RIN4. When XopR hijacks and fluidizes the RIN4-RPM1 condensates, Arabidopsis shows reduced RIN4 phosphorylation and diminished RPM1-activated defense in vivo, consistent with XopR-impaired RIN4 phosphorylation by RIPK. Our research illuminates the mechanism underlying the dynamic interplay between bacterial T3Es and plant receptor complex condensates during infection.

Poster #7

The Kinase Activity of SERK4 is Required for the Potentiation of PEPR Pathway Upon BAK1 Depletion

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BAK1 and SERK4 are co-receptors for multiple LRR-PRRs, thus their integrity is key to maintain plant immune homeostasis. Depletion of BAK1 abolishes PTI, yet triggering strong PEPR-mediated DTI responses and cell death, thereby ensuring basal resistance to pathogens. However, the precise activation mechanism of potentiated PEPR pathway upon BAK1 depletion remains largely unknown. By screening the bak1-4 EMS mutant library, we identified suppressors carrying mutations in SERK4, which lead to compromised SERK4 kinase activity, completely inhibit Pep2-induced DTI and cell death. We report that in the absence of BAK1, SERK4 trans-phosphorylates PEPR1/2 and phosphorylates RLCKs BIK1/PBL1, activating the canonic PEPR-SERK-RLCK receptor complex and subsequent downstream DTI signaling. Meantime, BTL2, an LRR-RLK with autoimmune inducibility yet constrained by BAK1/SERK4-mediated phosphorylation, is dissociated from SERK4, thereby unleashing the suppression to activate strong immune responses and cell death. Notably, subtle kinase activity of SERK4 is sufficient for the phosphorylation and inhibition on BTL2 to sustaining the normal growth of bak1-4. Thus, our study uncovers the specific regulation of DTI and cell death by the co-receptor SERK4 upon BAK1 depletion, underscoring the differential regulation mechanisms of phosphorylation governing PTI and DTI signaling pathways.

Poster #8

The SlZF14-SlERF.B5-SlProDH1/2 Transcriptional Cascade Enhances Cold Tolerance in Tomato by Promoting Proline Accumulation

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Cold stress during the winter and spring seasons poses a significant challenge to the overwintering cultivation of crops. In this study, we demonstrate that the C2H2-type zinc finger protein ZF14 positively modulates cold tolerance in tomato by promoting proline accumulation. Notably, ZF14 does not directly regulate the expression of genes involved in proline synthesis or metabolism. Through screening via ChIP-seq and RNA-seq, we identified the transcription factor ERF.B5 as a downstream target of ZF14. ERF.B5 is dually activated by cold and ZF14, and functions to suppress the expression of the proline catabolic genes ProDH1 and ProDH2. This inhibition of proline degradation ultimately reinforces ZF14-mediated cold tolerance in tomato. Our results provide a key strategy for cold signal transduction in tomato.

Poster #9

A Stochastic Particle Model for the Emergence of Distinct Cell Morphology and Size of Confluent Cell Sheet

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Collective migration of confluent epithelial sheets underlies processes from wound healing to cancer invasion. A striking feature of migrating epithelia is their emergent heterogeneity: peripheral cells stretch and elongate while bulk cells remain compact and ordered. Existing simulation models either capture cell shape without scalability or efficiency without morphology. Here we bridge this divide with a stochastic particle–Voronoi framework that unifies efficiency with explicit geometry. Remarkably, size and shape heterogeneity emerge from mechanical interactions alone — no prescribed target geometries are required. Peripheral cells emerge larger, more irregular, and more polarized, while bulk cells remain smaller and more hexagonal. Tuning division thresholds and neighbor coupling strength reveals simple rules that link local mechanics to global morphology. By connecting minimal dynamics to emergent tissue organization, our model offers a new lens on how epithelial monolayers coordinate structure and motion during collective migration.

Poster #10

The Small GTP-binding Protein GhARAC3 is Involved in Cotton Resistance to Verticillium dahliae by Regulating Lignin Metabolism

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Cotton, a vital global crop for natural fiber and oil production, faces severe yield loss from Verticillium wilt caused by Verticillium dahliae. Plants have evolved complex immune systems where Rac/Rop GTPases act as key molecular switches, yet how ubiquitination regulates their function in cotton immunity remains unclear. This study elucidates a ubiquitination-mediated regulatory mechanism governing the cotton Rac/Rop GTPase GhARAC3 in resistance to Verticillium dahliae. Proteomic modification analysis revealed that GhARAC3 ubiquitination levels were significantly reduced following Verticillium dahliae inoculation. Furthermore, GhARAC3 interacts with the laccase protein GhLAC14 to regulate lignin biosynthesis and deposition. Silencing either gene impaired lignin accumulation and altered monomer composition, particularly under early infection. Transcriptomic profiling revealed enrichment in phenylpropanoid biosynthesis, ubiquitin-dependent proteolysis, and plant–pathogen interaction pathways in GhARAC3-manipulated plants. Our results identify a novel regulatory pathway in which ubiquitin modification of GhARAC3 coordinates GTPase signaling with lignin biosynthesis to mediate cotton resistance to Verticillium wilt, offering fresh perspectives on post-translational regulation of plant immunity and suggesting promising genetic targets for enhancing crop disease resistance.

Poster #11

Drought-smart: Using Synthetic Biology to Engineer Stomatal Production to Enhance Plant Drought Resilience

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Drought-smart-Using synthetic biology to engineer stomatal production for optimal drought resistance plant Abstract: Stomata are the gatekeepers of plant water and carbon balance, coordinating gas exchange and transpiration to sustain growth under fluctuating environments. By modulating pore aperture in response to light, humidity, and drought, they maintain homeostasis and productivity; notably, optogenetic tuning of stomatal kinetics has been shown to enhance carbon assimilation, water use, and growth. Leveraging these principles, we apply synthetic biology to engineer a regulatory circuit that amplifies abscisic acid (ABA) biosynthesis in Arabidopsis thaliana specifically within meristemoids and epidermal cells. Building on our prior discovery that drought activates SnRK2 kinases to phosphorylate the master regulator SPEECHLESS (SPCH)—and that SPCH primes stomatal precursors to perceive long-distance dehydration signals—we design a synthetic positive-feedback loop that reinforces endogenous ABA signaling to tighten control of stomatal development. This targeted enhancement improves stomatal regulation and water-use efficiency under water limitation, offering a generalizable strategy for drought resilience. More broadly, our work demonstrates how rational circuit design can rewire hormone networks to couple developmental decisions with stress responses in plants.

Poster #12

Glucose-G protein Signaling Plays a Crucial Role in Tomato Resilience to High Temperature and Elevated CO2.

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Elevated CO_2 mitigates heat stress (HT) in tomato by raising apoplastic glucose (Glc). Exogenous Glc mimics this protection. Glc binds the membrane receptor RGS1, triggering its endocytosis and dissociation from the G-protein α subunit GPA1. RGS1 negatively, and GPA1 positively, controls thermotolerance; both are indispensable for CO_2-Glc benefits. Transcriptome and chlorophyll fluorescence analyses show GPA1 orchestrates photosynthetic and photoprotective genes to sustain carbon assimilation and prevent photo-oxidative damage under HT. Thus, a Glc–RGS1–GPA1 signaling module converts CO_2 fertilization into acquired thermotolerance, offering a clear engineering target for climate-resilient crops.

Poster #13

Site-specific Phosphorylation of LRP Regulates FLC Chromatin Looping and Flowering

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Emerging evidence suggests that multiple RNA recognition motif (RRM)-containing proteins are involved in transcriptional regulation, yet the underlying mechanisms remain largely unclear. Here, we show that the previously uncharacterized LATE-FLOWERING RRM-CONTAINING PROTEIN (LRP) prevents 5'-3' chromatin looping of the key floral repressor gene FLOWERING LOCUS C (FLC) via direct association with its 5' and 3' genomic regions. Loss of LRP function leads to increased 5'-3' gene looping, reduced RNA polymerase II (Pol II) occupancy at the FLC locus, thereby increasing FLC transcription and delaying flowering in Arabidopsis thaliana. Furthermore, site-specific phosphorylation of LRP at serine 17, mediated by the kinase PRP4KA, is essential for LRP protein stability, and its function in preventing FLC chromatin looping and Pol II recruitment. Our findings reveal that site-specific phosphorylation of LRP by PRP4KA precludes FLC gene loop formation, constituting a key mechanism for FLC transcriptional repression to ensure timely flowering.

Poster #14

Functional Characterization of the Deubiquitinase OTU2 Role in A. Thaliana SGs Biology

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Functional characterization of the deubiquitinase OTU2 role in SGs biology. Abiotic stress can reduce plant yield and biomass, threatening global food security. To cope with it, plants developed adaptive mechanisms, including stress granules (SGs) formation—membrane-less, dynamic, and reversible condensates. SGs are thought to transiently sequester cellular components during stress-induced shutdowns, making their proper assembly and disassembly vital for recovery. In mammals, SGs dynamics are regulated by post-translational modifications such as ubiquitination. In plants, the deubiquitinase Ovarian-Tumor-2 (OTU2) was identified as a heat-induced SGs component, however; its role in SG biology is still unknown. Confocal imaging shows that OTU2 foci are heat-specific and RNA-dependent. OTU2 only partially co-localizes with mRNA-containing SGs or RBP47b-marked SGs, suggesting rather different nature of OTU2 condensates. Interestingly, the otu2 mutant line, present more and smaller in size SGs in comparison to wild-type and OTU2-overexpressing lines. Notably, SGs in both, OTU2 OE and in otu2 background disassemble at similar times. This indicates a possibility of so far unknown regulation of OTU2. While SGs biology is well understood in non-plant systems, its role in plant stress responses remains less explored. Understanding OTU2's function may provide new insights into SGs dynamics and enhance crop resilience under adverse conditions.

Poster #15

Multi-omics Brain Tumor Microenvironment Interrogation Identifies Anti-tumor Phagocytic Modulators

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Glioma-associated macrophages (MAC) are largely considered immunosuppressive, despite their anti-tumor potentials, which remains elusive. In this pursuit, our transcriptomics (n=145,00) and cytometry studies of glioma-associated leukocytes (n=54) revealed 22 distinct cell types mediate brain immunity. Microglia decreased with glioma recurrence, whereas monocytic derivatives increased with glioma severity. MAC acquired antigen presentation-like phenotype upon tumor recurrence, with a concomitant increase in CD8+ T cells. Besides dissecting relapse associated immunity patterns, we provide a faithful clinical genomics framework for redefining macrophage polarization beyond M1/M2 states such as palmitic- and oleic-acid modules. Beyond canonical LM22 (leukocyte gene matrix), we curated glioma specific leukocyte signatures termed GlioTIME-36 (glioma tumor immune microenvironment-36) for deconvolution of brain transcriptomic datasets. Furthermore, we discovered that TREM2 and Galectin-9 expression in microglia correlated with enrichment of phagocytosis pathways. Using ex vivo and in vivo brain tumor models, we confirmed that TREM2+ and Galectin-9+ microglia efficiently phagocytosed glioma cells. In summary, besides providing the advanced optics of pan-glioma immune contexture for downstream translational and clinical applications, our reverse translational approach also identifies actionable anti-glioma phagocytic circuits for developing brain tumor immunotherapies.

Poster #16

Manipulation of UBP1C Low-Complexity Domains Alters Stress Granule Dynamics and Enhances Heat Stress Resilience in Arabidopsis

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High temperature rewires gene expression, represses translation initiation, and promotes the assembly of stress granules (SGs). SGs are cytoplasmic biomolecular condensates where untranslated mRNAs are stored. Although SGs are widely associated with stress responses, the molecular features that determine their dynamics and functional relevance in plants remain unclear. Here, we investigated the role of a low-complexity domain (LCD) in modulating the behavior of the RNA-binding protein UBP1C, a well-described Arabidopsis SG marker. We generated mCherry-tagged UBP1C variants with polyglutamine (polyQ) expansions and found that altering LCD length influenced SG dynamics. PolyQ expansions increased the size and number of UBP1C granules during heat shock but impaired their disassembly during recovery. Proteomic analysis of purified SGs revealed that polyQ-expanded UBP1C recruited an expanded set of SG components. Notably, Arabidopsis plants expressing polyQ-expanded UBP1C variants exhibited enhanced survival following heat stress. To explore the mechanisms underlying this enhanced heat tolerance, we analyzed the accumulation of mRNAs and their association with ribosomes in lines expressing either wild-type or polyQ-expanded UBP1C during the progression of heat stress and recovery. This analysis uncovered distinct patterns of transcript recruitment into translation, which may link increased SG persistence with delayed recovery of protein synthesis but improved stress resilience.

Poster #17

Curvature-Coupled Condensation Drives Podosome Enrichment on Nanotopography

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Liquid-liquid phase separation is recognized as a common mechanism for organizing biomolecules at membranes to regulate adhesion assembly. For instance, phase separation of adhesive proteins such as talin and paxillin promotes focal adhesion formation. Podosomes are membrane-associated adhesion structures in immune cells with an actin-rich core and adhesive ring. It has been found to form along surface topographies, transitioning from individual ring-dot structure to more connected architectures. However, their reorganization mechanism in response to topographical cues remains unclear. In our study, we engineered vertical nanostructures to dissect the impact of surface topography on podosome components. We found that topographical surfaces triggered podosome proteins (actin and vinculin) exhibit negative curvature-dependent enrichment around patterns. In addition, live-cell imaging of podosome-related actin showed distinct frequencies of merging/splitting phenomenon around topographical surfaces. To understand the mechanism behind, we use pharmacological modulation of protein multivalency in podosomes. Upon treatment of 1,6-Hexanediol, which disrupts weak hydrophobic interactions globally in the cells, we observed that partially disassembled podosomes, where vinculin ring dissolution with the enlarger of actin core. These findings suggest that multivalent protein interactions and phase separation contribute to podosome reorganization in response to surface topography.

Poster #18

Decoding Phase Separation Evolution in Signaling via AI and System Biology

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Macromolecular condensation plays a pivotal role in signalling pathways, driving diverse developmental and adaptive processes in plants. While experimental studies have elucidated detailed mechanisms of phase separation (PS) regulation, their low-throughput nature limits a comprehensive understanding of PS across the broader scope of life and complex signalling networks. To address this, we first developed an advanced protein PS predictor MolPhase (https://molphase.sbs.ntu.edu.sg/), which integrates diverse physicochemical PS features. Furthermore, we employed the large language model combine with vision language model for literature-based data mining to build up the most comprehensive database. With EMS3 for clustering, we develop MolPhase2 with enhanced performance. Expanding MolPhase2 to analyze proteomes from 1,106 species across six major kingdoms, we identified a co-expansion of PS proteins with genome size along evolution. By integrating PS protein data with experimental omics and interactome databases, we identified conserved, PS regulated signalling hubs across multiple model species including Arabidopsis. To facilitate exploration of these findings, we developed PhaseHub, a user-friendly interface that highlights key scaffold proteins and binders to predict potential multicomponent phase separation-based plant signalling hubs.

Poster #19

Membrane Curvatures Orchestrate Actin Nucleation via N-WASP–FBP17 Nanoclusters

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Membrane surface topography plays a critical role in guiding local actin remodeling, which underpins numerous signaling pathways in cells. However, the spatiotemporal coordination between membrane deformation and actin nucleation remains poorly understood. By employing nanolithography to precisely manipulate membrane curvature, we developed an in vitro reconstitution system to study actin polymerization on membranes with defined nanoscale features. Our results show that curved membrane sites promote localized actin nucleation through the synergistic action of N-WASP, FBP17, and Cdc42, mediated by multivalent interactions that drive nanoscale clustering. When Cdc42 is globally distributed, localized curvature cues selectively initiate N-WASP clustering through its interactions with the curvature-sensing BAR-domain protein FBP17. We further demonstrate that the enhancement of actin nucleation is sensitive to the stoichiometry between FBP17 and N-WASP, which is modulated according to the curvature radius. These findings uncover how nanoscale membrane geometry can differentially regulate global versus localized actin assembly, providing insight into the coordination of membrane shape and cytoskeletal dynamics during complex cellular functions.

Poster #20

Nanoscale Curvatures Enrich the Membrane-Associated Condensation of LAT/Grab2/SOS1 *in vitro*

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Membrane-associated protein condensation plays a pivotal role in diverse biological processes including immune activation, cell adhesion, and synapse formation, which has been shown to induce membrane deformation through attractive and repulsive interactions. The interplay between membrane shape and protein condensation is increasingly recognized, yet how pre-existing membrane curvature influences protein condensation remains elusive. This raises a critical question about whether membrane geometry can modulate biochemical reactions through protein condensation. Here, we investigate the condensation of the well-studied LAT/Grb2/SOS1 system on curved membrane guided by designed nanostructures in vitro. This condensation is known as key players in TCR-related signalling on T cell membrane that contains highly curved microvilli with 50 nm – 350 nm in diameter. Remarkably, the condensation of LAT/Grb2/SOS1 preferentially enriched at curved membrane with 250nm diameter but not on those with 850nm diameter. Such curvature-guided condensation was found highly dependent on both the conditions of individual molecules (e.g. protein density, membrane mobility) and the intermolecular interactions (e.g. crosslinking strength, cluster diffusion). Our findings indicate that membrane-associated protein condensation can be effectively guided by membrane curvature, suggesting membrane geometry regulation as a new strategy of cells to manipulate signalling transduction.

Poster #21

SnRK1α1-mediated RBOH1 Phosphorylation Regulates Reactive Oxygen Species to Enhance Tolerance to Low Nitrogen in Tomato

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Nitrogen is essential for plant growth and development. SnRK1 is an evolutionarily conserved protein kinase pivotal for regulating plant responses to nutrient deffciency. Here, we discovered that the expression and activity of the SnRK1α1 increased in response to low-nitrogen stress. SnRK1α1 overexpression enhanced seedling tolerance, nitrate uptake capacity, apoplastic ROS accumulation, and NADPH oxidase activity in tomato under low-nitrogen stress compared to wild type plants, while snrk1α1 mutants exhibited the opposite phenotypes. Mutation of the NADPH oxidase gene RBOH1 suppressed numerous nitrate uptake and metabolism genes during low-nitrogen stress. rboh1 mutants displayed lower NADPH oxidase activity, apoplastic ROS production, and seedling tolerance to low nitrogen. Silencing RBOH1 expression also compromised SnRK1α1-mediated seedling tolerance to low-nitrogen stress. SnRK1α1 interacts with and activates RBOH1 through phosphorylation of three N-terminal serine residues, leading to increased apoplastic ROS production and enhanced tolerance to low nitrogen conditions. Furthermore, RBOH1-dependent ROS oxidatively modiffed the transcription factor TGA4 at residue Cys-334, which increased NRT1.1 and NRT2.1 expression under low-nitrogen stress. These ffndings reveal a SnRK1α1-mediated signaling pathway and highlight the essential role of RBOH1-dependent ROS production in enhancing plant tolerance to low nitrogen.

Poster #22

Holliday Junction Resolvase RuvC Targets Biofilm eDNA and Confers Plant Resistance to Vascular Pathogens

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Plant vascular bacterial pathogens such as Ralstonia solanacearum and Xanthomonas oryzae pv. oryzae (Xoo) cause severe crop yield reduction. Biofilm lifestyle is critical for bacterial pathogens to colonize and protect themselves from host immunity and antimicrobial chemicals in plants and animals. The formation and regulation mechanism of phytobacterial biofilm are still obscure. Here, we found that Ralstonia solanacearum Resistance to ultraviolet C (RuvC) is highly abundant in biofilm and positively regulates pathogenicity by governing systemic movement in tomato xylem. RuvC protein accumulates at the later stage of biofilm and specifically targets the Holliday junction (HJ) like structures to disrupt biofilm extracellular DNA (eDNA) lattice, thus facilitating biofilm dispersal. Heterologous expression of R. solanacearum or Xanthomonas oryzae pv. oryzae RuvC with plant secretion signal in tomato or rice confers resistance to bacterial wilt or bacterial blight disease, respectively. Our novel finding reveals a critical pathogenesis mechanism of R. solanacearum and provides an efficient biotechnology strategy to improve plant resistance to bacteria vascular disease.

Poster #23

A Novel LRR-RLK BRAK Reciprocally Phosphorylates PSKR1 to Enhance Growth and Defense in Tomato

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Plants constantly encounter pathogens that impair growth and yield. Leucine-rich repeat receptor-like kinases (LRR-RLKs) play key roles in development and immunity, but their roles against necrotrophic fungi remain unclear. We identified an LRR-RLK (Solyc06g069650) in tomato, strongly induced by Botrytis cinerea, and named it BRAK (B. cinerea resistance-associated kinase). Loss of BRAK reduced growth and increased susceptibility to B. cinerea, whereas overexpression enhanced growth, fruit yield, and resistance. Yeast two-hybrid and functional analyses revealed BRAK interacts with the phytosulfokine receptor PSKR1. Growth and defense responses triggered by PSK were impaired in pskr1, brak, and double mutants, as well as in PSKR1-overexpressing plants with BRAK silenced. Microscale thermophoresis showed that BRAK and PSKR1 phosphorylate each other, strengthening their interaction. This reciprocal phosphorylation proved essential for promoting growth and resistance. Together, our findings identify BRAK as a novel regulator linking yield and fungal resistance, offering promising strategies for breeding disease-tolerant crops without yield penalty.

Poster #24

A RabGAP–Rab–ATG8 Module Balances Autophagy and Immune Secretion in Plants

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Plants rely on autophagy and membrane trafficking to maintain cellular homeostasis, adapt to stress, and mount immune responses. However, how these two pathways intersect at the molecular level remains poorly understood. Using an AI-guided discovery approach, we identified Rab3GAPL as a conserved regulator that links membrane trafficking with autophagy in plants. Rab3GAPL suppresses autophagy by directly binding ATG8, a core autophagy adaptor, and inactivating Rab8a, a small GTPase essential for autophagosome formation and defense-related secretion. Loss of Rab3GAPL function enhances autophagic activity and confers improved heat stress recovery in Marchantia polymorpha, indicating a physiological role in stress adaptation. In addition to its function in autophagy, Rab3GAPL negatively regulates focal immune responses against the oomycete pathogen Phytophthora infestans by restricting secretion of defense cargo. These findings establish Rab3GAPL as a molecular switch that fine-tunes the balance between autophagic flux and immune exocytosis through Rab8a-mediated trafficking. The identification of this RabGAP–Rab–ATG8 regulatory module provides new insight into how membrane trafficking coordinates autophagy and immunity in plants.

Poster #25

The Mechanisms of SlBBX17 in Regulation of Pollen Development in Tomato

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Pollen development is crucial for plant sexual reproduction, encompassing microsporogenesis, microgametogenesis and pollen maturation stages. The precise regulation of signaling molecules, transcription factors, and metabolites during each stage is central to ensuring pollen formation and function. BBX transcription factors, a class of zinc-finger proteins containing a Box domain, integrate signals such as light and temperature and have been reported to function in seed germination, photomorphogenesis, and flowering. Although a relatively complete DYT1-TDF1-AMS transcriptional regulatory network has been elucidated in Arabidopsis, studies on the effects of transcription factors on sexual reproduction in tomato remain scarce. In particular, the role of the BBX family in pollen development warrants further investigation. Therefore, based on existing transcriptomic data showing high expression of BBX17 in flowers, we hypothesized its potential functional role. Subsequent observation of BBX17 mutants revealed severe flower and fruit drop, along with reduced pollen counts. Scanning electron microscopy (SEM) revealed abnormal pollen structure in BBX17 mutants. FDA staining indicated decreased pollen viability, with significantly reduced pollen germination rates both in vitro and in vivo, ultimately leading to reduced fruit weight and seed number. The specific mechanism by which BBX17 influences tomato pollen development will be further investigated.

Poster #26

Phosphocode of a Tomato Receptor Kinase Distinguishes the Invasion of Bacterial and Fungal Pathogens

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Ralstonia solanacearum is a soil-borne bacterial plant pathogen with a worldwide distribution and infects more than 250 plant species belonging to over 50 different families. However, our understanding of how tomato plants perceive the bacterial wilt pathogen requires further research. Exopolysaccharide (EPS), a major virulence factor of R. solanacearum, elicits pattern-triggered immunity (PTI) in tomato, but the means by which EPS is recognized in the plant remain poorly understood. We found that tomato non-RD receptor kinase SlLYK4 mediates the perception of R. solanacearum EPS and positively regulates resistance to bacterial wilt. The RD receptor kinases SlLYK1 and SlLYK13 are required for EPS-triggered immune responses and form complexes with SlLYK4. These receptor kinase complexes have dual functions in recognizing bacterial EPS and fungal chitin. Phosphorylation of Ser320 in the juxtamembrane domain of SlLYK4 is essential in EPS- and chitin-mediated signaling, while phosphorylation of Ser334 or Ser634 in the C-terminal domain is required for chitin or EPS signaling, respectively. Our results reveal the mechanism underlying EPS recognition in tomato, and provide insight into how a phosphocode-dependent receptor kinase differentiates anti-bacterial and anti-fungal immunity.

Poster #27

The PyShell Governs Pyrenoid Morphology via the Modulation of Liquid-Liquid Phase Separation in the Diatom Phaeodactlyum tricornutum

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Ribulose-1,5-bisphosphate carboxylase/oxygenase (Rubisco) catalyzes the entry of inorganic carbon into the biosphere. However, RuBisCO is slow and non-specific, frequently incorporating O_2 instead of CO_2 which necessitates the energetically costly process of photorespiration. Thus, many phototrophs have evolved CO_2-concentrating mechanisms (CCMs) which saturate Rubisco active sites with CO_2. Most algae possess biophysical CCMs, where inorganic carbon is actively pumped into a liquid-liquid phase separated Rubisco-rich compartment, the pyrenoid. The diatom P. tricornutum (Pt) pyrenoid is characterized by the presence of a multivalent linker protein PYCO1 (Oh et al. 2023) and a proteinaceous shell (Shimakawa et al. 2024). In vivo, the PtPyrenoid posseses unique architecture with its elongated morphology and shell patterning at the condensate rim, where this PyShell has been proposed as a CO2 diffusion barrier Here, we show that the addition of purified PtPyShell proteins into homotypic PYCO1 droplets displayed surfactant-like properties, leading to the formation of smaller in vitro droplets. In addition, the titration of PtRubisco into PtPyShell-PYCO1 droplets pushes the PyShell protein to the rim of the condensate. This work furthers our understanding of the architecture of a red type pyrenoid and may inform future efforts to engineer a synthetic CCM into crop plants.

Poster #28

Selectively Targeting UDP-glucose 4-epimerase MoUGE1 for Controlling Rice Blast Disease

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Rice blast, caused by the fungal pathogen Magnaporthe oryzae, is a major threat to global food security. Current management strategies, including resistant rice varieties and fungicides, are challenged by emerging fungicide-resistant strains. This study identifies MoUGE1, a UDP-glucose 4-epimerase in M. oryzae, as a critical determinant of fungal pathogenicity. MoUGE1 is essential for maintaining cell wall integrity and synthesizing galactosaminogalactan (GAG), a component crucial for appressorium adhesion, host penetration and immune evasion. Deletion of MoUGE1 impaired appressorium function and invasive growth, reducing fungal virulence. Metabolomic analyses revealed that MoUGE1 deletion disrupted cell wall dynamics, altered soluble sugar components, and affected cell membrane fluidity. Furthermore, virtual screening and AI-assisted molecular docking identified inhibitor UGE1i, a small-molecule compound with high binding affinity to MoUGE1. UGE1i selectively inhibits M. oryzae growth and pathogenicity without affecting other fungal pathogens, suggesting its potential as a novel, specific fungicide. This study highlights MoUGE1 as a promising target for developing fungicides, offering a new strategy for sustainable rice blast management.

Poster #29

The Application of Pogostone in the Control of Rice false smut

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Rice false smut is one of the most important diseases in global rice production, prevalent in more than forty rice-growing countries across Asia, the Americas, Africa, and Europe. This disease not only causes yield losses but, more critically, the toxins produced in the false smut balls exhibit toxic and teratogenic effects on animal cells, posing a serious threat to food safety. However, at present, there is a severe shortage of resistant rice varieties and genetic resources against false smut, and no plant-derived inhibitors have been identified for practical use.In this study, pogostone, a functional component derived from patchouli essential oil, significantly inhibited the mycelial growth of Ustilaginoidea virens and its pathogenicity in rice. It also induced morphological alterations in the spores of the pathogen, causing surface shrinkage and deformation. The inhibitory effects are primarily attributed to the activation of autophagic activity, disruption of mitochondrial integrity, and accumulation of reactive oxygen species (ROS) in the fungus.

Poster #30

An Effector in Ustilaginoidea virens Suppresses Rice Immunity by Altering the Protein Conformation

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Rice false smut, caused by Ustilaginoidea virens, is a devastating disease affecting rice (Oryza sativa) worldwide. However, the molecular mechanisms underlying the U.virens-rice interaction remain largely unknown. In this study, we identified a secreted protein, UvHp1, as a critical virulence factor. UvHp1 is successfully secreted into rice cells, and its heterologous expression in rice enhances susceptibility to rice false smut, indicating that UvHp1 suppresses rice immunity and promotes U.virens infection. Further analysis revealed that UvHp1 targets the rice OSKβ2 (SnRK1β) and alters its protein conformation, thereby promoting the interaction between OSKβ2 and OSK1 (SnRK1α) and inhibiting the kinase activity of OSK1, ultimately suppressing rice immunity. Our study unveils a novel strategy by which the U.virens effector protein inhibits rice immunity, providing new insights for future control of rice false smut.

Poster #31

Sec24A Enhances Plant Thermotolerance by Stabilizing COPII Complex Through Liquid-liquid Phase Separation

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Rising global temperatures pose severe threats to plant growth and survival. Plants have evolved complex thermotolerance mechanisms, including the endoplasmic reticulum-to-Golgi vesicular trafficking system that maintains cellular proteostasis under heat stress. The Coat Protein Complex II (COPII), central to secretory protein transport, plays a pivotal role in secretory efficiency and stress response. However, how COPII stability is maintained under heat stress remains unclear. Our previous work revealed that the core COPII component Sec24A undergoes phase separation, forming liquid-like droplets in vitro. Heat stress triggered Sec24A phase separation in Arabidopsis protoplasts, increasing the proportion of cells exhibiting phase separation from <10% to ~80% (40% in yeast cells). Notably, these condensates dissipated upon returning to optimal temperatures, suggesting dynamic regulation. This study investigates how Sec24A stabilizes COPII via liquid-liquid phase separation to enhance thermotolerance, addressing a critical knowledge gap between secretory trafficking and heat stress response. Furthermore, modulating Sec24A phase separation through gene editing may provide a strategy for developing heat-resistant crops, offering significant implications for sustainable agriculture under climate change.

Poster #32

WRKY33 Confers Root-knot NematodeResistance by Upregulating scopolin and fraxin in Tomato

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Root-knot nematodes (RKNs; Meloidogyne incognita) are major agricultural pathogens, inflicting substantial economic losses annually in a wide range of crops. WRKY transcription factors (TFs) play crucial roles in the growth and development of plants and their response to biotic and abiotic stresses, yet the role of WRKY in host plant responses to RKN infection remains poorly explored. The present study reveals that WRKY33 confers tomato resistance to RKNs by directly suppressing nematode invasion through upregulating the biosynthesis of scopolin and fraxin. Compared to wild-type plants, wrky33 mutants exhibited heightened susceptibility to RKNs, while WRKY33-overexpressing lines showed enhanced resistance. Nematode infection triggered the production of scopolin and fraxin, which accumulated significantly more in WRKY33-overexpressing roots, as revealed by LC-MS analysis. Further evidence indicates that WRKY33 transcriptionally activates key biosynthetic genes COSY and S8H. Remarkably, complementing wrky33 mutants with these genes restored resistance. Bioassays confirmed that scopolin and fraxin directly inhibit egg hatching and reduce nematode accumulation, thereby limiting colonization. Thus, WRKY33 orchestrates a TF–metabolite–resistance pathway that strengthens RKN defense in tomato.

Poster #33

Harnessing Microbiomes to Shift the Thermal Tipping Point in seagrasses

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Seagrass meadows are foundational coastal ecosystems that stabilize shorelines, store blue carbon, and support marine biodiversity. Their persistence is increasingly threatened by climate-driven stressors. Seagrass research has focused largely on below-ground microbiomes and nutrient cycling. However, the role of microbiomes in enhancing host health and stress resilience, which is well established in terrestrial plants, macroalgae, and phytoplankton, remains poorly understood in tropical seagrasses. We used the primary colonizer and habitat-forming seagrass, Halophila ovalis, to investigate how plant-associated and environmental microbiomes influence thermal tolerance. In controlled aquaria experiments, plant-associated microbiome extended H. ovalis's temperature tolerance by 4 °C beyond the tipping point observed for microbiome-disturbed individuals. Inclusion of sediment and seawater microbiomes further increased tolerance by 2 °C. When only seawater microbiome was intact, seagrass's temperature tipping point differed by only 1 °C from untreated plants and Photosystem II efficiency was restored nearly to the optima of untreated plants after 5 days, highlighting the critical role of above-ground microbiomes. Ongoing molecular analyses aim to identify bacterial taxa contributing to thermal resilience. Our findings show that microbiomes enhance seagrass thermal tolerance, providing a basis for microbiome-assisted strategies to support seagrass persistence in a warming ocean.

Poster #34

Warm Temperature Activates the TCP15-HDA4 Module to Suppress Shoot Branching Through Promoting auxin Biosynthesis and Signaling in Tomato

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Shoot branching, as an important agronomic trait, is controlled by environment. Epigenetic modifications play a pivotal role in governing transcriptional responses to light and temperature cues for plant growth. Nevertheless, the contribution of epigenetic modifiers in regulating shoot branching under varying temperatures remains elusive. Our study reveals that elevated temperature suppresses lateral bud outgrowth in tomato (Solanum lycopersicum), accompanied by increased levels of HISTONE DEACETYLASE 4 (HDA4). Loss of function of SlHDA4 augmented lateral bud outgrowth resulting from a reduced auxin response. Notably, increased lateral bud outgrowth observed in slhda4 mutants was insensitive to an increase in temperature but was restored by SlHDA4 overexpression. Furthermore, the histone deacetylase SlHDA4 interacts with SlTCP15 transcription factor to suppress the expression of genes encoding light receptor SlPHYB1 and auxin signaling repressor SlIAA12 by decreasing the H3K9ac levels at their promoters. In summary, the SlTCP15-SlHDA4 module participates in warm temperature regulation of lateral bud outgrowth by enhancing auxin signaling in tomato.

Poster #35

Identification of Strigolactone Signaling Components and Their Role in Sugar Regulation of Shoot Branching in Tomato

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SL signaling pathways are primarily characterized in model and crop species. However, the SL signaling components in tomato, an important horticultural crop, remain uncharacterized. Here, we demonstrate that SlD14 could bind rac-GR24 and acts as a functional SL receptor to suppress shoot branching in tomato. Two homologs of MAX2 (SlMAX2.1 and SlMAX2.2), and SlSMXL1 and SlSMXL2 that are analogous to SMXL proteins involved in repressing SL signaling, were identified in tomato. SlMAX2.1 and SlMAX2.2 exhibit functional redundancy in suppressing shoot branching, whereas knocking out SlSMXL1, but not SlSMXL2, resulted in reduced bud growth. Furthermore, silencing of SlSMXL1 reversed the enhanced bud growth in SL-related mutants. Notably, SlD14, SlMAX2.1/2.2, and SlSMXL1 are likely to form a ternary complex. Additionally, SlD14 and SlMAX2.1/2.2 were found to promote the degradation of SlSMXL1. Under low light, bud growth was suppressed, concomitant with upregulation of SL-related genes, whereas this suppression was attenuated in SL mutants. Low light also induced SlSnRK1.1 whose overexpression inhibited bud growth and induced the expression of SL-related genes, while silencing SlSnRK1.1 diminished these responses under low light. Taken together, the core SL signaling components were elucidated in tomato and SlSnRK1.1 modulates shoot branching through regulating SL-related genes under low light.

Poster #36

Trans-kingdom Functionality of STING in Innate Immunity

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Stimulator of interferon genes (STING) is conserved for innate immunity in animals and bacteria, but appears to be absent in plants. Here, we studied human STING in plants. Transient expression of STING in the plant Nicotiana benthamiana induced robust immune responses, cell death and disease resistance, and was involved in plant Ca2+ signaling. In transgenic N. benthamiana, Arabidopsis, potato, and rice plants, STING conferred resistance to viral, bacterial, oomycete, and fungal pathogens, demonstrating STING's broad roles in plant immunity. Mechanistically, STING is activated by small nucleotide molecules in plants. The H+ channel activity of STING but not its canonical pathway was required for cell death induction. Furthermore, STING-mediated plant immunity is involved in autophagy. Finally, using protein design, we engineered a designer STING protein that functions specifically in plants. These results deepen our understanding of STING-triggered innate immunity across the tree of life and provides a new strategy for engineering multipathogen resistance in crops. Our work links plant proton channels to plant cell autophagy, providing new insights for plant immunity.

Poster #37

Unravelling the Complex Sub-compartmentalization of the CO2-fixing Pyrenoid in Red-lineage Phytoplankton

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The CO2-concentrating mechanism of the diatom Phaeodactylum tricornutum involves sequestration of the catalytically inefficient CO2-fixation enzyme Rubisco into a pyrenoid. We had previously identified a pyrenoid linker protein PYCO1 which can undergo heterotypic liquid-liquid phase separation (LLPS) with Rubisco, leading to the formation of Rubiscondensates. From our investigation into the physiological functions of PYCO1, we tangentially discovered that the pyrenoid architecture is supported by not only PYCO1, but also a multitude of other pyrenoid proteins. These novel proteins all bare Rubisco LSU-binding motifs that are variants of those found on PYCO1, suggesting Rubisco to be a central organizer of the pyrenoid. A deeper characterization of PYCO2 revealed it to be capable of decreasing the LLPS propensity of Rubiscondensates, hinting at its role as a modulator of pyrenoid dynamics. Mechanistically, PYCO2 competes directly with PYCO1 for Rubisco binding, thereby regulating the effective number of binding sites that are available for maintenance of a system-spanning protein network.

Poster #38

A dephosphorylation-dependent Molecular Switch for FT Repression Mediates Flowering in Arabidopsis

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The reproductive success of flowering plants relies greatly on precise timing of the floral transition, which is finely modulated by a complex network of floral regulators. As amain floral integrator, FLOWERING LOCUST (FT) is also an essential constituent of the florigen that is transported from leaves to shoot apices to induce flowering. FT is specifically transcribed in leaf vascular tissues, where its production is suppressed by many flowering repressors, including the MYB transcription factor EARLY FLOWERING MYB PROTEIN (EFM). Here, we show that a plant CTD phosphatase, C-TERMINAL DOMAIN PHOSPHATASE-LIKE 2 (CPL2), suppresses FT expression in leaf vascular tissues by modulating the binding activity of EFM. CPL2 interacts with and dephosphorylates EFMto facilitate the binding of dephosphorylated EFM to FT chromatin, thereby inhibiting flowering. Our results suggest that CPL2-mediated dephosphorylation of the floral repressor EFM serves as a molecular switch, adding another layer of regulation to fine-tune FT transcription and ensure that flowering occurs at an appropriate time.

Poster #39

IPAMD: A Plugin-Based Software for Biomolecular Condensate Simulations

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The study of intrinsically disordered proteins (IDPs) and their role in biomolecular condensate formation has become a critical area of research, offering insights into fundamental biological processes and therapeutic development. Here, we present IPAMD (Intrinsically disordered Protein Aggregation Molecular Dynamics), a plugin-based software designed to simulate the formation dynamics of biomolecular condensates of IDPs. IPAMD provides a modular, efffcient, and customizable simulation platform speciffcally designed for biomolecular condensate studies. It incorporates advanced force fields, such as HPS-based and Mpipi models, and employs optimization techniques for large-scale simulations. The software features a user-friendly interface and supports batch processing, making it accessible to researchers with varying computational expertise. Benchmarking and case studies demonstrate the ability of IPAMD to accurately simulate and analyze condensate structures and properties.

Poster #40

Early Immunosuppressive Landscape Shaped by BRCA1/p53 Loss in Early Pre-Malignant Mammary Glands Permits Tumor Development

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Triple-negative breast cancer (TNBC) is an aggressive subtype with limited therapeutic options and poor prognosis. The early pre-malignant events that lead to TNBC remain elusive, largely due to a lack of tractable models that recapitulate stepwise tumor initiation in a natural tissue context. Here, we use a spontaneous mouse model with mammary-specific deletion of Brca1 and Trp53, which develops TNBC, together with single-cell RNA sequencing and multi-color flow cytometry to investigate the cellular and molecular landscape of the pre-tumoral mammary glands. Strikingly, the microenvironmental changes occur before any detectable tumors. Although macrophages remained proportionally comparable in the pre-tumoral lesions, their interactions with other populations were much reinforced. Brca1/Trp53 loss in epithelial cells generated unstable genome and DNA fragment due to impaired DNA damage repair, which was sensed by macrophages and triggered type I interferon expression. The reprogrammed macrophages expressed IL-10 to paralyze cytotoxic T cells, TGFβ to target mast cells, and CD137L to stimulate Tregs, contributing to a favorable tumor-initiating niche. Our study establishes a stepwise model of immune remodeling preceding TNBC onset and uncovers macrophage-centered signaling as a mechanistic axis linking genetic instability to a tumor-permissive niche. These findings provide insights into early intervention targets in high-risk breast cancer.

Poster #41

Identification and Functional Characterization of Pathogenicity-Associated Effectors in Ustilaginoidea virens Based on Extracellular Vesicle Proteomics

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Ustilaginoidea virens is a major fungal pathogen that causes significant yield losses in rice production. The extracellular vesicles (EVs) it secretes are hypothesized to play a crucial role in pathogen-host interactions. This study aimed to identify key effector proteins involved in pathogenesis by extracting and profiling the proteome of U. virens EVs. Mass spectrometry analysis identified 118 EV proteins, 63 of which contained a signal peptide. Using an Agrobacterium-mediated transient expression assay in tobacco, we functionally screened these proteins and identified two effectors that significantly suppressed tobacco necrosis. Knockout mutants of these two effectors markedly reduced the pathogenicity of U. virens. Concurrently, one effector was found to elicit necrosis in tobacco. This study is the first to identify effector proteins within U. virens EVs that possess both immunosuppressive and immune-activating functions, providing important insights for elucidating the molecular mechanisms by which U. virens utilizes EVs to infect rice.

Poster #42

Exploring the Genome of Dunaliella tertiolecta for Nutritional Applications

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With increasing demand for sustainable and natural sources of nutraceuticals, pigments, and functional ingredients, microalgae have emerged as promising alternatives due to their rich metabolic diversity and comparatively low environmental footprint. Dunaliella tertiolecta is a candidate of interest because of its metabolic plasticity, rapid growth, and absence of a rigid cell wall, which aids in downstream processing. The alga is remarkable for its ability to concurrently produce a diverse range of high-value compounds including omega 3-rich lipids for aquaculture, potent antioxidants for supplements, and biofuels. Despite its potential, genomic insights into D. tertiolecta remain limited, to enable precise metabolic engineering, we are employing a genomics-driven approach aimed at assembling and annotating the genome of D. tertiolecta using Illumina NovaSeq and Oxford Nanopore sequencing technologies; followed by the identification of candidate genes and biosynthetic pathways involved in the production of nutritionally and industrially relevant metabolites, including fatty acids, carotenoids, and proteins. Hybrid genome sequencing has produced an assembly which is undergoing annotation. The insights generated from this work will strengthen the genomic resources available for D. tertiolecta and provide a foundation for enhancing the production of target compounds, thereby supporting the integration of microalgae into the food industry as sustainable biological factories.

Poster #43

SlWRKY80 Modulates Cold Tolerance by Recruiting Histone Deacetylase SlHDA1 to Repress SlCBF Pathway in Tomato

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WRKY transcription factors play pivotal roles in plant stress responses, and histone deacetylases (HDACs) regulate plant stress responses by modifying both histone and nonhistone proteins, yet the functional impact of nonhistone deacetylation remains unclear. Here, we demonstrate that SlWRKY80, partners with SlHDA1, a HDAC, to suppress the SlCBF pathway, thus negatively regulates cold tolerance in tomato. In detail, SlWRKY80 decreases cold tolerance, and mechanistic investigations showed that SlWRKY80 interacts with SlHDA1, a key regulator in cold response, thus inhibiting its transcriptional activity. Collectively, we uncover the SlWRKY80-SlHDA1-SlCBF signaling module as a central regulator enabling plants to adapt to cold stress. This work deciphers a key mechanism for environmental signal integration in plants, thereby offering a promising biotechnological approach for enhancing plant resilience against cold.

Poster #44

Phase Separation of MYB73 Regulates Seed Oil Biosynthesis in Arabidopsis

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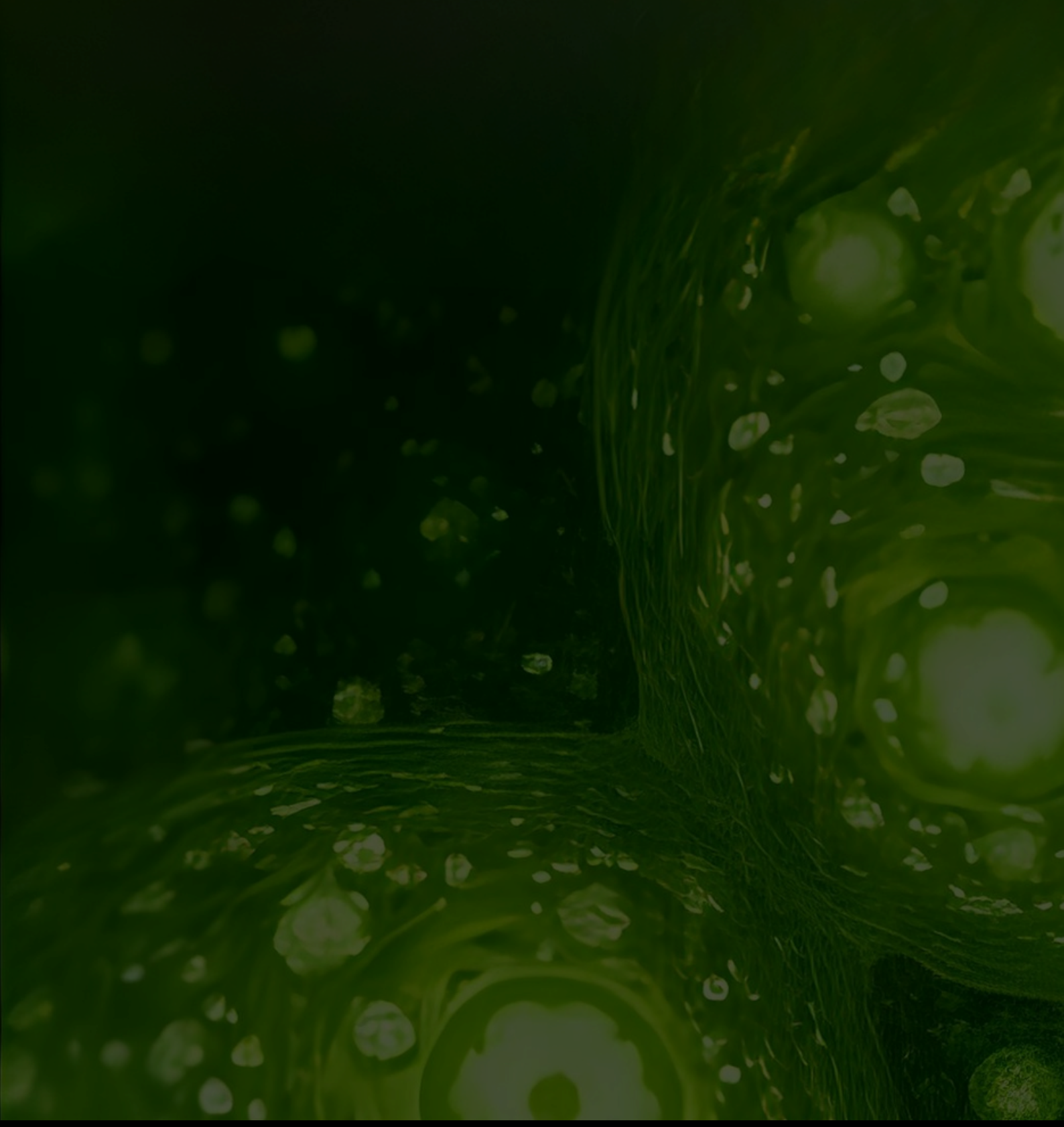
MYB family transcription factors play crucial roles in governing developmental processes, metabolic pathways, and responses to various stresses in plants. However, the involvement of MYBs in the regulation of fatty acid accumulation in seeds has remained largely unclear. Here, we demonstrated that transgenic Arabidopsis plants overexpressing MYB73 exhibit altered FATTY ACID ELONGATION1 (FAE1) expression, seed oil content, and seed fatty acid composition. Electrophoretic mobility shift assays showed that FAE1 is a direct target of MYB73, and functional assays revealed that MYB73 represses FAE1 promoter activity. Transcriptomic analysis of the MYB73-overexpressing plants detected significant changes in the expression of genes involved in fatty acid biosynthesis and triacylglycerol assembly. Furthermore, MYB73 expression was responsive to abscisic acid (ABA), and ABA-responsive element binding factor 2 directly bound to the ABA-responsive element in the MYB73 promoter to activate its expression. Additionally, we determined that MYB73 exhibits the hallmarks of an intrinsically disordered protein and forms phase-separated condensates with liquid-like characteristics, which are important in regulating target gene expression. Together, our findings suggest that MYB73 condensate formation likely fine-tunes seed oil biosynthesis.



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