

IPMB PROFILE 2026

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As the world confronts increasingly complex challenges, including climate change, emerging diseases, environmental sustainability, and the need to secure food production for a growing population, scientific advances in plant and microbial biology have become more important than ever. Plants and microorganisms play essential roles in agriculture, environmental adaptation, and many of the biological processes that sustain life, making them critical to understanding and addressing global challenges.

The Institute of Plant and Microbial Biology (IPMB), Academia Sinica, is dedicated to advancing fundamental knowledge of plant and microbial systems while exploring solutions to challenges that affect both society and the environment. Over the decades, the institute has contributed to a wide range of scientific discoveries, including plant genomics and breeding, plant-microbe interactions, microbial physiology, cellular regulation, and genome biology. These efforts have expanded our understanding of the biological mechanisms that govern growth, adaptation, and survival.

Today, IPMB brings together 22 research laboratories and several state-of-the-art core facilities that support a vibrant and collaborative research environment. The institute fosters interdisciplinary research and international partnerships while providing advanced infrastructure for scientific discovery. Through its research programs, training initiatives, and technological platforms, IPMB continues to cultivate scientific talent and contribute to the global advancement of plant and microbial biology.

IPMB at a Glance

Leadership



Erh-Min Lai
Director

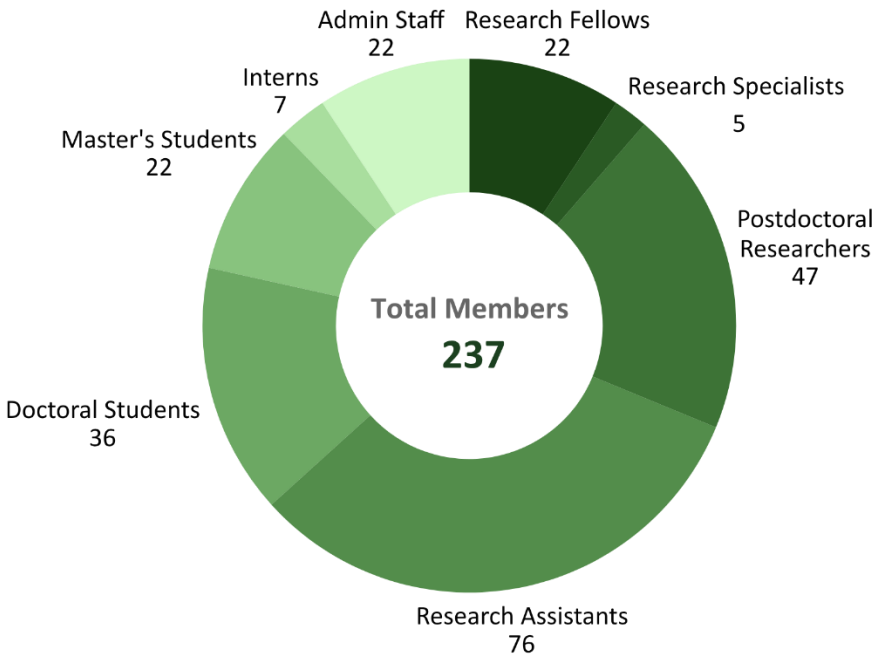


Chih-Horng Kuo
Deputy Director
Academic Affairs



Guang-Yuh Jauh
Deputy Director
Administrative Affairs

Personnel



(Data current as of June 30, 2026)

Education & Training

01 Taiwan International Graduate Program (TIGP) (https://tigp.sinica.edu.tw/)

02 Ph.D. Programs (NTU & NCU)

03 MS Programs (NTU, NCU, SCU & NCHU)

04 Undergraduate Internship Program (https://internship.ipmb.sinica.edu.tw)

05 High School Research Programs (https://hispj.project.sinica.edu.tw/)

Awards & Recognition (2022-2026)

INTERNATIONAL AWARDS		
YEAR	**RECIPIENT**	**AWARD / HONOR**
2026	Makoto Shirakawa	Young Investigator Award / JSPP
2024	Chih-Hang Wu	EMBO Global Investigator / EMBO
	Tuan-hua David Ho	Charles Reid Barnes Life Membership Award / ASPB
2023	Chin-Min Ho	EMBO Global Investigator / EMBO
	Chin-Min Ho	Women's Young Investigator Travel Award / ASPB
	Chih-Horng Kuo	Derrick Edward Award / IOM
2022	Chuan Ku	EMBO Global Investigator / EMBO
	Paul Verslues	Column Award for Distinguished Alumnus of the Division of Plant Science and Technology / University of Missouri
	Yue-Ie Caroline Hsing	Pioneer Award for Outstanding and Sustained Contributions to the Advancement of Rice Genome Biology / ISRFG

JSPP: Japanese Society of Plant Physiologist
EMBO: European Molecular Biology Organization
ASPB: American Society of Plant Biologists
IOM: International Organization for Mycoplasmology
ISRFG: International Symposium on Rice Functional Genomics

DOMESTIC AWARDS		
YEAR	**RECIPIENT**	**AWARD / HONOR**
2026	Guang-Yuh Jauh	Future Tech Award / NSTC
	Chih-Hang Wu	SEED – Young Scholars Program / NSTC
	Chin-Min Ho	27th Distinguished Young Women Award / The Ten Outstanding Young Women Association of ROC
	Tien-Shin Yu	Investigator Award / Academia Sinica
2025	Na-Sheng Lin	Outstanding Science and Technology Contribution Award / Executive Yuan
	Shu-Hsing Wu	Ho Chin-Tui Award / Ho Chin-Tui Foundation
	Tuan-hua David Ho	Lifetime Achievement Award / TSPB
	Chang-Hung Chou	Distinguished Alumnus / Institute of Plant Biology, NTU
	Chih-Hang Wu	Career Development Award / Academia Sinica
	Chuan Ku	International Outstanding Young Scholars (2030 Cross-Generation Young Scholars Program) / NSTC
	Chih-Hang Wu	Young Scholars' Creativity Award / Foundation for the Advancement of Outstanding Scholarship
2024	Ting-Ying Wu	Career Development Award / Academia Sinica
	Ooi-Kock Teh	Career Development Award / Academia Sinica
	Chuan-Chih Hsu	Technician Professional Award / Taiwan Society for Mass Spectrometry
	Chih-Hang Wu	Shang-Fa Yang Young Scientist Award / The Shang-Fa Yang Memorial Foundation
	Chih-Hang Wu	Outstanding Young Scholar Award / TSPB
	Tuan-hua David Ho	Distinguished Alumnus / Institute of Plant Biology, NTU
	Ming-Hsiun Hsieh	National Innovation Award / Institute for Biotechnology and Medicine Industry
	Shu-Hsing Wu	Frontier Science Research Program / NSTC
	Chuan Ku	Outstanding Teaching Award / NTU
2023	Na-Sheng Lin	Lifetime Achievement Award / TSPB

	Chin-Min Ho	Shang-Fa Yang Young Scientist Award / The Shang-Fa Yang Memorial Foundation
	Shu-Hsing Wu	Investigator Award / Academia Sinica
	Jian-Geng Chiou	Emerging Young Scholars (2030 Cross-Generation Young Scholars Program) / NSTC
2022	Wolfgang Schmidt	Investigator Award / Academia Sinica
	Chin-Min Ho	Career Development Award / Academia Sinica
	Yuki Nakamura	Outstanding Young Scholars Program / NSTC
	Chuan Ku	Outstanding Young Scholar Award / TSPB
	Yue-le Caroline Hsing	Lifetime Achievement Award / TSPB
	Shih-Long Tu	Outstanding Research Award / NSTC
	Chih-Hang Wu	Emerging Young Scholars (2030 Cross-Generation Young Scholars Program) / NSTC
	Yuki Nakamura	Outstanding Research Award / NSTC

NSTC: National Science and Technology Council **TSPB**: Taiwan Society of Plant Biologists
NTU: National Taiwan University

Academic Advisory Committee (2026-2028)



Blake Meyers (convener)
Director / Distinguished Professor
Genome Center / Department of Plant Sciences,
University of California, Davis, USA

Julia Bailey-Serres
Distinguished Professor of Genetics
Director
UC Riverside, USA





Susan Golden
Distinguished Professor
Chancellor's Associates Chair
UC San Diego, USA

David Jackson
Professor
Cold Spring Harbor Laboratory, USA





Robert Last
University Distinguished Professor
Barnett Rosenberg Chair
Michigan State University, USA



Jan Leach
Associate Dean for Research, College of Agricultural Sciences
Distinguished Professor,
Colorado State University, USA

Takayuki Kohchi
Professor, Graduate School of Biostudies,
Division of Integrated Life Science,
Kyoto University, Japan





Nick Talbot
Group leader and Executive Director
The Sainsbury Laboratory, UK

Dolf Weijers
Professor, Wageningen University
Netherlands





Shin-Han Shiu
Professor, Department of Plant Biology
Michigan State University, USA

ABOUT THE INSTITUTE

Evolution of IPMB

For more than eight decades, the Institute has evolved alongside the rapid advancement of biological science. Since its establishment as the Institute of Botany in 1944, the institute has continuously expanded its scientific scope, building upon its strong foundation in plant science while embracing new advances in genetics, genomics, microbiology, and systems biology. In 2005, to better reflect the Institute's research focus, the name was officially changed to the Institute of Plant and Microbial Biology (IPMB).

Throughout its history, the institute has adapted to emerging scientific questions and technological breakthroughs. Early research in plant taxonomy, cytogenetics, physiology, crop improvement, and microbiology helped establish a strong foundation for biological research in Taiwan. As biology entered the molecular era, new disciplines and technologies opened opportunities to explore life at increasingly deeper levels, from genes and cells to organisms and biological networks.

Today, IPMB brings together expertise spanning plant biology, microbial biology, genomics, cell biology, bioinformatics, and systems biology, fostering research that ranges from fundamental biological mechanisms to environmental adaptation and host-microbe interactions. While research tools and scientific questions have evolved dramatically over the decades, the institute's commitment remains steadfast: to deepen our understanding of living systems and generate knowledge that contributes to science, agriculture, environmental sustainability, and human well-being.

Key Milestones

1944

Institute of Botany Established

The Institute of Botany was officially established as an independent institute of Academia Sinica.



1962

Reestablished in Taiwan

The Institute of Botany was officially reestablished in Taiwan, marking the beginning of a new chapter in plant science research.

1974

Construction of Hsien-Wen Li Memorial Hall

Construction of a new research building began in summer 1974 with support from the National Science Council and was completed in 1975.



2005

Renamed IPMB

The institute was renamed the Institute of Plant and Microbial Biology to reflect its expanded research scope and interdisciplinary focus.

2009

Agricultural Technology Building Completed

The Agricultural Technology Building was completed, expanding research and core facility space.



2024

Celebrating the 80th Anniversary

Celebrating 80 years of scientific excellence and looking ahead to a future of discovery and impact.

Research Scope

IPMB research activities are organized into four major areas:

▶ **Chromosome, Genome, and Systems Biology**

Investigating genetic information, recombination mechanisms, and gene regulation in plants and microorganisms through multi-dimensional omics approaches, advanced microscopy, image analysis, and data-driven research.

▶ **Cell and Developmental Biology**

Exploring cellular functions, signal transduction, metabolism, growth regulation, and developmental processes in plants and microorganisms.

▶ **Plant-Environment Interactions**

Understanding how plants perceive and respond to environmental factors such as light, temperature, drought, nutrients, and other stress conditions.

▶ **Plant and Environmental Microbiology**

Studying microbial diversity, evolution, pathogenicity, plant immunity, and plant-microbe interactions to better understand microbial functions in natural and agricultural environments.

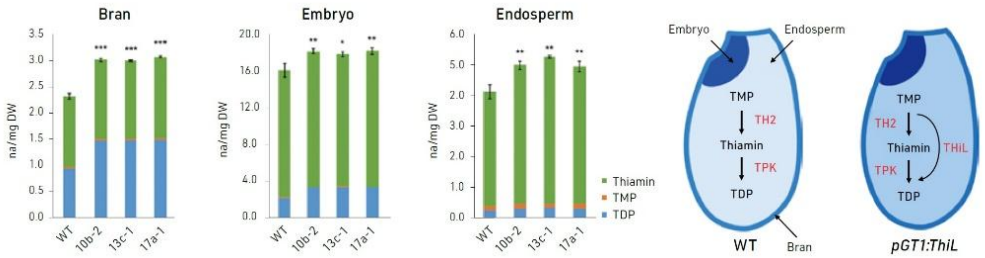
RESEARCH HIGHLIGHTS

2023 - 2025

Ectopic Expression of a Bacterial Thiamin Monophosphate Kinase Enhances Vitamin B1 Biosynthesis in Plants

Yi-Hsin Chung, Ting-Chieh Chen, Wen-Ju Yang, Soon-Ziet Chen, Jia-Ming Chang, Wei-Yu Hsieh and Ming-Hsiun Hsieh*

In plants, thiamin monophosphate (TMP) synthesized in the vitamin B1 biosynthetic pathway is first converted to thiamin by a phosphatase, which is then pyrophosphorylated to the bioactive thiamin diphosphate (TDP). In contrast, bacteria use a TMP kinase encoded by ThiL to phosphorylate TMP to TDP directly. Ectopic expression of E. coli ThiL driven by an endosperm-specific GLUTELIN1 (GT1) promoter enhanced TDP biosynthesis in rice. Total vitamin B1 increased by approximately 25-30% in the polished and unpolished seeds of the pGT1:ThiL transgenic rice compared to the wild type. These results suggest that genetic engineering of a bacterial vitamin B1 biosynthetic gene downstream of TMP can enhance vitamin B1 production in rice.



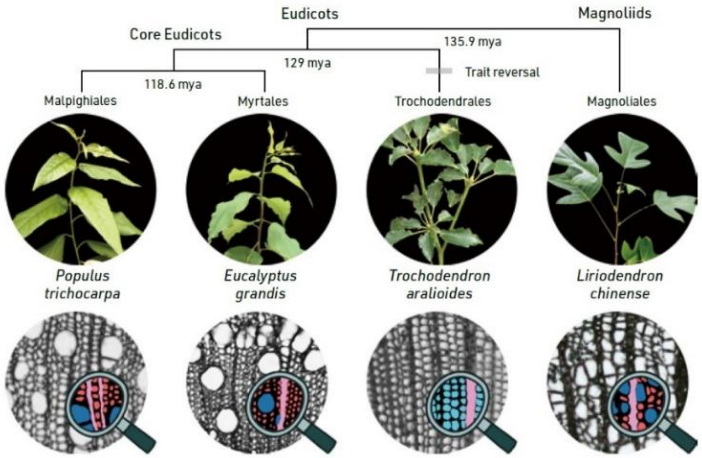
The *pGT1: ThiL* transgenic rice has increased vitamin B1 in the seed compared with the wild type (WT). The color gradient in the schematic diagram depicts the relative vitamin B1 content in the seed. TMP, thiamin monophosphate; TDP, thiamin diphosphate; TH2, TMP phosphatase; TPK, thiamin pyrophosphokinase; ThiL, TMP kinase.

The Plant Journal **117**, 1330-1343 (2024). DOI: 10.1111/tpj.16563

Development and Evolution of Xylem: the Most Abundant Tissue on Earth

Chia-Chun Tung, Shang-Che Kuo, Chia-Ling Yang, Jhong-He Yu, Chia-En Huang, Pin-Chien Liou, Ying-Hsuan Sun, Peng Shuai, Jung-Chen Su, Chuan Ku* and Ying-Chung Jimmy Lin*

Xylem is a plant tissue for mechanical support and water transportation, as well as a key natural resource and carbon sink. To understand xylem formation, our team analyzed single-cell transcriptomes of four tree species representing divergent lineages of flowering plant (angiosperm) evolution. The developmental trajectories of ray cells are highly conserved across angiosperms. The tracheids of *Trochodendron aralioides* (a native Taiwanese species without libriform fibers and vessel elements) exhibit strong transcriptomic similarity to vessel elements rather than libriform fibers of other eudicots. The results provide a cell atlas for xylem development and new perspectives for plant tissue evo-devo research.



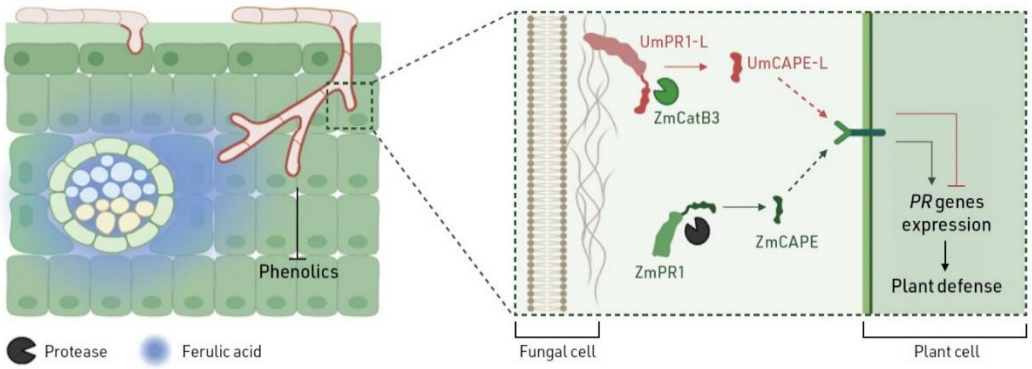
Above Four tree species that diverged over 100 million years ago. **Below** Cross-section of the xylem. The development of ray cells (pink) is more conservative than that of vessels (blue) and fibers (red). The tracheids of *T. aralioides* (light blue) are developmentally more similar to vessels.

Genome Biology **24**, 3 (2023). DOI: 10.1186/s13059-022-02845-1

Ustilago maydis PR-1-like Protein Has Evolved Two Distinct Domains for Dual Virulence Activities

Yu-Han Lin, Meng-Yun Xu, Chuan-Chih Hsu, Florensia Ariani Damei, Hui-Chun Lee, Wei-Lun Tsai, Cuong V. Hoang, Yin-Ru Chiang and Lay-Sun Ma*

Our discovery has elucidated the role of structurally conserved proteins in the ongoing co-evolutionary struggle between fungal pathogens and their host plants: the defensive role of plant PR1 and the virulence role of fungal PR1-like (PR1-L) protein. *U. maydis* covers its hyphae with PR1-L to resist toxic maize phenolics and hijacks the host protease CatB3 to release a mimetic peptide from PR1-L, counteracting the immunity-triggering peptide of host PR1s. This suppresses plant immunity and facilitates fungal colonization. These findings address gaps in our understanding of fungal parasitism in crops and the co-evolutionary dynamics of PR1-L and PR1 proteins in pathogens and their hosts, offering opportunities for strategic enhancements in crop defense against fungal pathogens.

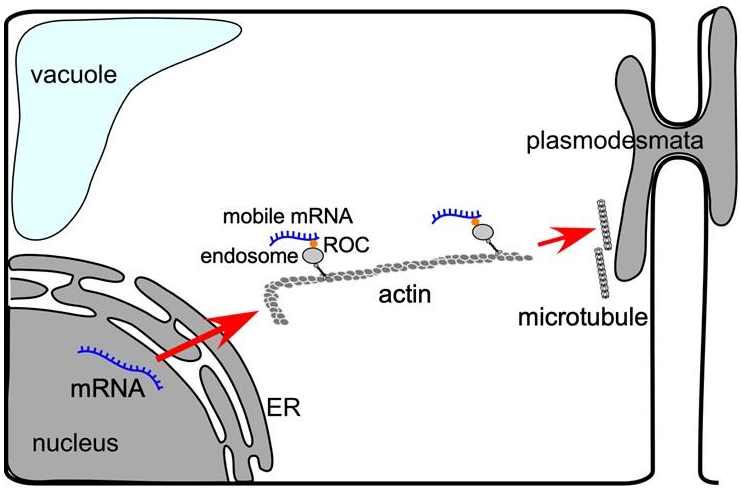


Nature Communications **14**, 5755 (2023). DOI: 10.1038/s41467-023-41459-4

A ROCing Ride to Plasmodesmata: The Organelle Hitchhiking of Mobile mRNA Transport

Kai-Ren Luo, Nien-Chen Huang, Yu-Hsin Chang, Yu-Wen Jan and Tien-Shin Yu*

In plants, mobile mRNAs travel between cells through intercellular pores, plasmodesmata, and a long distance via phloem in the vascular tissue, to modulate plant development systemically. However, how mobile mRNAs target plasmodesmata to initiate cell-to-cell movement is unclear. By using mRNA live-imaging system, we unveiled the machinery supporting the intracellular transport of mobile mRNAs. We identified endosomal RNA-binding proteins ROCs specifically bridge mobile mRNAs onto the surface of endosomes. The organelle-bound mobile mRNA complex co-transports with endosomes through cytoskeleton networks toward plasmodesmata. This study reveals a hitchhiking strategy is used to direct mobile mRNAs for intercellular delivery.

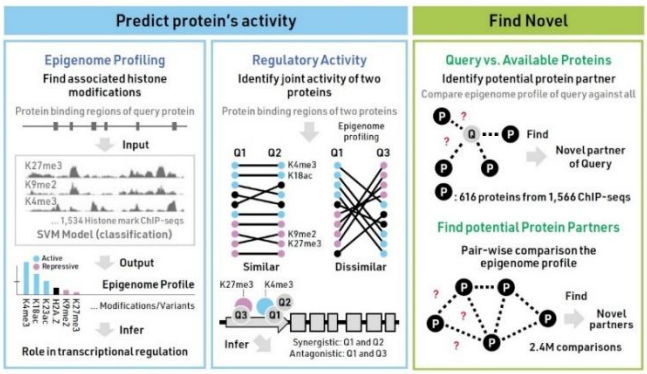


Nature Plants **10(1)**, 161-171 (2024). DOI: 10.1038/s41477-023-01597-5

Predicting Protein Synergistic Effect in *Arabidopsis* Using Epigenome Profiling

Chih-Hung Hsieh, Ya-Ting Sabrina Chang, Ming-Ren Yen, Jo-Wei Allison Hsieh and Pao-Yang Chen*

Understanding how regulatory proteins interact with histone modifications is essential for decoding the complex mechanisms of gene expression in plants. Although ChIP-seq has enabled genome-wide mapping of histone marks, it remains difficult to predict how specific proteins contribute to gene regulation or cooperate with other factors—largely due to the lack of integrative, predictive tools. To address this, we developed QHistone (https://qhistone.paoyang.ipmb.sinica.edu.tw), a machine learning-driven platform based on 1,534 ChIP-seq datasets covering 27 histone modifications in *Arabidopsis thaliana*. QHistone allows users to predict the epigenomic profile of any regulatory protein, infer its potential function, identify synergistic or antagonistic relationships between protein pairs, and discover previously unknown co-regulators across the genome. By also integrating gene expression data from various plant tissues, the platform enables users to validate predictions in a biologically meaningful context. This research not only fills a long-standing gap in plant epigenetics by providing a powerful predictive framework, but also offers a valuable resource for the broader scientific community. QHistone represents a significant breakthrough in computational epigenomics, enhancing our ability to understand gene regulation at a systems level and advancing functional genomics in plant biology.



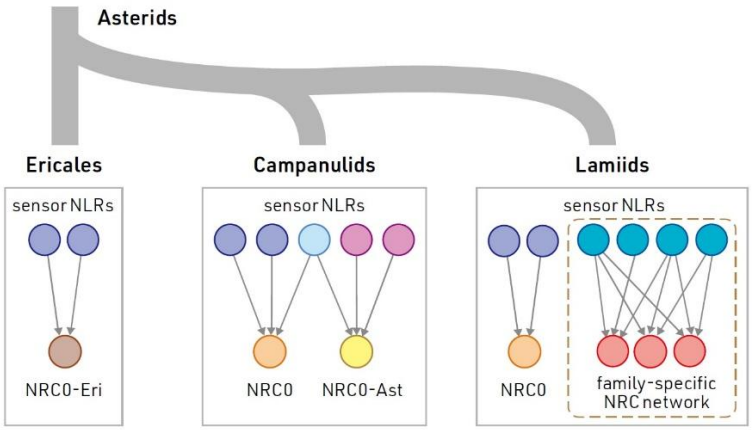
Nature Communications **15(1)**, 9160 (2024). DOI: 10.1038/s41467-024-53565-y

The Expansion of a Complex Plant Immune Receptor Network

Foong-Jing Goh, Ching-Yi Huang and Chih-Hang Wu*

In nature, plants are continuously exposed to pathogenic microbes that threaten crop productivity and global food security. To protect themselves, plants have evolved immune receptors called NLRs. In solanaceous species, these receptors form a complex “NRC immune network” that acts cooperatively to fend off pathogens. However, the evolution and function of such networks in other plant lineages remain poorly understood.

Through comparative genomic analyses across diverse asterids species, we found that the NRC network has undergone significant expansion in the lamiids, while it remains relatively simple in other groups. Notably, some NRCs exhibit partial functional compatibility across species, whereas others do not. These insights highlight the evolutionary diversification of plant immune systems and provide a critical foundation for future work in disease-resistance breeding and interspecies gene transfer.

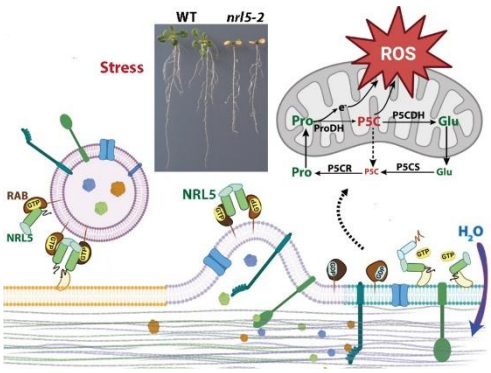


The Plant Cell **36(9)**, 3399-3418 (2024). DOI: 10.1093/plcell/koae179

The Nonphototrophic Hypocotyl 3 (NPH3) Domain Protein NRL5 Is a Trafficking-Associated GTPase Essential for Drought Resistance

Neha Upadhyay-Tiwari , Xin-Jie Huang, Yi-Chen Lee, Shashi Kant Singh, Chuan-Chi Hsu, Shih-Shan Huang, and Paul E. Verslues*

Plant productivity is impaired by even small decreases in water availability during drought. While this is of increasing global concern because of climate change, our ability to improve plant stress resistance is limited by a lack of understanding of how plant cells detect and respond to water limitation. The Verslues laboratory found that mutation of the Non-Phototrophic Hypocotyl3 (NPH3)-domain protein NRL5 causes plants to become hypersensitive to drought stress because of mis-regulated proline metabolism. The NPH3-domain is a protein feature that is unique to plants and was of unknown function despite the fact that NPH3-domain proteins have been implicated in important signaling pathways such as phototropism and hormone response. We demonstrated that NRL5, and other NPH3-domain proteins, have GTPase activity despite having no similarity to known GTPases. The NPH3 domain was required for NRL5 to interact with and control the function of proteins involved in vesicle trafficking. Trafficking interactions are in turn important for NRL5 polar localization. These results demonstrate that NPH3 proteins constitute a previously unsuspected layer of regulation controlling intracellular trafficking and cellular polarization in plants. The results also demonstrate that correct regulation of proline metabolism is critically important for drought resistance.

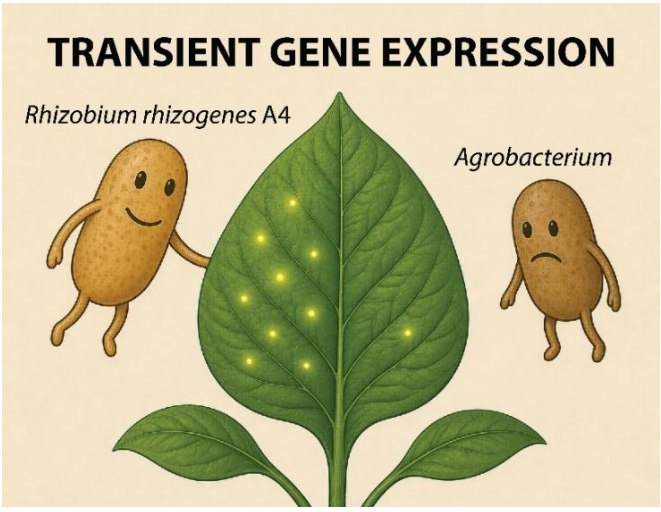


Science Advances, **10(32)**, eado5429.
DOI: 10.1126/sciadv.ado5429

A New Tool for Plant Gene Research: *Rhizobium rhizogenes* A4 Shows Superior Performance in Gene Delivery

Juan Carlos Lopez-Agudelo, Foong-Jing Goh, Sopio Tchabashvili, Yu-Seng Huang, Ching-Yi Huang, Kim-Teng Lee, Yi-Chieh Wang, Yu Wu, Hao-Xun Chang, Chih-Horng Kuo, Erh-Min Lai, and Chih-Hang Wu*

Agroinfiltration is a widely used technique in plant gene research. It involves using bacteria to temporarily introduce foreign genes into plant leaves, allowing scientists to observe how these genes function within the plant quickly. Traditionally, the most commonly used bacterium for this purpose has been *Agrobacterium tumefaciens*. However, our recent research has revealed that a strain of *Rhizobium rhizogenes*, a relative of *A. tumefaciens*, performs even better. This breakthrough provides plant scientists with a more flexible and efficient tool for gene function studies. It holds particular promise for research and breeding in solanaceous crops, accelerating crop improvement and promoting sustainable agriculture.

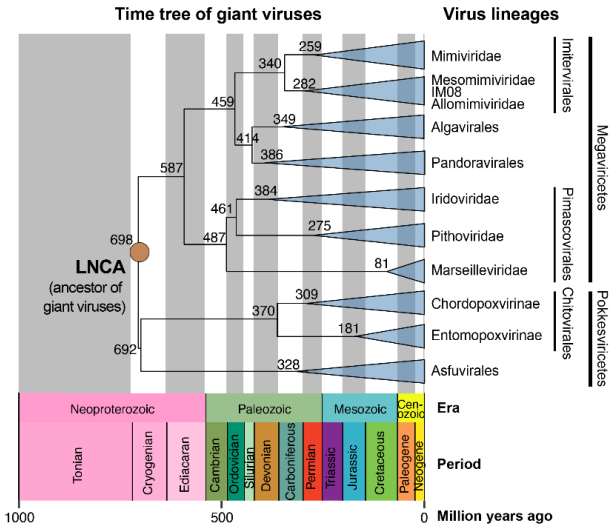


Plant Biotechnology Journal **24(1)**, 131-144 (2026). DOI:10.1111/pbi.70083

New Dating Method Reconstructs the Evolutionary History of Giant Viruses

Hwee Sze Tee and Chuan Ku*

Viruses have important impacts on human health, food security, and the Earth's environment. To better understand when viruses originated, we developed a host-calibrated dating method and used it to infer the evolutionary timescale of giant viruses (phylum *Nucleocytoviricota*). These viruses possess large DNA genomes and infect a wide variety of eukaryotic organisms. We found that *Nucleocytoviricota* originated in an era of significant rise in atmospheric oxygen on Earth, which may have enabled giant viruses to harness more mitochondrial energy for their replication. Although giant viruses originated much later than eukaryotes, they have spread across all major eukaryotic lineages over the last hundreds of millions of years through extensive host shifts (from amoebae to animals, algae, fungi, and other organisms), resulting in their exceptional host diversity.



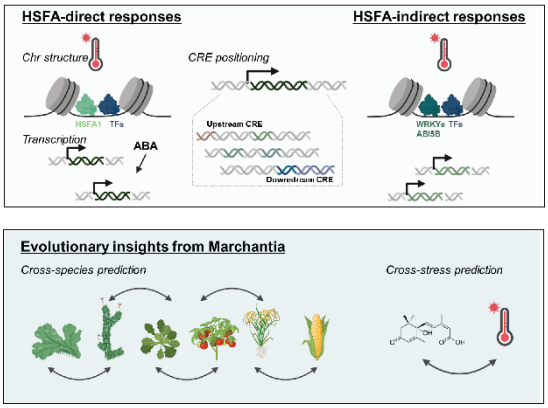
A time tree of giant viruses (*Nucleocytoviricota*) shows the divergence times of viral lineages in the last billion years. The last *Nucleocytoviricota* common ancestor (LNCA) may have infected unicellular amoebae, while its descendants later spread to diverse lineages of eukaryotes.

Molecular Biology and Evolution **42(2)**, msaf033 (2025).
DOI: 10.1093/molbev/msaf033

Conserved HSFA1-Dependent Chromatin Dynamics Drive Heat Stress Responses in Plants

Ming-Ren Yen, Kuan-Hung Lin, Lavakau Thalimaraw, Hsiu-Ru Yang, Kulaporn Boonyaves, Chia-Yi Cheng and Ting-Ying Wu*

Plants, like all living organisms, must respond quickly when their environment becomes stressful, such as during extreme heat. One way they do this is by changing how their DNA is packaged, which helps turn important genes on or off. In this study, we found that a transcription factor called HSFA1 plays a central role in helping plants respond to heat stress. Using both a simple land plant and a flowering plant, we showed that HSFA1 controls which parts of the DNA become accessible during heat stress. This mechanism is highly conserved and is also found in animals, including humans. We also discovered that some plant hormones, such as ABA, influence heat-responsive genes without changing DNA structure. By combining these data with machine learning, we were able to predict how genes respond to stress across species. Our findings reveal a shared and ancient strategy that living organisms use to survive in hot environments.



The graphic summarizes the main findings of this study. We found that (I) HSFA1 is required for HS-induced chromatin remodeling, while ABA did not induce genome-wide chromatin changes. (II) MpABI5B and MpWRKY10 are required for MpHSFA1-parallel HS regulation. (III) HSFA1 is required for the accessibility of HS-related CREs in *Marchantia*. Additionally, we demonstrated that by using information from CREs, it is possible to predict gene expression at the transcriptional level across plant species and stress types.

Cell Reports **44(12)**, 116714 (2025). DOI: 10.1016/j.celrep.2025.116714

FACULTY & RESEARCH



Pao-Yang Chen

Research Fellow

Email: paoyang@gate.sinica.edu.tw

Education

D. Phil., Statistics (Computational Biology), Oxford University, UK (2008)

Professional Experience

Visiting Professor**,** UCLA-DOE Institute for Genomics and Proteomics, Los Angeles, California, USA

Research Overview

#Epigenomics #Bioinformatics #Genomics #Structural Bioinformatics

My research focuses on developing computational and statistical approaches to understand how epigenomic information regulates gene expression and cell state. A major challenge in epigenomics is that genome-wide datasets are rapidly increasing, but the functional meaning of epigenomic patterns is still difficult to interpret. This is especially true because DNA methylation, histone modifications, chromatin regulators, and developmental context often act together in a complex and combinatorial manner.

To address this challenge, I develop predictive epigenomics frameworks that convert large-scale sequencing data into quantitative models of regulatory function. My work includes MeH, a method that captures DNA methylation heterogeneity beyond average methylation levels, and QHistone, a framework that predicts chromatin regulatory function from epigenomic profiles. Using these approaches, I have studied transformation-induced epigenomic changes in rice, combinatorial chromatin regulation in *Arabidopsis*, and developmental timing in mammalian systems. Together, these studies show that epigenomic variation is

not random, but structured, interpretable, and predictive across species. Moving forward, I aim to develop AI-based methods that identify minimal and interpretable rules of epigenomic regulation, with the long-term goal of predicting and controlling cell state.

Selected Publications

Chatterjee D, Zhang Z, Lin PY, Wang PH, Sidhu GK, Yennawar NH, Hsieh JA, Chen PY, Song R, Meyers BC, Chopra S. Maize *unstable factor for orange1* encodes a nuclear protein that affects redox accumulation during kernel development. *Plant Cell.* 2024 Dec 23;37(1):koae301. doi: 10.1093/plcell/koae301.

Hsieh CH, Chang YS, Yen MR, Hsieh JA, Chen PY. Predicting protein synergistic effect in *Arabidopsis* using epigenome profiling. *Nat Commun.* 2024 Oct 24;15(1):9160. doi: 10.1038/s41467-024-53565-y.

Hsieh JA, Yen MR, Hung FY, Wu K, Chen PY. Epigenetic factors direct synergistic and antagonistic regulation of transposable elements in *Arabidopsis*. *Plant Physiol.* 2024 Nov 4;196(3):1939-1952. doi: 10.1093/plphys/kiae392.

Lin PY, Chang YT, Huang YC, Chen PY. Estimating genome-wide DNA methylation heterogeneity with methylation patterns. *Epigenetics Chromatin*. 2023 Nov 09; 16(1): 44. doi:10.1186/s13072-023-00521-7.

Hsieh JA, Chang P, Kuang LY, Hsing YC, Chen PY. Rice transformation treatments leave specific epigenome changes beyond tissue culture. *Plant Physiol.* 2023 Sep 22;193(2):1297-1312. doi: 10.1093/plphys/kiad382.

Kuo FC, Huang YC, Yen MR, Lee CH, Hsu KF, Yang HY, Wu LW, Lu CH, Hsu YJ, Chen PY. Aberrant overexpression of *HOTAIR* inhibits abdominal adipogenesis through remodelling of genome-wide DNA methylation and transcription. *Mol Metab.* 2022 Jun:60:101473. doi: 10.1016/j.molmet.2022.101473.



Jian-Geng Chiou

Assistant Research Fellow

Email: jchiou@as.edu.tw

Education

Ph.D., Duke University, USA (2019)

Professional Experience

Postdoctoral Researcher, University of California San Diego, USA

Research Overview

#Cell polarity #Biofilm development #Pattern formation
#Turing systems #Reaction-diffusion #Mathematical modeling
#Microbial development #Biophysics

The Chiou Lab studies how pattern formation principles generate developmental organization in microbial systems. The lab combines live-cell microscopy, quantitative analysis, and mathematical modeling to examine how molecular components self-organize across scales, with emphasis on cases where shared mathematical rules transcend conventional biological boundaries.

One major direction investigates cell polarity in Ascomycete fungi. Building on mass-conserved Turing and reaction-diffusion frameworks, the lab asks how conserved polarity machinery can support distinct growth modes, including unipolar budding, multipolar growth, equalization, and splitting of polarity sites.

A second direction focuses on Bacillus subtilis biofilm development. Biofilms can behave as multicellular communities, producing concentric segmentation patterns through clock-and-wavefront mechanisms that scale with growth conditions and guide cellular differentiation. Current questions center on how individual

molecular clocks synchronize to generate sharp collective patterns under live imaging.

Together, these projects use microbial systems to define general biophysical principles of development, polarity, robustness, and scalable patterning.

Selected Publications

Chiou JG, Chou TK, Garcia-Ojalvo J, Süel GM. Intrinsically robust and scalable biofilm segmentation under diverse physical growth conditions. *iScience*. 2024 Nov 13;27(12):111386. doi: 10.1016/j.isci.2024.111386.

Chou KT, Lee DD, Chiou JG, Galera-Laporta L, Ly S, Garcia-Ojalvo J, Süel GM. A segmentation clock patterns cellular differentiation in a bacterial biofilm. *Cell*. 2022 Jan 6;185(1):145-157.e13. doi: 10.1016/j.cell.2021.12.001

Chiou JG, Moran KD, Lew DJ. How cells determine the number of polarity sites. *Elife*. 2021 Apr 26:10:e58768. doi: 10.7554/eLife.58768.

Chiou JG, Ramirez SA, Elston TC, Witelski TP, Schaeffer DG, Lew DJ. Principles that govern competition or co-existence in Rho-GTPase driven polarization. *PLoS Comput Biol*. 2018 Apr 12;14(4):e1006095. doi: 10.1371/journal.pcbi.1006095.

Chiou JG, Balasubramanian MK, Lew DJ. Cell polarity in yeast. *Annu Rev Cell Dev Biol*. 2017 Oct 6:33:77-101. doi: 10.1146/annurev-cellbio-100616-060856.

Honors and Awards

Emerging Young Scholar Award, 2030 Cross-generation Young Scholars Program, Ministry of Science and Technology, Taiwan



Hsiu-An Chu

Associate Research Fellow

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Education

Ph.D., Biochemistry, University of California, Riverside, USA (1994)

Professional Experience

Postdoctoral Researcher, University of California, Riverside, USA

Postdoctoral Researcher, Michigan State University, USA

Research Overview

#Cyanobacteria #Photosynthesis #Comparative Genomics #Extremophile

As global warming and environmental extremes intensify, understanding the mechanisms that enable life to thrive under stress is increasingly important. Cyanobacteria are among the most resilient photosynthetic organisms, capable of sustaining oxygenic photosynthesis under extreme heat, high salinity, and desiccation. Our research focuses on the molecular and evolutionary mechanisms underlying photosynthetic adaptation to extreme environments. Major contributions include (1) elucidating the molecular mechanisms of photosynthetic water oxidation, (2) defining the structural and photoprotective functions of cytochrome b_{559} in Photosystem II, and (3) uncovering novel cyanobacterial diversity and adaptation strategies in Taiwan's unique geothermal and marine ecosystems. These studies provide fundamental insights into photosynthetic resilience and adaptation under environmental extremes.

Our current research focuses on newly identified thermophilic and thermotolerant cyanobacteria, with particular emphasis on the molecular mechanisms governing phototaxis, photoprotection, and thermo-saline

adaptation. Through the integration of physiology, functional genomics, and biochemistry, we aim to discover novel strategies that enable cyanobacteria to thrive under environmental extremes while developing biological resources for carbon capture and sustainable biotechnology.

Selected Publications

Chu HA. Fourier transform infrared difference spectroscopy for studying the molecular mechanism of photosynthetic water oxidation. *Front Plant Sci*. 2013 May 21:4:146. doi: 10.3389/fpls.2013.00146.

Cheng YI, Chou L, Chiu YF, Hsueh HT, Kuo CH, Chu HA. Comparative genomic analysis of a novel strain of Taiwan hot-spring cyanobacterium *Thermosynechococcus* sp. CL-1. *Front Microbiol*. 2020 Jan 31:11:82. doi: 10.3389/fmicb.2020.00082.

Chiu YF, Fu HY, Skotnicová P, Lin KM, Komenda J, Chu HA. Tandem gene amplification restores photosystem II accumulation in cytochrome b_{559} mutants of cyanobacteria. *New Phytol*. 2022 Jan;233(2):766-780. doi: 10.1111/nph.17785.

Chiu YF, Chu HA. New structural and mechanistic insights into functional roles of cytochrome b_{559} in photosystem II. *Front Plant Sci*. 2022 Jun 8:13:914922. doi: 10.3389/fpls.2022.914922.

Cheng YI, Lin YC, Leu JY, Kuo CH, Chu HA. Comparative analysis reveals distinctive genomic features of Taiwan hot-spring cyanobacterium *Thermosynechococcus* sp. TA-1. *Front Microbiol*. 2022 Aug 11:13:932840. doi: 10.3389/fmicb.2022.932840.

Chen CN, Lin KM, Lin YC, Chang HY, Yong TC, Chiu YF, Kuo CH, Chu HA. Comparative genomic analysis of a novel heat-tolerant and euryhaline strain of unicellular marine cyanobacterium *Cyanobacterium* sp. DS4 from a high-temperature lagoon. *BMC Microbiol*. 2025 May 8;25(1):279. doi: 10.1186/s12866-025-03993-7.



Chin-Min Kimmy Ho

Associate Research Fellow

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Education

Ph.D., Biochemistry and Molecular Biology, University of California, Davis, USA (2011)

Professional Experience

Postdoctoral Researcher, Stanford University, USA

Research Overview

#Leaf development #Plant cell biology

My research centers on a simple question: can we build a better leaf by understanding how epidermal cell fate decisions, cuticle formation, and tissue architecture are coordinated during development? I use the leaf epidermis as a model system because cell state transitions can be directly linked to tissue organization and physiological performance.

I first investigated cell fate regulation in the *Arabidopsis* stomatal lineage and showed that stomatal lineage ground cells (SLGCs) occupy a poised state between proliferation and differentiation, revealing how developmental plasticity is encoded at the molecular level. I subsequently identified a chromatin-associated factor, HDL, that regulates heterochromatin organization and cell fate decisions, establishing a link between nuclear architecture and developmental trajectories.

I then explored how epidermal differentiation influences tissue function. By uncovering a regulatory connection between cuticle formation and stomatal development through MYB16, I demonstrated that epidermal mechanics and

biochemical signaling are tightly integrated during leaf development. Extending this work to the tissue scale, I showed that stomatal patterning is coordinated with substomatal cavity formation and mesophyll organization, contributing to improved water-use efficiency and environmental adaptation.

Together, these studies connect chromatin organization, cell fate decision, tissue architecture, and the leaf function across multiple biological scales.

Selected Publications

Tsai MY, Kuan C, Guo ZL, Yang HA, Chung KF, Ho CK. Stomatal clustering in *Begonia* improves water use efficiency by modulating stomatal movement and leaf structure. *Plant Environ Interact*. 2022 Jul 4;3(4):141-154. doi: 10.1002/pei3.10086.

Yang SL, Tran N, Tsai MY, Ho CK. Misregulation of *MYB16* expression causes stomatal cluster formation by disrupting polarity during asymmetric cell divisions. *Plant Cell*. 2022 Jan 20;34(1):455-476. doi: 10.1093/plcell/koab260.

Ho CK, Bringmann M, Oshima Y, Mitsuda N, Bergmann DC. Transcriptional profiling reveals signatures of latent developmental potential in *Arabidopsis* stomatal lineage ground cells. *Proc Natl Acad Sci USA*. 2021 Apr 27;118(17):e2021682118. doi: 10.1073/pnas.2021682118.

Honors and Awards

2026 27th Distinguished Young Women Award, The ten outstanding young women association of R.O.C.

2024 EMBO Global Investigator Network.

2023 SHANG-FA YANG Outstanding Young Scientist Award.

2023 American Society of Plant Biologists (ASPB) Women's Young Investigator Travel Award (WYITA), Plant Biology 2023, Savannah, Georgia, USA.

2022 Academia Sinica Career Development Award.

2021 Outstanding Young Scholar Award, Taiwan Society of Plant Biologists (TSPB).



Ming-Hsiun Hsieh

Research Fellow

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Education

Ph.D., Biology, New York University, USA (1998)

Professional Experience

Postdoctoral Research Fellow, Department of Molecular Biology, Massachusetts General Hospital, Boston, USA

Research Overview

#Plant nutrition #Glutamine #Glutamate #Signal transduction

Glutamine (Gln) is the first organic nitrogen (N) compound synthesized during primary N assimilation. While the metabolic functions of N compounds have been extensively characterized, the signaling roles of Gln in plants remain poorly understood. We demonstrated that extracellular Gln elicits defense responses in rice and *Arabidopsis*, in contrast to the effects of NH_4NO_3 treatments (Kan et al., 2015; Liao et al., 2024). These observations suggest that Gln functions not merely as a metabolic intermediate but also as a signaling molecule that modulates plant defense. We hypothesize that Gln is perceived by a specific receptor located on the plasma membrane, which subsequently activates downstream signaling cascades to reprogram gene expression or interacts with defense hormones to modify growth and defense processes (Fig. 1). The objective of our research is to elucidate the molecular mechanisms underlying Gln perception and signaling in plants.

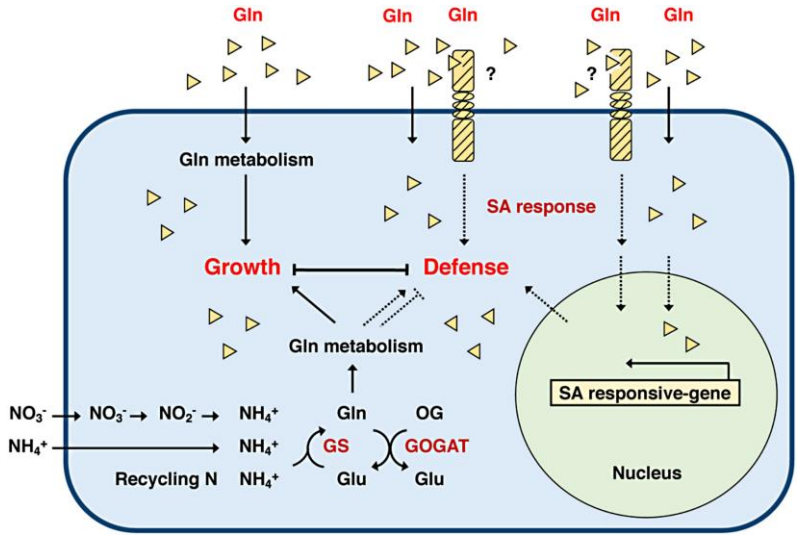


Fig. 1 A working model of Gln-induced defense in plants.

We hypothesize that Gln receptors (hatched diagrams) on the plasma membrane can detect extracellular Gln, activate the SA pathway, and trigger the plant's defense responses. GS, Gln synthetase; GOGAT, Gln:2-oxoglutarate aminotransferase; SA, salicylic acid.

Selected Publications

Kan CC, Chung TY, Juo YA, Hsieh MH. Glutamine rapidly induces the expression of key transcription factor genes involved in nitrogen and stress responses in rice roots. *BMC Genomics*. 2015 Sep 25;16(1):731. doi: 10.1186/s12864-015-1892-7.

Lee KT, Liao HS, Hsieh MH. Glutamine metabolism, sensing, and signaling in plants. *Plant Cell Physiol*. 2023 Dec 21;64(12):1466-1481. doi: 10.1093/pcp/pcad054.

Liao HS, Lee KT, Chung YH, Chen SZ, Hung YJ, Hsieh MH. Glutamine induces lateral root initiation, stress responses, and disease resistance in *Arabidopsis*. *Plant Physiol*. 2024 Jun 28;195(3):2289-2308. doi: 10.1093/plphys/kiae144.

Honors and Awards

Presidential Scholar, Academia Sinica, Taipei, Taiwan (2025-2028)

National Innovation Award, Research Center for Biotechnology and Medicine Policy, Taiwan (2024)



Yu-Ying Hsieh

Assistant Research Fellow

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Education

Ph.D., Molecular & Cellular Biology, Harvard University, USA (2019)

Professional Experience

Postdoctoral Fellow, Fred Hutchinson Cancer Center, USA

Research Overview

#Fungal-bacterial interactions #Microbial evolution #Experimental evolution #Antibiotic resistance #Plant-microbe interactions #Pseudomonas #Polymicrobial communities #Host-microbe interactions

My research aims to understand how interactions between fungi and bacteria shape microbial evolution, host–microbe interactions, and antimicrobial resistance. Using microbial genetics, functional genomics, and experimental evolution, I investigate the molecular mechanisms that govern competition within polymicrobial communities. My work discovered that fungal sequestration of magnesium (Mg^{2+}) represents a widespread mechanism of nutritional competition that can unexpectedly increase bacterial resistance to last-resort antibiotics while altering evolutionary trajectories. Building on these findings, my laboratory studies how diverse plant- and human-associated Pseudomonas species interact with fungal competitors and how these cross-kingdom interactions influence bacterial adaptation, virulence, and host immune responses. By integrating in vitro and in vivo infection models with evolutionary and genetic approaches, we seek to uncover general principles of microbial competition and leverage this knowledge to develop sustainable strategies for controlling infectious diseases in both medical and agricultural systems.

Selected Publications

Hsieh YY. Potassium controls skin adaptation in *Candida auris*. *Proc Natl Acad Sci USA*. 2026 Jun 9;123(23):e2611972123. doi: 10.1073/pnas.2611972123.

Hsieh YY, O'Keefe IP, Wang Z, Sun W, Yang H, Vu LM, Smalley NE, Ernst RK, Dandekar AA, Malik HS. Magnesium depletion by *Candida albicans* unleashes two unusual modes of colistin resistance in *Pseudomonas aeruginosa* with different fitness costs. *PLoS Biol*. 2026 Mar 3;24(3):e3003673. doi: 10.1371/journal.pbio.3003673.

Hsieh YY, Sun W, Young JM, Cheung R, Hogan DA, Dandekar AA, Malik HS. Widespread fungal-bacterial competition for magnesium lowers bacterial susceptibility to polymyxin antibiotics. *PLoS Biol*. 2024 Jun 20;22(6):e3002694. doi: 10.1371/journal.pbio.3002694.

Hsieh YY, Makrantoni V, Robertson D, Marston AL, Murray AW. Evolutionary repair: changes in multiple functional modules allow meiotic cohesin to support mitosis. *PLoS Biol*. 2020 Mar 10;18(3):e3000635. doi: 10.1371/journal.pbio.3000635.

LaBar T, Phoebe Hsieh YY, Fumasoni M, Murray AW. Evolutionary repair experiments as a window to the molecular diversity of life. *Curr Biol*. 2020 May 18;30(10):R565-R574. doi: 10.1016/j.cub.2020.03.046.

Hsieh YY, Hung PH, Leu JY. Hsp90 regulates nongenetic variation in response to environmental stress. *Mol Cell*. 2013 Apr 11;50(1):82-92. doi: 10.1016 /j.molcel.2013.01.026.

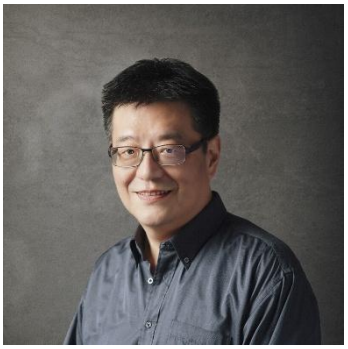
McDonald MJ, Hsieh YY, Yu YH, Chang SL, Leu JY. The evolution of low mutation rates in experimental mutator populations of *Saccharomyces cerevisiae*. *Curr Biol*. 2012 Jul 10;22(13):1235-40. doi: 10.1016/j.cub.2012.04.056.

Honors and Awards

Cystic Fibrosis Foundation Postdoc-to-Faculty Transition Award (2024)

Cystic Fibrosis Foundation Postdoctoral Research Fellowship (2021)

The Hutch SPAC Course Scholarship Award (2021)



Guang-Yuh Jauh

Research Fellow

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Education

Ph.D., Botany and Plant Sciences, University of California, Riverside, USA (1997)

Professional Experience

Postdoctoral Researcher in the laboratory of Dr. John C. Rogers, Institute of Biological Chemistry, Washington State University, Pullman, Washington, USA

Research Overview

#Plant sexual reproduction #Plant development #Plant cell biology

Seeds and grains, essential food sources globally, are produced through successful double fertilization, in which a highly reduced male gametophyte, the pollen tube, delivers two sperm cells to fertilize the egg and central cell within the embryo sac. Understanding the cellular processes underlying pollination offers new insights into fundamental processes of fertilization and embryogenesis, which are crucial for plant breeding. Several years ago, we adopted a bioinformatics-driven strategy to systematically identify T-DNA insertional mutants across the Arabidopsis genome, with a particular focus on those with potential defects in gametophytic or embryogenetic development. Through this approach, we identified a subset of mutants that exhibited severe reproductive abnormalities and failed to produce homozygous progeny, which we termed '*no homozygote progeny*' mutants (*nhp*s). These *NHP*s serve as valuable resources for uncovering essential genes involved in fertility, cell division, and embryonic patterning (Hsu et al., 2025).

Reproductive barriers are essential for maintaining species boundaries by blocking gene flow between different species, thereby protecting species integrity.

Understanding these barriers, which are vital to speciation, is a captivating area for biologists. We have identified a bioactive component, stigmin, in the secreted stigma exudate, a natural fluid released by the stigma that plays a crucial role in facilitating pollen-pistil communication. Stigmin has been shown to stimulate polarized cell growth, notably pollen germination in Easter lily and root hair elongation in *Arabidopsis*, making it an excellent tool for understanding cell polarity and growth signaling cascades in plant cells. We are currently working to elucidate the molecular identity, signaling pathway, and mode of action of this compound, as well as its potential cross-species activity. By integrating genetic, cellular, and biochemical approaches, we hope to uncover fundamental mechanisms that underlie plant reproductive success. Deepening our understanding of these processes will not only advance basic plant biology but also offer innovative strategies for enhancing crop productivity, stress resilience, and reproductive efficiency. Ultimately, our commitment to basic research with translational potential aspires to contribute toward sustainable agriculture and the long-term well-being of our environment and society.

Selected Publications

Hsu YW, Juan CT, Guo CL, Wang HJ, Jauh GY. HYCCIN2 is essential for recruiting the SH3P2-DRP1A complex to the cell plate in *Arabidopsis* embryos. *New Phytol*. 2025 Sep;247(6):2781-2796. doi: 10.1111/nph.70367.

Yen CC, Hsu YW, Leu KC, Chen SS, Chen TY, Juan CT, Wang C, Kuan C, Shaw JF, Ho C-M K, Jauh GY. Guard-cell phytosterol homeostasis is critical for proper stomatal development. *bioRxiv*. 2024 Aug 30. doi: 10.1101/2024.08.29.610202.

INTELLECTUAL PROPERTY: Jauh GY, Yen CC, Chen SS. Methods of enhancing pollen viability of plants. Application No: 63/394,069. Filed on August 1, 2022.

Honors and Awards

Knowledge Feast-Popular Science Lecture, Academia Sinica, Taipei, Taiwan. November 26, 2019.



Yu-Ming Ju

Research Fellow

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Education

Ph.D., Department of Plant Pathology, Washington State University, Pullman, WA, USA (1995)

Professional Experience

Postdoctoral Researcher, Washington State University, Pullman, USA

Research Overview

#Mycology #Systematics #Termite-fungus interaction

My research focuses on fungal taxonomy, biodiversity, evolution, and phylogenetics, with particular emphasis on the systematics of ascomycetous fungi. Over the course of my career, I have published more than 130 peer-reviewed papers and described over 100 fungal species new to science. My recent research has also explored the mutualistic relationship between the black-winged subterranean termite (*Odontotermes formosanus*) and edible *Termitomyces* mushrooms, contributing to a better understanding of fungal-insect symbioses.

Since 2023, my work has advanced knowledge of the ecologically important genus *Xylaria*. I investigated the taxonomic diversity and evolutionary relationships of termite-associated *Xylaria* species that produce medicinal sclerotia known as Wulingshen, demonstrating that these structures originate from multiple closely related species sharing a common ancestry. I also conducted the first global revision of leaf- and petiole-inhabiting *Xylaria*, recognizing 45 species and clarifying their classification through morphological and phylogenetic analyses. In

addition, I described several new terrestrial and termite-associated *Xylaria* species and resolved their phylogenetic relationships within the genus.

Beyond research, I actively promote mycology through university teaching, public outreach, and editorial service. I currently teach mycology at National Taiwan University and serve as Editor-in-Chief of *Fungal Science*, supporting fungal research and education in Taiwan and internationally.

Selected Publications

Ju YM, Hsieh HM, Newman DS, Singer H, Paxton K, Paxton C, Tighe D. *Poronia phosphorea*, a newly recombined name from *Xylaria phosphorea*. *Nova Hedwigia*. 2026 Apr 26, 122:409-439. doi: 10.1127/nova_hedwigia/1191.

Ju YM, Hsieh HM, Lin CR, Huang CY. *Graphostroma formosanum*, a newly described xylariaceous fungus in Taiwan. *Fung Sci*. 2025, 40:9-14. https://mycology.sinica.edu.tw/taiwanmycosoc/FungalScience/FS40(1)009-014.pdf.

Okane I, Hsieh HM, Ju YM, Lin CR, Huang CY, Kuan IC. *Xylaria iriomotensis* sp. nov. from termite nests and notes on *X. angulosa*. *Bot Stud*. 2025 Jan 17;66(1):4. doi: 10.1186/s40529-024-00447-7.

Hsieh HM, Lin CR, Huang CY, Ju YM. *Annulohypoxylon annulatoides* newly described in Taiwan. *Fung Sci*. 2024, 39: 027-033. https://mycology.sinica.edu.tw/TaiwanMycoSoc/Download.aspx?Target=39(1)027-033.

Hsieh HM, Lin CR, Tang YY, Ju YM. *Xylaria chiuyuanii* sp. nov., a fasciculate terrestrial *Xylaria* species found in Taiwan. *Fung Sci*. 2024, 39: 9-26. https://mycology.sinica.edu.tw/taiwanmycosoc/Download.aspx?Target=39(1)009-026.



Chuan Ku

Associate Research Fellow

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Education

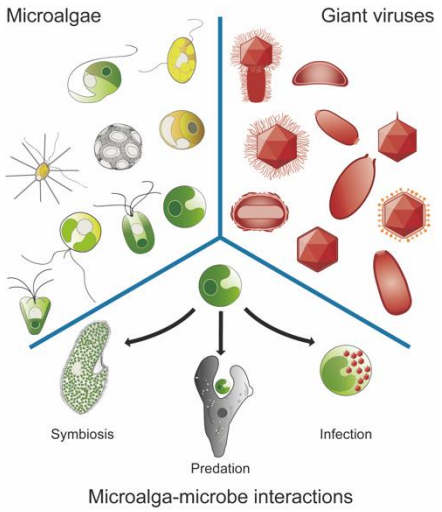
Ph.D., Biology, University of Düsseldorf, Germany (2016)

Professional Experience

Postdoctoral Researcher, Weizmann Institute of Science, Israel

Research Overview

#Algae #Giant viruses #Microbial interactions
#Eukaryote genome evolution #Single-cell biology #Aquatic microbiology



Microalga-microbe interactions

Microorganisms have been shaping Earth's atmosphere and oceans for four billion years. While invisible to the naked eye, microalgae contribute to nearly half of the global primary production and carbon fixation. Their organic carbon and stored energy are passed on to other members of the aquatic food webs through microbial interactions. To better understand the biology of microalgae, we combine lab culturing, omics, and single-cell methods to investigate the molecular, cellular, and environmental regulators of algal physiology and interactions with symbiotic hosts and viruses. We also use bioinformatics tools to elucidate the evolution of microbes across different timescales in the Earth history, with the goal to predict their potential interactions and responses to climate and other environmental changes. We particularly focus

on ecologically important microbes that are globally distributed across marine or freshwater ecosystems, including 1) coccolithophore microalgae that can store carbon in $CaCO_3$ plates, 2) giant viruses (*Nucleocytoviricota*) with large DNA genomes that infect diverse algae and other eukaryotes, and 3) large unicellular eukaryotes that host microalgal endosymbionts.

Selected Publications

Tee HS, Ku C. Host-calibrated time tree caps the age of giant viruses. *Mol Biol Evol*. 2025 Feb 3;42(2):msaf033. doi: 10.1093/molbev/msaf033.

Kao S, Kao CF, Chang W, Ku C. Widespread distribution and evolution of poxviral entry-fusion complex proteins in giant viruses. *Microbiol Spectr*. 2023 Apr 13;11(2):e0494422. doi: 10.1128/spectrum.04944-22.

Tung CC, Kuo SC, Yang CL, Yu JH, Huang CE, Liou PC, Sun YH, Shuai P, Su JC, Ku C, Lin YJ. Single-cell transcriptomics unveils xylem cell development and evolution. *Genome Biol*. 2023 Jan 9;24(1):3. doi: 10.1186/s13059-022-02845-1.

Kao TT, Wang TH, Ku C. Rampant nuclear-mitochondrial-plastid phylogenomic discordance in globally distributed calcifying microalgae. *New Phytol*. 2022 Aug;235(4):1394-1408. doi: 10.1111/nph.18219.

Ku C, Sebé-Pedrós A. Using single-cell transcriptomics to understand functional states and interactions in microbial eukaryotes. *Philos Trans R Soc Lond B Biol Sci*. 2019 Nov 25;374(1786):20190098. doi: 10.1098/rstb.2019.0098.

Honors and Awards

Research Grant for International Outstanding Young Scholars (with a salary award), 2030 Cross-Generation Young Scholars Program, National Science and Technology Council, Taiwan

Outstanding Teaching Award, National Taiwan University (2024)

Early Career Travel Grant Award, Association for the Sciences of Limnology and Oceanography (ASLO) Meeting (June 2-7, 2024), Madison, Wisconsin, USA

Global Investigator, European Molecular Biology Organization (2023)

Outstanding Young Scholar Award, Taiwan Society of Plant Biologists, Taiwan

Young Scholars' Creativity Award, Foundation for the Advancement of Outstanding Scholarship, Taiwan



Chih-Horng Kuo

Research Fellow

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Education

Ph.D., Genetics, University of Georgia, USA (2008)

Professional Experience

Postdoctoral Researcher, University of Arizona, USA

Research Overview

#Evolutionary and functional genomics #host-associated bacteria

Our research addresses the genomic basis of bacterial diversity and microbe-host interactions, combining evolutionary genomics, comparative transcriptomics, and molecular genetics across bacteria with contrasting lifestyles and pathogenic potential.

Agrobacteria and rhizobia. These plant-associated bacteria span pathogenicity to nitrogen-fixing symbiosis. We study their genomic diversity and the genetic basis of microbe-plant and microbe-microbe interactions, including the type IV and type VI secretion systems and the regulatory networks behind them, work that also informs *Agrobacterium*-mediated transformation (AMT) technologies.

Mollicutes. With phytoplasmas as our primary focus, we examine genome organization and dynamics, the molecular evolution driving divergence among lineages, mobile genetic elements in horizontal gene transfer, and effectors that reprogram host development. Genome-based taxonomy of this group supports accurate classification and molecular diagnostics.

Microbial diversity. Beyond our primary systems, our expertise underpins broad collaborations spanning microbiome, symbiosis, taxonomy, and applied microbiology.

Selected Publications

Pei SC, Li NP, Li TT, Yang YC, Hung TH, Kuo CH. Comparative genomics of a poinsettia-associated phytoplasma and functional validation of its SAP11-homologous effectors that induce plant branching. *Microb Genom*. 2026 Mar;12(3):001675. doi: 10.1099/mgen.0.001675.

Wu Y, Chang HY, Wu CH, Lai EM, Kuo CH. Comparative transcriptomics reveals context- and strain-specific regulatory programmes of *Agrobacterium* during plant colonization. *Microb Genom*. 2025 Aug;11(8):001485. doi: 10.1099/mgen.0.001485.

Yan XH, Pei SC, Yen HC, Blanchard A, Sirand-Pugnet P, Baby V, Gasparich GE, Kuo CH. Delineating bacterial genera based on gene content analysis: a case study of the *Mycoplasmatales–Entomoplasmatales* clade within the class Mollicutes. *Microb Genom*. 2024 Nov;10(11):001321. doi: 10.1099/mgen.0.001321.

Weisberg AJ, Wu Y, Chang JH, Lai EM, Kuo CH. Virulence and ecology of agrobacteria in the context of evolutionary genomics. *Ann Rev Phytopathol*. 2023 Sep 5:61:1-23. doi: 10.1146/annurev-phyto-021622-125009.

Chou L, Lin YC, Haryono M, Santos MNM, Cho ST, Weisberg AJ, Wu CF, Chang JH, Lai EM, Kuo CH. Modular evolution of secretion systems and virulence plasmids in a bacterial species complex. *BMC Biol*. 2022 Jan 13;20(1):16. doi: 10.1186/s12915-021-01221-y.

Honors and Awards

Derrick Edward Award, International Organization for Mycoplasmology (2023)

Robert F. Whitcomb Award, International Organization for Mycoplasmology (2021)

Professor Chu-Yung Lin Memorial Award, Chu-Yung Lin Plant Science Education Foundation and Taiwan Society of Plant Biologists (2019)

Research Award for Junior Research Investigators, Academia Sinica (2017)



Erh-Min Lai

Research Fellow

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Education

Ph.D., Plant Pathology, University of California, Davis, USA (1999)

Professional Experience

Postdoctoral Researcher, University of Michigan, Ann Arbor, USA

Visiting Scientist, Massachusetts General Hospital, USA

Research Overview

#Agrobacteria #Plant transformation #Protein secretion #Plant-microbe interactions #microbe-microbe interactions

Microorganisms profoundly influence plant health, productivity, and evolution. Understanding how microbes interact with plants and competing microorganisms is essential for advancing both fundamental biology and sustainable agriculture. Our research investigates the molecular mechanisms underlying microbe–microbe and plant–microbe interactions, with a particular focus on agrobacterial biology, bacterial secretion systems, and plant genetic transformation.

We integrate genetics, molecular biology, genomics, and multi-omics approaches to uncover how agrobacteria survive and compete in complex microbial communities while successfully colonizing plants and transferring DNA into host cells. A major focus is the Type VI Secretion System (T6SS), a bacterial nanoweapon used for interbacterial competition. Our studies have identified novel antibacterial effectors, elucidated mechanisms of effector delivery, and revealed the ecological roles of T6SS in microbial community dynamics and disease development. In parallel, we develop innovative technologies to improve

Agrobacterium-mediated transformation and plant genome engineering. These efforts include the AGROBEST transient expression system, identification of factors affecting transformation efficiency, engineering of highly efficient agrobacterial strains, and strategies to enhance genome editing through developmental optimization and immune evasion.

Together, our research bridges microbial ecology, host-microbe interactions, and plant biology, advancing fundamental knowledge while enabling technologies that accelerate crop improvement and sustainable agriculture.

Selected Publications

Liu MS, Huang TK, Wang YC, Wang SC, Wu CH, Kuo CH, Lai EM. Floral stage optimization and immune evasion enhance *Agrobacterium*-mediated genome editing in *Arabidopsis. New Phytol*. 2026 Feb;249(4):2125-2139. doi: 10.1111/nph.70795.

Huang TK, Lai EM. Cooperation and antagonism in *Agrobacterium*-mediated transformation. *Nat Plants*. 2025 May;11(5):946-948. doi: 10.1038/s41477-025-01998-8.

Lai X, Yu M, Cheng CP, Lai EM. Distinct strategies of diguanylate cyclase domain proteins on inhibition of virulence and interbacterial competition by agrobacteria. *mBio*. 2025 May 14;16(5):e0003925. doi: 10.1128/mbio.00039-25.

Ali J, Yu M, Sung LK, Cheung YW, Lai EM. A glycine zipper motif is required for the translocation of a T6SS toxic effector into target cells. *EMBO Rep*. 2023 Jun 5;24(6):e56849. doi: 10.15252/embr.202356849.

Wang SC, Chen AP, Chou SJ, Kuo CH, Lai EM. Soil inoculation and blocker-mediated sequencing show effects of the antibacterial T6SS on agrobacterial tumorigenesis and gallobiome. *mBio*. 2023 Apr 25;14(2):e0017723. doi: 10.1128/mbio.00177-23.

Honors and Awards

Presidential Scholar, Academia Sinica (2021-2023; 2024-2027)
Outstanding Research Award, MOST/NSTC (2017)
Investigator Award, Academia Sinica (2018-2022)
Young Investigators Award, Shang-Fa Yang Foundation (2011)
Junior Research Investigators Award, Academia Sinica (2010)



Ka-Wai Ma

Assistant Research Fellow

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Education

Ph.D., Plant Pathology, University of California, Riverside, USA (2015)

Professional Experience

Postdoctoral Researcher, University of California, Riverside, USA

Postdoctoral Researcher, Max Planck Institute of Plant Breeding Research, Germany

Research Overview

#Plant innate immunity #Bacterial Pathogenesis #Plant Microbiome

Higher-level organisms, including terrestrial plants, live in close association with multifaceted microbial communities known as the **microbiota** / **microbiome**. Plants actively invest a substantial portion of their resources to attract and nourish these microbial cohorts in exchange of beneficial microbial services, including boosted disease protection against diseases, improved stress tolerance and enhanced nutrient uptake. Plants also mount robust immunity to fend off pathogens, maintaining healthy plant-microbiome interaction.

Our group used *Arabidopsis thaliana* as the model plant system together with an established microbial culture collection to reconstitute these interactions. We utilized multi-omics and genetics to understand the mechanistic basis underlying healthy plant-microbiome interaction. Using these approaches, we revealed the role of innate immunity and proper hormonal balance to maintain healthy plant-microbiome interactions.

To facilitate high-throughput genetic perturbation, we also developed CRISPR-based gene editing pipeline to study multi-gene interactions involved in these processes. Our ultimate goal is to manipulate the composition of the plant microbiome to improve plant fitness.



Selected Publications

Lu TT, Isip M, Han CJ, Shih HJ, Syukur S, Trinh LL, Perin S, Lin YC, Lin PA, Ma KW. Upregulated jasmonate signaling shifts *Arabidopsis* microbiota interactions and stress adaptations through a positive feedback loop. *ISME J*. 2026 Jan 14;20(1):wrag146. doi: 10.1093/ismejo/wrag146.

Copeland C, Schulze-Lefert P, Ma KW. Potential and challenges for application of microbiomes in agriculture. *Plant Cell*. 2025 Aug 4;37(8):koaf185. doi: 10.1093/plcell/koaf185.

Ordon J, Logemann E, Maier LP, Lee T, Dahms E, Oosterwijk A, Flores-Uribe J, Miyauchi S, Paoli L, Stolze SC, Nakagami H, Felix G, Garrido-Oter R, Ma KW, Schulze-Lefert P. Conserved immunomodulation and variation in host association by Xanthomonadales commensals in *Arabidopsis* root microbiota. *Nat Plants*. 2025 Mar;11(3):612-631. doi: 10.1038/s41477-025-01918-w.

Ma KW, Niu Y, Jia Y, Ordon J, Copeland C, Emonet A, Geldner N, Guan R, Stolze SC, Nakagami H, Garrido-Oter R, Schulze-Lefert P. Coordination of microbe-host homeostasis by crosstalk with plant innate immunity. *Nat Plants*. 2021 Jun;7(6):814-825. doi: 10.1038/s41477-021-00920-2.

Honors and Awards

Postdoctoral fellowship, EMBO (2018-19)

Postdoctoral fellowship, Alexander von Humboldt Foundation (2019-20)

Eigene Stelle, German Research Foundation (2022-23)



Lay-Sun Ma

Associate Research Fellow

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Education

Ph.D., Molecular Microbiology, National Chung-Hsing University and Academia Sinica Taiwan International Graduate Program, Taiwan (2011)

Professional Experience

Postdoctoral Researcher, Max Planck Institute, Germany

Postdoctoral Researcher, Institute of Plant and Microbial Biology, Academia Sinica, Taiwan

Research Overview

#Plant immunity #Fungal virulence

The interaction between plants and pathogenic fungi is an ongoing molecular arms race: plants continuously refine their immune surveillance to restrict invasion, while adapted fungi counter by evolving sophisticated strategies to disarm host defenses. Using the biotrophic corn smut fungus *Ustilago maydis* as a model system, our laboratory investigates these molecular battlegrounds. We focus primarily on how this pathogen coordinates and deploys a diverse arsenal of secreted effector proteins to manipulate host cell processes and suppress immunity. Specifically, we aim to identify cell-surface sensors that detect host signals to drive pathogenic morphological transitions, decipher the regulatory networks controlling sequential waves of effector expression, and elucidate how extracellular effectors deactivate apoplastic defenses at the primary infection interface. Ultimately, by uncovering conserved virulence mechanisms across

biotrophic fungi, our work provides foundational insights to guide targeted, innovative crop protection strategies.

Selected Publications

Bhaskar C, Teoh EY, Chau MQ, Yeh CH, Tsai WL, Teh OK, Ma LS. N-glycosylation mediates smut effector adaptation toward a host pectin methylesterase inhibitor. *Plant Cell*. 2026 Aug 4;38(8):koag234. doi: 10.1093/plcell/koag234.

Bhaskar C, Chandrasekharan N, Chau MQ, Ma LS. Molecular puppeteering: Roles of Ustilago maydis effectors. *Curr Opin Plant Biol*. 2025 Dec;88:102792. doi: 10.1016/j.pbi.2025.102792.

John E, Chau MQ, Hoang CV, Chandrasekhar N, Bhaskar C, Ma LS. Fungal cell wall-associated effectors: sensing, integration, suppression, and protection. *Mol Plant Microbe Interact*. 2024 Mar;37(3):196-210. doi: 10.1094/MPMI-09-23-0142-FI.

Lin YH, Xu MY, Hsu CC, Damei FA, Lee HC, Tsai WL, Hoang CV, Chiang YR, Ma LS. *Ustilago maydis* PR-1-like protein has evolved two distinct domains for dual virulence activities. *Nat Commun.* 2023 Sep 16;14(1):5755. doi: 10.1038/s41467-023-41459-4.

Ma LS, Tsai WL, Damei FA, Kalunke RM, Xu MY, Lin YH, Lee HC. Maize antifungal protein AFP1 elevates fungal chitin levels by targeting chitin deacetylases and other glycoproteins. *mBio*. 2023 Apr 25;14(2):e0009323. doi: 10.1128/mbio.00093-23.



Makoto Shirakawa

Assistant Research Fellow

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Education

Ph.D. in Science, Kyoto University, Nara, Japan (2009)

Professional Experience

Assistant Professor, Nara Institute of Science and Technology, Japan

Postdoctoral Fellow, University of British Columbia, Canada

Postdoctoral Research Fellow, Kyoto University, Japan

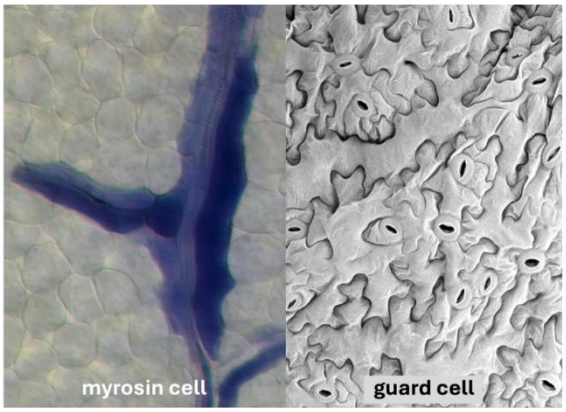
Research Overview

#Cell differentiation #Specialized cells #Transcription factor

Plant Idioblast Biology

Our vision is to establish "Plant Idioblast Biology" as a new field to advance understanding of plant cell diversity and adaptation.

Plants have evolved conserved and species-specific specialized cells to adapt to diverse environments. Idioblasts are specialized plant cells with distinct morphology and functions, often associated with unique metabolic or structural features. However, their developmental mechanisms and evolutionary trajectories remain largely unknown. One well-characterized example of a highly specialized cell is the guard cell, which adjusts stomatal aperture to regulate CO_2 uptake. Another example is the myrosin cell, a Brassicales-specific defense cell type, which has been a central focus of our research (Figure). Our laboratory was launched on September 1st, 2025, at the Institute of Plant and Microbial Biology, Academia Sinica, with the mission to uncover how plants rewire and evolve transcriptional networks to give rise to novel idioblasts that enable adaptation.



Our vision is to establish “Plant Idioblast Biology” as a new field that advances our understanding of plant cell diversity and adaptation. By exploring a wide range of idioblast types, we will reveal the molecular mechanisms—such as gene co-option and neofunctionalization, including exon shuffling—that generate novel specialized cells. In doing so, we aim to illuminate the fundamental principles that create plant diversity and firmly establish Plant Idioblast Biology as a transformative new discipline.

Selected Publications

Shirakawa M, Oguro T, Sugano SS, Yamaoka S, Sagara M, Tanida M, Sunuma K, Iwami T, Nakanishi T, Horiuchi K, Kumaishi K, Yoshida S, Watanabe M, Tohge T, Suzuki T, Ichihashi Y, Takemiya A, Yamaguchi N, Kohchi T, Ito T. Co-option and neofunctionalization of stomatal executors for defense against herbivores in Brassicales. *Nat Plants*. 2025 Mar;11(3):483-504. doi: 10.1038/s41477-025-01921-1.

Moriya KC, Shirakawa M, Loue-Manifel J, Matsuda Y, Lu YT, Tamura K, Oka Y, Matsushita T, Hara-Nishimura I, Ingram G, Nishihama R, Goodrich J, Kohchi T, Shimada T. Stomatal regulators are co-opted for seta development in the astomatous liverwort *Marchantia polymorpha*. *Nat Plants*. 2023 Feb;9(2):302-314. doi: 10.1038/s41477-022-01325-5.

Horiuchi Y, Shirakawa M. Divergent routes to specialization: guard cells, myrosin cells, and beyond. *Curr Opin Plant Biol*. 2026 Feb:89:102853. doi: 10.1016/j.pbi.2025.102853.

Honors and Awards

Young Investigator Award, Japanese Society of Plant Physiologist (2026)
Bioscience Division Award, Nara Institute of Science and Technology (2025)
NAIST PRESIDENT’S FELLOW, Nara Institute of Science and Technology (2023)
HIRASE Award, Japanese Society of Plant Morphology (2023)



Ooi-Kock Teh

Assistant Research Fellow

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Education

DPhil., Plant Sciences, University of Oxford, United Kingdom (2007)

Professional Experience

JSPP Postdoctoral Researcher, Kyoto University, Kyoto, Japan

Postdoctoral Researcher, Swedish University of Agricultural Sciences, Uppsala, Sweden

Postdoctoral Researcher, Leibniz Institute of Plant Biochemistry, Halle, Germany

Assistant Professor, Hokkaido University, Sapporo, Japan

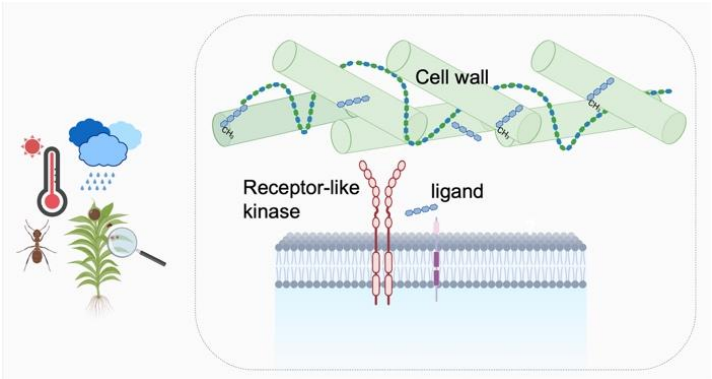
Research Overview

#Plant development #Cell wall signalling #Receptor #Signal transduction

A defining feature of plant cells is their polysaccharide-rich cell wall, a dynamic structure that not only provides mechanical support and protection but also serves as a sophisticated platform for sensing and responding to environmental cues. Changes in cell wall composition triggered by pathogens, abiotic stresses, or developmental processes are detected by specialized receptor-like kinases and associated signalling proteins, which coordinate cellular responses essential for growth, adaptation and survival.

Our laboratory uses *Physcomitrium patens* as a powerful model system to uncover the molecular mechanisms underlying cell wall signalling. By integrating phosphoproteomics, biochemistry, genetics and advanced live cell imaging techniques, we investigate how signalling networks are activated and regulated following cell wall perturbation.

The overarching goal of our research is to identify the key signalling components that control the strength, specificity, and dynamics of cellular responses to environmental challenges. By elucidating the mechanisms of cell wall signalling in *Physcomitrium patens*, we generate fundamental insights into the evolution of signalling pathways across the plant kingdom and establish conceptual frameworks that can inform future strategies for enhancing plant resilience, adaptation, and productivity.



Selected Publications

Yu CY, Maharjan M, Liu CH, Teh OK. Glycosylation-dependent sorting of an Arabinogalactan protein SLEEPING BEAUTY mediates apical tip growth and osmosensing in *Physcomitrium patens*. *bioRxiv*. 2025, doi: 10.1101/2025.07.08.663806.

Teh OK, Singh P, Ren J, Huang LT, Ariyarathne M, Salamon BP, Wang Y, Kotake T, Fujita T. Surface-localized glycoproteins act through class C ARFs to fine-tune gametophore initiation in *Physcomitrium patens*. *Development*. 2022 Dec 15;149(24):dev200370. doi: 10.1242/dev.200370.

Ginanjar EF, Teh OK, Fujita T. Characterisation of rapid alkalinisation factors in *Physcomitrium patens* reveals functional conservation in tip growth. *New Phytol*. 2022 Mar;233(6):2442-2457. doi: 10.1111/nph.17942.



Shih-Long Tu

Research Fellow

Email: tsl@as.edu.tw

Education

Ph.D., Molecular Biology, Graduate Institute of Life Science, National Defense Medical Center, Taipei, Taiwan (2001)

Professional Experience

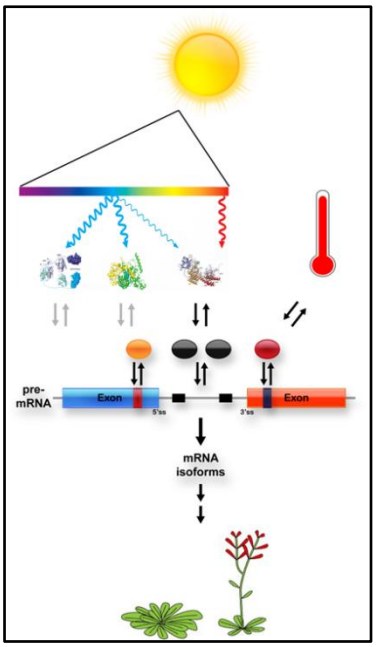
Postdoctoral Researcher, University of California, Davis, USA

Research Overview

#pre-mRNA splicing #photoreceptor #thermomorphogenesis

Plant responses to environmental changes involve complex network of signal perception, transduction, and gene expression regulation. While interactions between signaling pathways and gene expression have been extensively studied, recent evidence highlights that post-transcriptional regulation—specifically at the precursor mRNA (pre-mRNA) splicing level—plays a pivotal role in how plants adapt to fluctuating environments. However, the precise regulatory mechanisms remain poorly understood.

Our team investigates the functions and regulatory mechanisms of pre-mRNA splicing in plant responses to light and temperature. By integrating genome-wide, cell biology, biochemical, molecular genetics, and physiological approaches, we aim to uncover the fundamental mechanisms underlying pre-mRNA splicing regulation required for plant environmental responses. Our ultimate goal is to translate these discoveries into agricultural applications, optimizing the growth, development, and resilience of important crops through targeted pre-mRNA splicing control.



Selected Publications

Chang P, Hsieh HY, Tu SL. The U1 snRNP component RBP45d regulates temperature-responsive flowering in *Arabidopsis*. *Plant Cell*. 2022 Feb 3;34(2):834-851. doi: 10.1093/plcell/koab273.

Shih CJ, Chen HW, Hsieh HY, Lai YH, Chiu FY, Chen YR, Tu SL. Heterogeneous nuclear ribonucleoprotein H1 coordinates with phytochrome and the U1 snRNP complex to regulate alternative splicing in *Physcomitrella patens*. *Plant Cell*. 2019 Oct;31(10):2510-2524. doi: 10.1105/tpc.19.00314.

Wu HP, Su YS, Chen HC, Chen YR, Wu CC, Lin WD, Tu SL. Genome-wide analysis of light-regulated alternative splicing mediated by photoreceptors in *Physcomitrella patens*. *Genome Biol.* 2014 Jan 7;15(1):R10. doi: 10.1186/gb-2014-15-1-r10.

Honors and Awards

Outstanding Research Award, National Science and Technology Council (2022)

Asian and Oceania Society for Photobiology Award for Young Scientist, Asian and Oceania Society for Photobiology (2017)

Junior Research Investigators Award, Academia Sinica (2013)

The 5th Shang-Fa Yang Bio-Agricultural Young Scientist Award, Shang-Fa Yang Foundation (2012)



Paul Verslues

Research Fellow

Email: paulv@gate.sinica.edu.tw

Education

Ph.D., Plant Biology, University of California, Riverside (2004)

Professional Experience

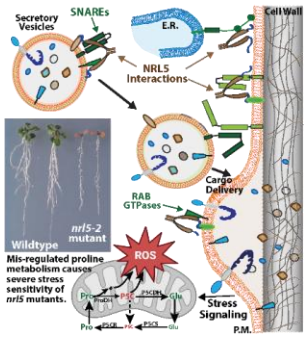
Postdoctoral Researcher, University of California, Riverside, USA

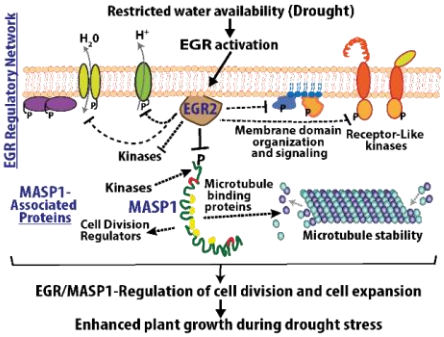
Research Overview

#Drought Stress #Plant Physiology #Cell Biology

The core interest of the Verslues laboratory is to understand the cellular mechanisms plants use to sense and respond to drought stress. We are particularly interested in drought-responsive protein phosphorylation as well as intracellular trafficking and drought-related signaling at the cell wall-plasma membrane-cytoskeleton interface. One particular interest is the Clade E Growth-Regulating (EGR) protein phosphatases and their regulatory network that controls plant growth during moderate water limitation, as well as role of the EGR-regulated protein MASP1 in controlling meristem cell production. We also are investigating the NPH3-domain protein NRL5, which we have found to be a novel type of GTPase and novel component of plant intracellular trafficking, and how it is involved in trafficking of stress-related proteins and its function at ER-PM contact sites. Other work in the lab is focused on stress-related protein kinases and regulation of drought-induced proline accumulation. Overall, our focus on growth and metabolic responses to moderate water limitation offer a different, and more translationally relevant, view of molecular drought responses than studies focused on survival of severe stress. As our genetic analyses often lead to

proteins of unknown function, another contribution of our research is to establish the cellular function of uncharacterized, often plant-specific, proteins.





Selected Publications

Upadhyay-Tiwari N, Huang XJ, Lee YC, Singh SK, Hsu CC, Huang SS, Verslues PE. The nonphototrophic hypocotyl 3 (NPH3) domain protein NRL5 is a trafficking-associated GTPase essential for drought resistance. *Sci Adv*. 2024 Aug 9;10(32):eado5429. doi: 10.1126/sciadv.ado5429.

Longkumer T, Chen CY, Biancucci M, Bhaskara GB, Verslues PE. Spatial differences in stoichiometry of EGR phosphatase and Microtubule-Associated Stress Protein 1 control root meristem activity during drought stress. *Plant Cell*. 2022 Feb 3;34(2):742-758. doi: 10.1093/plcell/koab290.

Bhaskara GB, Wen TN, Nguyen TT, Verslues PE. Protein Phosphatase 2Cs and *Microtubule-Associated Stress Protein 1* control microtubule stability, plant growth, and drought response. *Plant Cell*. 2017 Jan;29(1):169-191. doi: 10.1105/tpc.16.00847.

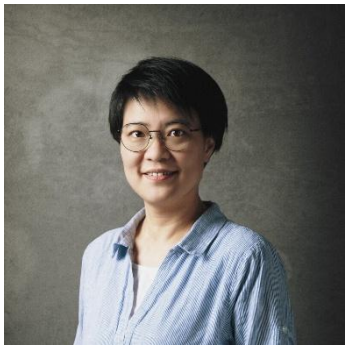
Honors and Awards

Co-chair of the Gordon Research Conference on Salt and Water Stress in Plants (with Siobhan Brady of UC-Davis), 2026

Visiting professor of the Institute of Global Innovation Research (GIR) program at Tokyo University of Agriculture and Technology, 2025

Column Award for Distinguished Alumnus of the Division of Plant Science and Technology; College of Agriculture, Food and Natural Resources; University of Missouri, 2022

Plant Cell, senior editor for focus issue on Climate Change and Abiotic Stress; Reviewing Editor, 2020-present



Chung-Ju Wang

Associate Research Fellow

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Education

Ph.D., Plant Biology, National Taiwan University, Taiwan (2003)

Professional Experience

Postdoctoral Researcher, University of California, Berkeley, USA

Research Overview

#Meiosis #Anther development #Chromosome Biology #Sexual reproduction

Sexual reproduction in plants relies on successful meiosis to produce viable haploid spores. Our research investigates meiotic recombination and meiotic cell cycle control in the context of anther development, aiming to elucidate the mechanisms governing crossover formation and distribution, the signals controlling meiotic entry, progression, and exit, and the somatic and germline coordination essential for male meiosis.

To dissect these mechanisms, we combine classical genetics with cutting-edge technologies, including multi-omics, epigenomics, single-cell approaches, and super-resolution microscopy. We primarily use maize, taking advantage of its exceptional cytological resolution and rich natural variation, and further expand selected projects to rice and Brassicaceae species. Additionally, we are developing AI-assisted image analysis pipelines for expansion microscopy data, enabling sophisticated investigation of crossover-designation processes and chromosome synapsis at nanoscale resolution. This approach yields unprecedented structural

and molecular insights, allowing us to resolve the spatiotemporal dynamics of recombination and uncover the mechanisms that designate crossover sites. Beyond fundamental research, we are establishing a plant synthetic biology platform to translate mechanistic insights into crop engineering. Through these studies, we aim to uncover fundamental principles of meiotic regulation and recombination, ultimately contributing to more efficient breeding strategies and improved agricultural productivity.

Selected Publications

Du Q, Wang M, Tiang CL, Sheehan MJ, Altendorf P, Yu JK, Hudecz O, Roitinger E, Wang C JR, Bukowski R, Meeley RB, Ko C, Golubovskaya IN, Pawlowski WP. PAM1 regulates meiosis by coupling RNA processing to the chromosome axis. *Proc Natl Acad Sci USA.* 2026 May 19;123(20):e2535316123. doi: 10.1073/pnas.2535316123.

Ku JC, Ronceret A, Golubovskaya I, Lee DH, Wang CT, Timofejeva L, Kao YH, Angoa AKG, Kremling K, Williams-Carrier R, Meeley R, Barkan A, Cande WZ, Wang C JR. Dynamic localization of SPO11-1 and conformational changes of meiotic axial elements during recombination initiation of maize meiosis. *PLoS Genet.* 2020 Apr 20;16(4):e1007881. doi: 10.1371/journal.pgen.1007881.

Jing JL, Zhang T, Kao YH, Huang TH, Wang C JR, He Y. *ZmMTOPVIB* enables DNA double-strand break formation and bipolar spindle assembly during maize meiosis. *Plant Physiol*. 2020 Dec;184(4):1811-1822. doi: 10.1104/pp.20.00933.

Lee DH, Kao YH, Ku JC, Lin CY, Meeley R, Jan YS, Wang C JR. The axial element protein DESYNAPTIC2 mediates meiotic double-strand break formation and synaptonemal complex assembly in maize. *Plant Cell*. 2015 Sep;27(9):2516-29. doi: 10.1105/tpc.15.00434.

Honors and Awards

Innovative Research Award, Professor Chiu-Lung Lin Foundation (2018)
Noteworthy Maize Primary Literature, MaizeGDB (2016)
Young Scientist Award, Shang-Fa Yang Foundation (2016)
Society Excellent Youth Award, Youth National Salvation Corps (2013)
Career Development Award, Academia Sinica (2013)



Chih-Hang Wu

Associate Research Fellow

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Education

Ph.D., Biology, University of East Anglia, United Kingdom (2017)

Professional Experience

Postdoctoral Researcher, The Sainsbury Laboratory, United Kingdom

Research Overview

#Plant immunity #NLR immune receptors #Hypersensitive cell death #Plant-microbe interactions #Evolutionary biology #Agrobacterium biotechnology

Plants rely on sophisticated immune systems to recognize invading pathogens and activate defense responses. Our research aims to uncover the molecular, cellular, and evolutionary mechanisms that govern plant immunity, with a particular focus on nucleotide-binding leucine-rich repeat (NLR) immune receptors and their associated signaling networks. A major area of our work investigates NRC helper–sensor NLR networks, a complex immune receptor system that provides resistance against diverse pathogens. We combine genetics, biochemistry, genomics, structural prediction, and advanced live-cell imaging to understand how these receptors function, evolve, and coordinate immune responses. More recently, we have focused on the cell biology of resistosomes, elucidating how their activation triggers calcium influx, organelle remodeling, and hypersensitive cell death at single-cell resolution. In parallel, we develop innovative technologies for plant functional genomics and biotechnology, including inducible gene expression systems and improved agrobacteria-based transformation platforms.

Selected Publications

Chen YF, Lin KY, Huang CY, Hou LY, Yuen ELH, Sun WJ, Chiang BJ, Chang CW, Wang HY, Bozkurt TO, Wu CH. Subcellular calcium dynamics and organelle perturbations in resistosome-mediated cell death. P*roc Natl Acad Sci USA*. 2026 Mar 24;123(12):e2523470123. doi: 10.1073/pnas.2523470123.

Lopez-Agudelo JC, Goh FJ, Tchabashvili S, Huang YS, Huang CY, Lee KT, Wang YC, Wu Y, Chang HX, Kuo CH, Lai EM, Wu CH. *Rhizobium rhizogenes* A4-derived strains mediate hyper-efficient transient gene expression in *Nicotiana benthamiana* and other solanaceous plants. *Plant Biotechnol J*. 2026 Jan;24(1):131-144. doi: 10.1111/pbi.70083.

Goh FJ, Huang CY, Derevnina L, Wu CH. NRC immune receptor networks show diversified hierarchical genetic architecture across plant lineages. *Plant Cell*. 2024 Sep 3;36(9):3399-3418. doi: 10.1093/plcell/koae179.

Chiang BJ, Lin KY, Chen YF, Huang CY, Goh FJ, Huang LT, Chen LH, Wu CH. Development of a tightly regulated copper-inducible transient gene expression system in *Nicotiana benthamiana* incorporating suicide exon and Cre recombinase. *New Phytol*. 2024 Oct;244(1):318-331. doi: 10.1111/nph.20021.

Huang CY, Huang YS, Sugihara Y, Wang HY, Huang LT, Lopez-Agudelo JC, Chen YF, Lin KY, Chiang BJ, Toghani A, Kourelis J, Wang CH, Derevnina L, Wu CH. Subfunctionalization of NRC3 altered the genetic structure of the *Nicotiana* NRC network. *PLoS Genet*. 2024 Sep 12;20(9):e1011402. doi: 10.1371/journal.pgen.1011402.

Honors and Awards

Young Scholars' Creativity Award, Foundation for the Advancement of Outstanding Scholarship (2025)

EMBO Global Investigator, European Molecular Biology Organization (2024)

Shang-Fa Yang Outstanding Young Scientist Award (2024)

Outstanding Young Scholar Award, Taiwan Society of Plant Biologists (2024)

Emerging Young Scholar, National Science and Technology Council, Taiwan (2022)



Shu-Hsing Wu

Distinguished Research Fellow

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Education

Ph.D., Plant Biology, University of California, Davis, USA (1997)

Professional Experience

Director, Institute of Plant and Microbial Biology, Academia Sinica

Deputy Executive Secretary, Central Academic Advisory Committee, Academia Sinica

Discipline coordinator, Department of Life Sciences, National Science and Technology Council

Research Overview

#Light responses #Translation control #Photomorphogenesis #Circadian clock

Our research dissects three vital processes driving plant growth and developmental competitiveness: skotomorphogenesis, photomorphogenesis, and the establishment of the circadian clock. Having previously mapped the first plant translatome in de-etiolating *Arabidopsis* seedlings and identified core clock regulators such as LWD proteins, our future initiatives focus on uncovering the molecular principles that govern developmental transitions and clock robustness. Central to this program is the investigation of the dynamic formation of biomolecular condensates within the nucleus and cytosol. Specifically, we will dissect how LWD1-containing condensates generate wave-like transcription to maintain temporal precision in circadian oscillations. Concurrently, we will investigate multifaceted translational control mechanisms during light-mediated

seedling development. This includes delineating how processing bodies (P-bodies) selectively sequester mRNAs and stall their translation, evaluating how ribosome collisions and chemical modifications modulate protein output, and tracking localized translation adjacent to the nucleus and chloroplasts. Ultimately, this integrated program will clarify how macromolecular condensation and spatiotemporal mRNA triage shape the transcriptome and translatome, providing paradigm-shifting insights into the mechanisms ensuring timely environmental adaptation and developmental precision in plants.

Selected Publications

Lu KJ, Hsu CW, Jane WN, Peng MH, Chou YW, Huang PH, Yeh KC, Wu SH, Liao JC. Dual-cycle CO_2 fixation enhances growth and lipid synthesis in *Arabidopsis thaliana*. *Science*. 2025 Sep 11;389(6765):eadp3528. doi: 10.1126/science.adp3528.

Wu HW, Fajiculay E, Wu JF, Yan CCS, Hsu CP, Wu SH. Noise reduction by upstream open reading frames. *Nat Plants*. 2022 May;8(5):474-480. doi: 10.1038/s41477-022-01136-8.

Jang GJ, Yang JY, Hsieh HL, Wu SH. Processing bodies control the selective translation for optimal development of *Arabidopsis* young seedlings. *Proc Natl Acad Sci USA*. 2019 Mar 26;116(13):6451-6456. doi: 10.1073/pnas.1900084116.

Chen GH, Liu MJ, Xiang Y, Sheen J, Wu SH. TOR and RPS6 transmit light signals to enhance protein translation in deetiolating *Arabidopsis* seedlings. *Proc Natl Acad Sci USA*. 2018 Dec 11;115(50):12823-12828. doi: 10.1073/pnas.1809526115.

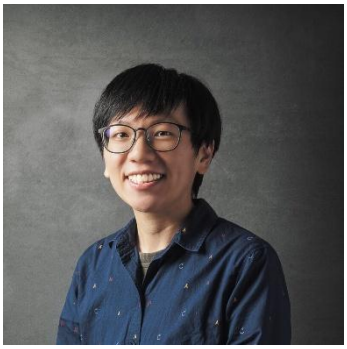
Wu JF, Tsai HL, Joanito I, Wu YC, Chang CW, Li YH, Wang Y, Hong JC, Chu JW, Hsu CP, Wu SH. LWD-TCP complex activates the morning gene *CCA1* in *Arabidopsis*. *Nat Commun*. 2016 Oct 13:7:13181. doi: 10.1038/ncomms13181.

Honors and Awards

Ho Chin Tui Outstanding Research Award, Ho Chin Tui Foundation (2025)

Enid MacRobbie Corresponding Membership, American Society of Plant Biologists (2021)

The 59th Academic Awards, Ministry of Education, Taiwan (2015)



Ting-Ying Wu

Assistant Research Fellow

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Education

Ph.D., Biology, ETH Zurich (ETHZ), Switzerland (2017)

Professional Experience

Adjunct Assistant Professor, Genome and Systems Biology Program, National Taiwan University, Taiwan

Research Fellow, Temasek Life Sciences Laboratory, National University of Singapore

Research Overview

#Plant evolutionary systems biology #Abiotic stress adaptation #Gene regulatory networks #Multi-omics #Predictive modeling #Bryophytes #Land plant evolution

My research investigates the evolutionary logic that enables land plants to adapt to dynamic environments, particularly heat and drought stress. Using an integrative approach spanning systems biology, multi-omics, and predictive computational modeling, my laboratory works to formulate a quantitative understanding of biological networks across ecological, evolutionary, and physiological scales.

To decode the deep evolutionary architecture of heat stress networks, we established that a conserved transcription factor physically remodels chromatin across species from bryophytes to mammals. Furthermore, a lineage-specific driver recruits distinct proteins to separately govern development and thermal

resistance, revealing how early plants repurposed ancestral stress networks during terrestrialization.

In parallel, my laboratory develops open-source computational toolkits to translate high-dimensional multi-omics datasets into quantitative biological insights. These tools significantly expand accessible proteome diversity and accelerate the discovery of novel stress regulators. My ultimate goal is to bridge evolutionary insights with predictive biology to deliver strategies for engineering climate-resilient crops.

Selected Publications

Yen MR, Lin KH, Thalimaraw L, Yang HJ, Boonyaves K, Cheng CY, Wu TY. Conserved HSFA1-dependent chromatin dynamics drive heat stress responses in plants. *Cell Rep*. 2025 Dec 23;44(12):116714. doi: 10.1016/j.celrep.2025.116714.

Wu TY, Li YR, Chang KJ, Fang JC, Urano D, Liu MJ. Modeling alternative translation initiation sites in plants reveals evolutionarily conserved *cis*-regulatory codes in eukaryotes. *Genome Res*. 2024 Mar 20;34(2):272-285. doi: 10.1101/gr.278100.123.

Wu TY, Hoh KL, Boonyaves K, Krishnamoorthi S, Urano D. Diversification of heat shock transcription factors expanded thermal stress responses during early plant evolution. *Plant Cell*. 2022 Sep 27;34(10):3557-3576. doi: 10.1093/plcell/koac204.

Wu TY, Goh H, Azodi CB, Krishnamoorthi S, Liu MJ, Urano D. Evolutionarily conserved hierarchical gene regulatory networks for plant salt stress response. *Nat Plants*. 2021 Jun;7(6):787-799. doi: 10.1038/s41477-021-00929-7.

Yen MR, Li YR, Cheng CY, Wu TY, Liu MJ. *TISCalling*: leveraging machine learning to identify translational initiation sites in plants and viruses. *Plant Mol Biol*. 2025 Aug 1;115(4):102. doi: 10.1007/s11103-025-01632-3.

Wang PW, Tien HC, Cheng CY, Wu TY. Modular cytokinin evolution: integrating heat stress and development during plant terrestrialization. *Trends Plant Sci*. 2026 Jun 11:S1360-1385(26)00168-8. doi: 10.1016/j.tplants.2026.05.007.



Tien-Shin Yu

Research Fellow

Email: tienshin@gate.sinica.edu.tw

Education

Ph.D., Institute of Life Science, National Defense Medical College, Taiwan (2000)

Professional Experience

Postdoctoral Researcher, University of California, Davis, USA

Postdoctoral Researcher, Institute of Molecular Biology, Academia Sinica, Taiwan

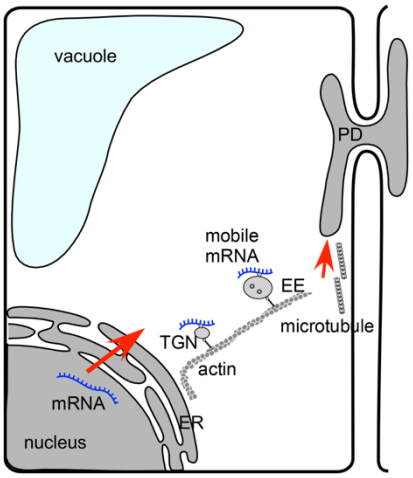
Research Overview

#mobile mRNA #RNA trafficking #plasmodesmata #live-cell imaging

Multicellular organisms rely on systemic communication systems to coordinate cellular processes with environmental dynamics. Our research focuses on understanding how mobile mRNAs function as systemic signaling molecules and how they are selectively transported between cells and organs. By combining genetics, cell biology, biochemistry, genomics, and advanced imaging approaches, we investigate both the biological significance and molecular mechanisms of RNA trafficking in plants.

A major goal of our work is to uncover how specific mRNAs are recognized, transported, and delivered to distant tissues through plasmodesmata and the phloem. Our studies have shown that key developmental regulators, including florigen, antiflorigen and some floral regulators, act as mobile RNA signals that control flowering and developmental transitions. More recently, we discovered that mobile mRNAs are actively transported through an organelle-hitchhiking

mechanism and identified cyclophilin RNA-binding proteins as critical regulators linking RNA transport to organelle dynamics and intercellular communication.



In parallel, we develop innovative live-cell RNA imaging technologies to directly visualize RNA movement in living plants. Our research advances fundamental understanding of systemic communication, while providing a foundation for engineering mobile RNAs for crop improvement and for developing novel approaches to prevent plant viral infection.

Selected Publications

Luo KR, Huang NC, Chang YH, Jan YW, Yu TS. *Arabidopsis* cyclophilins direct intracellular transport of mobile mRNA via organelle hitchhiking. *Nat Plants*. 2024 Jan;10(1):161-171. doi: 10.1038/s41477-023-01597-5.

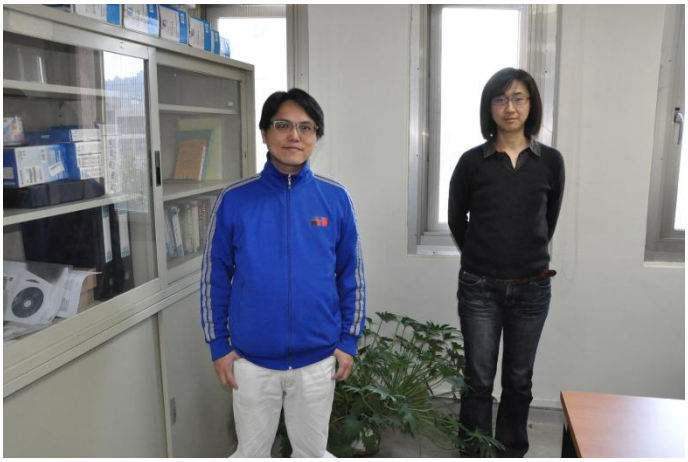
Huang NC, Tien HC, Yu TS. *Arabidopsis* leaf-expressed *AGAMOUS-LIKE 24* mRNA systemically specifies floral meristem differentiation. *New Phytol*. 2024 Jan;241(1):504-515. doi: 10.1111/nph.19293.

Huang NC, Luo KR, Yu TS. Mobility of antiflorigen and PEBP mRNAs in tomato-tobacco heterografts. *Plant Physiol*. 2018 Oct;178(2):783-794. doi: 10.1104/pp.18.00725.

Luo KR, Huang NC, Yu TS. Selective targeting of mobile mRNAs to plasmodesmata for cell-to-cell movement. *Plant Physiol*. 2018 Jun;177(2):604-614. doi: 10.1104/pp.18.00107.

CORE FACILITY
&
TECHNICAL SUPPORT

Bioinformatics Core Lab



Core Team

Wen-Dar Lin (Associate Research Specialist)

Yung-I Lin (Research Assistant)

Core Facility Overview

#Bioinformatics #Statistics #high-performance computation #structure prediction

The Bioinformatics Core Facility was established in early 2007. We provide computational expertise for advancing plant and microbial research. Our mission is to integrate bioinformatics know-how and knowledge into biological discovery by offering consultation, data analyses, customized tool development, and access to high-performance computing resources.

The core facility supports a wide range of analysis services, including genome assembly, SNP and structural variation detection, bulk and single-cell RNAseq data processing, and ChIP-seq data interpretation. Beyond analyses of sequencing data, we also provide systems biology services such as co-expression clustering, protein-protein interaction networks, motif discovery, and functional enrichment studies. We also developed open-source tools such as GOBU for easy-to-use GO

enrichment, MACCU for co-expression clustering, and RackJ for alternative-splicing comparisons.

Building on recent advances in artificial intelligence and machine learning, the facility now also offers structure-related computational services, including protein structure prediction, protein-protein interaction prediction, and protein-ligand docking computation.

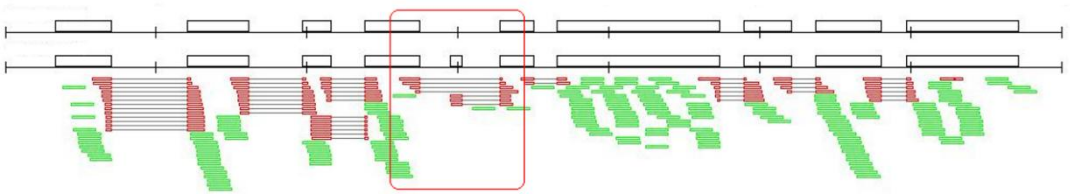


Figure 1. An alternative-splicing event detected by RackJ

Services / Capabilities

scRNAseq/RNAseq/DNAseq data processing
Protein structure/interaction prediction
Systems biology
Customized application development

Selected Publications

Vélez-Bermúdez IC, Lin WD, Chou SJ, Chen AP, Schmidt W. Transcriptome and translatome comparison of tissues from *Arabidopsis thaliana*. *Sci Data*. 2025 Mar 25;12(1):504. doi: 10.1038/s41597-025-04805-3.

Kanno T, Chiou P, Wu MT, Lin WD, Matzke A, Matzke M. A *GFP* splicing reporter in a *coilin* mutant background reveals links between alternative splicing, siRNAs, and coilin function in *Arabidopsis thaliana*. *G3 (Bethesda)*. 2023 Sep 30;13(10):jkad175. doi: 10.1093/g3journal/jkad175.

Huang CK, Lin WD, Wu SH. An improved repertoire of splicing variants and their potential roles in *Arabidopsis* photomorphogenic development. *Genome Biol*. 2022 Feb 9;23(1):50. doi: 10.1186/s13059-022-02620-2.

Cell Biology Core Lab
Electron Microscope Division



Division Team

Wann-Neng Jane (Research Specialist)

Chia-Mei Hsu (Assistant) / Hsiao-Jung Yen (Assistant)

Division Facility Overview

#TEM #SEM #Cryo SEM #STEM #HPF-FS #Sample Preparation #Negative staining #Immunolabeling #Freeze Fracture/Etching

The Electron Microscope Division was established in 1972, and the lab had the second TEM in Taiwan. The lab's mission is to provide up-to-date knowledge on EM methods for cell biology and immunocytochemistry, in particular the use of cryogenic techniques. The staff of the Electron Microscope Division consists of one research specialist and two research assistants. Their work includes maintaining the instruments and the laboratory for sample preparation, microtomy, and various cryogenic methods; training new users to make best use of our instruments and various techniques; assisting users in choosing the right methods and protocols for their research; and supplying a range of reagents specific for the relevant EM methods and protocols. The facilities are composed of a transmission EM, two cryo scanning EMs, and various instruments related to sample preparation, including high pressure freezer, freeze fracture/etching

system, freeze substitution system, microwave biological sample preparation system, ultramicrotomes, freeze dryer, critical point dryer, ion sputter, carbon coater, and glow discharge system. We have various techniques related to electron microscopy and provide the related services, including ultramicrotomy, negative staining, shadow casting, freeze substitution, freeze etching, immunogold labeling, cryo SEM, high pressure freezing, electron tomography, array tomography, and etc.

Services / Capabilities

Transmission Electron Microscopy
Scanning Electron Microscopy
Cryo Scanning Electron Microscopy
Sample Preparation of Block Sectioning using Chemical and Freezing Fixation
Negative Staining; Shadow Casting; Freeze Facture/Etching
Immunolabeling for Ultrathin Sectioning, Negative Staining, Freeze Facture/Etching

Selected Publications

Lu KJ, Hsu CW, Jane WN, Peng MH, Chou YW, Huang PH, Yeh KC, Wu SH, Liao JC. Dual-cycle CO2 fixation enhances growth and lipid synthesis in *Arabidopsis thaliana*. *Science*. 2025 Sep 11;389(6765):eadp3528. doi: 10.1126/science.adp3528.

Chu WH, Lin YS, Guo J, Jane WN, Wang WJ, Lin YY, Liu PH, Huang PY, Chiang WC. The ubiquitin-binding protein ANKRD13A mediates VCP-dependent mitochondrial outer membrane rupture during PINK1/Parkin-mediated mitophagy. *J Biol Chem*. 2025 Nov;301(11):110739. doi: 10.1016/j.jbc.2025.110739.

Kuo YP, Dai SS, Lin EJ, Jane WN, Tsai WH, Tsai WT, Imana ZN, Tung WJ, Su YS, Tien CF, Yu CY, Chen CH, Yu GY. Pathogenic dengue virus TW2015 strain infection triggers anaerobic glycolysis and enhances mortality in diabetic mice. *J Virol*. 2025 Dec 23;99(12):e0117725. doi: 10.1128/jvi.01177-25.

Comprehensive Flow Cytometry Laboratory



Core Manager

Yu-Fang Tseng

Core Facility Overview

#Single-Cell Analysis #Cell Sorting (FACS) #Large-Particle Imaging & Sorting

The Comprehensive Flow Cytometry Laboratory provides advanced flow cytometry analysis and cell sorting services to support cutting-edge research across the life sciences. As a core facility of Academia Sinica, our laboratory specializes in the characterization, quantification, and isolation of diverse biological particles and cells, including viruses, bacteria, algae, fungi, plant cells, animal cells, and small organisms. With one of the broadest sample-sorting service in Taiwan, we support a wide range of research applications spanning microbiology, plant biology, biotechnology, environmental sciences, and biomedical research.

Our facility is equipped with state-of-the-art instrumentation, including the CytoFLEX S high-sensitivity multicolor flow cytometer, the CytoFLEX SRT high-precision cell sorter, and the COPAS VISION 1000 large-particle imaging and sorting system, enabling studies from single cells to multicellular organisms. By integrating advanced analytical platforms with expert consultation and data

interpretation, we assist researchers in generating high-quality datasets and meaningful biological insights. Through professional service, technical innovation, and comprehensive research support, the facility contributes to scientific discovery and advances in life science research.

Figure 1. Comprehensive Flow Cytometry Laboratory workflow & services

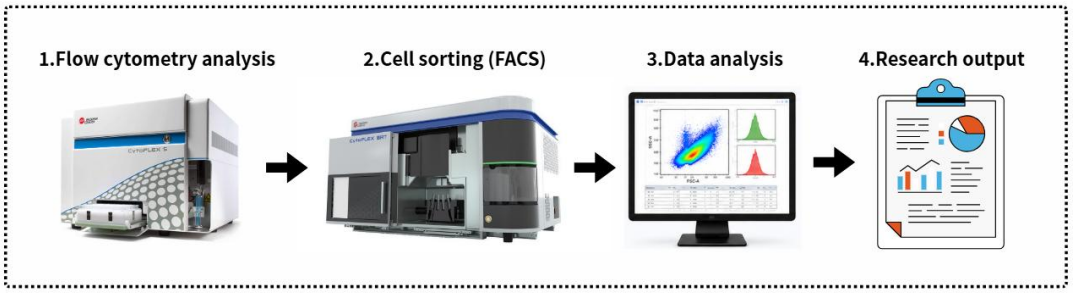
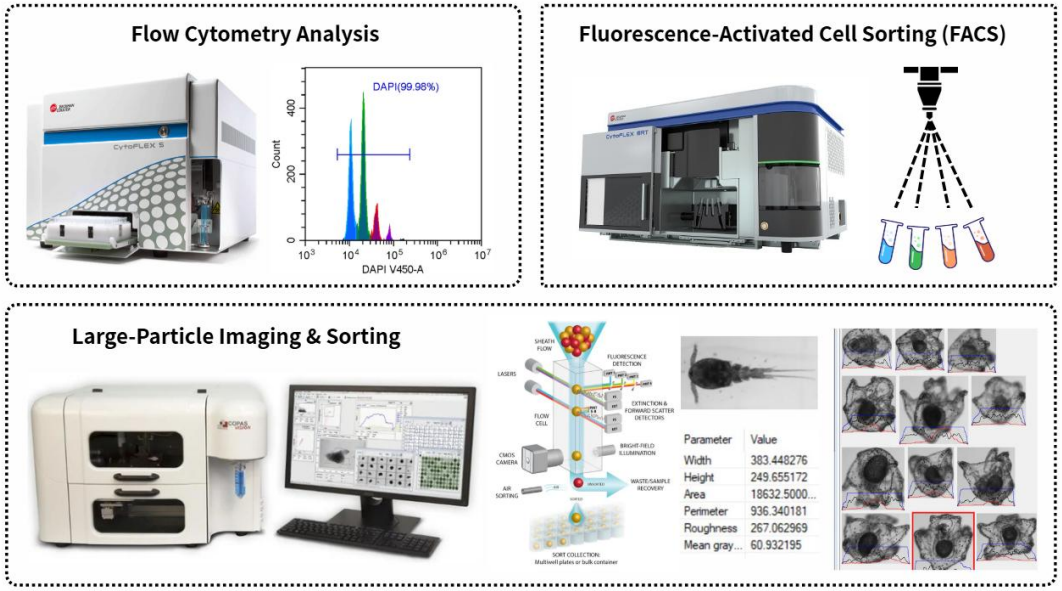
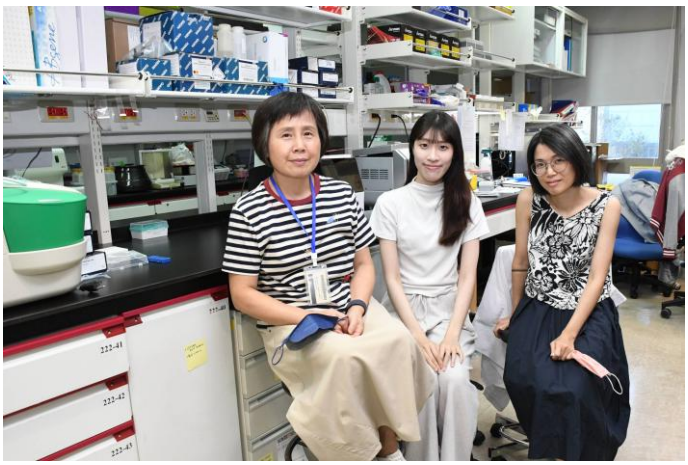


Figure2. Key Technologies



Genomic Technology Core Lab
Microarray and Sequencing Division



Core Team

Shu-Jen Chou (Research Specialist)

Ai-Ping Chen (Research Assistant)

Herng-Shiuan Ting (Research Assistant)

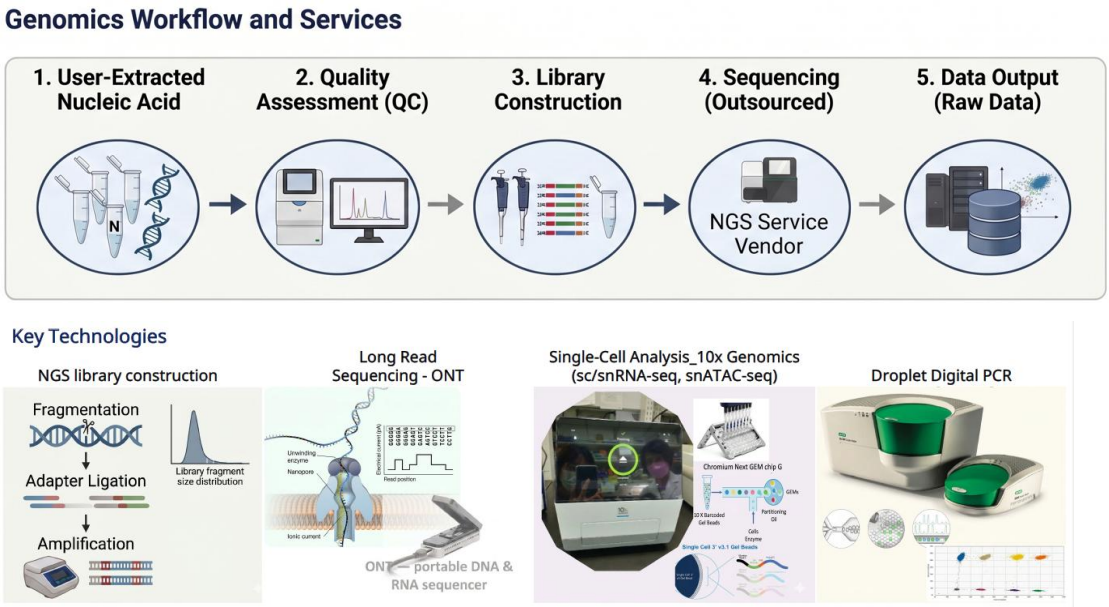
Core Facility Overview

#Genomics #Transcriptomics #Next Generation Sequencing #Long-Read Sequencing

The Genomic Technology Core (Microarray and Sequencing Division) delivers comprehensive genomic and transcriptomic solutions to advance plant and microbial research. Our facility offers end-to-end services, encompassing rigorous nucleic acid quality assessment, droplet digital PCR (ddPCR), next-generation sequencing (NGS) library construction, and long-read sequencing via Oxford Nanopore Technologies (ONT). These platforms empower researchers to deeply investigate transcriptomic profiles, structural variations, transcript diversity, and complex regulatory mechanisms.

We support diverse applications, including bulk and single-cell/single-nucleus analysis, small RNA analysis, epigenomic profiling, and full-length transcriptome characterization. Recognizing the unique challenges of plant and microbial

samples, we utilize standardized workflows and optimized protocols to consistently yield high-fidelity genomic data. Beyond technical execution, our division serves as a collaborative partner, offering expert consultation across the entire experimental workflow—from study design and sequencing strategy selection to sample evaluation and data interpretation—thereby facilitating high-impact studies in functional genomics, transcriptomics, and gene regulatory mechanisms.



Services / Capabilities

NGS Library Construction

Long-Read Sequencing: ONT Library Construction and Sequencing

Single-Cell Analysis: 10X Genomics

Droplet Digital PCR (ddPCR)

Live-Cell-Imaging Core Lab



Core Team

Mei-Jane Fang (Research Assistant)

Ji-Ying Huang (Research Assistant)

Core Facility Overview

#Confocal microscopy #Fluorescence imaging #Live-cell imaging #Time-lapse imaging #Fluorescence lifetime imaging (FLIM) #Image analysis #3D reconstruction #Quantitative microscopy

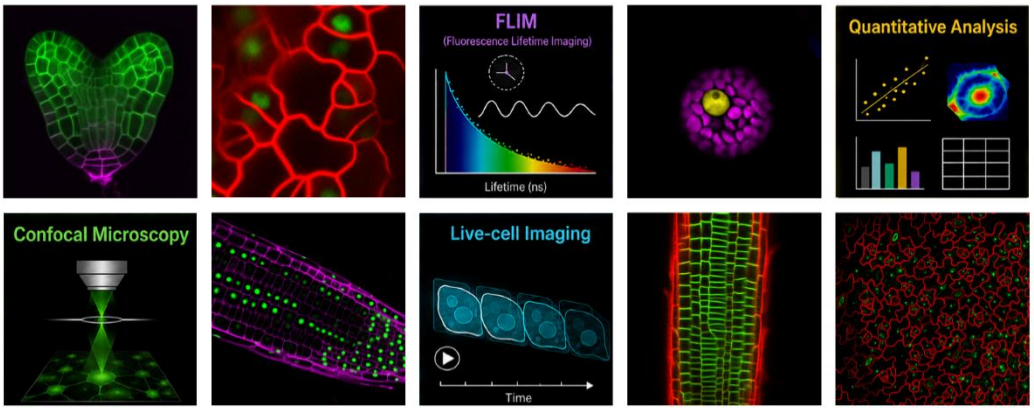
The Live-Cell Imaging Core Laboratory at the Institute of Plant and Microbial Biology, Academia Sinica, provides advanced imaging services to support a wide range of biological and biomedical research. The facility specializes in high-resolution light and fluorescence microscopy, including confocal imaging, live-cell imaging, time-lapse acquisition, and fluorescence lifetime imaging (FLIM), enabling visualization and quantitative analysis of dynamic cellular processes in living systems.

The core is equipped with state-of-the-art imaging platforms, including confocal laser scanning microscopy, deconvolution microscopy, and laser microdissection systems. These technologies allow users to perform detailed structural and

functional studies at cellular and subcellular levels across plant and microbial systems.

In addition to image acquisition, the facility provides training, technical consultation, and support for experimental design, imaging optimization, image analysis, and quantitative data extraction. Dedicated image-processing workstations further support three-dimensional reconstruction, quantitative imaging, and advanced image analysis workflows.

The facility supports diverse research fields including plant biology, microbiology, and cell biology, contributing to studies of cellular organization, protein localization, molecular interactions, and dynamic biological processes.



Services / Capabilities

- Confocal microscopy
- Fluorescence imaging
- Live-cell imaging and time-lapse imaging
- Fluorescence lifetime imaging (FLIM)
- Image analysis and quantitative microscopy

Proteomics Core Lab



Core Team

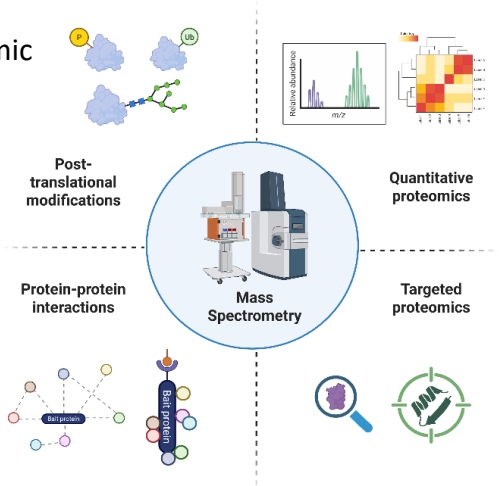
Chuan-Chih Hsu (Associate Research Specialist)
Pei-Yi Lin (Associated R&D Scientist)
Chin-Wen Chen (Assistant R&D Scientist)
Ting-An Chen (Research Assistant)
Po-Tsang Chen (Research Assistant)

Core Facility Overview

#Proteomics #Mass Spectrometry #LC-MS/MS
#Quantitative Proteomics #PTM Proteomics #Targeted Proteomics

The Proteomics Core Laboratory (PCL) provides state-of-the-art liquid chromatography tandem mass spectrometry (LC-MS/MS) services to researchers across the Institute of Plant and Microbial Biology (IPMB) and the Agricultural Biotechnology Research Center (ABRC). Our facility delivers discovery and targeted proteomics, including protein identification, global expression quantification, post-translational modification (PTM) analysis, protein interactome mapping, and large-scale phosphoproteomics and N-glycoproteomics profiling from plants, bacteria, and fungi. Operating a Bruker timsTOF HT and a Thermo Q-Exactive Orbitrap with DIA-PASEF and data-rich acquisition, we support deep, quantitative proteome coverage across diverse sample types. Beyond routine

services, PCL develops advanced workflows such as the tandem S-Trap-IMAC and TIMAHAC dual enrichment strategies, enabling sensitive, high-throughput plant PTM analysis. We also offer consultation on experimental design, sample preparation, and data interpretation, alongside user training in modern proteomic techniques, supporting research in plant stress signaling, microbial biology, and protein function.



Services / Capabilities

Protein identification
Post-translational modification analysis
Global proteomic quantification
Protein interactome mapping
Targeted peptide/protein analysis
Proteomics data analysis
Proteomics method development

Selected Publications

Chen CW, Chen TA, Lin PY, Lin SY, Hsu CC. Integrated single-tip IMAC-HILIC enables simultaneous analysis of plant phosphoproteomics and N-glycoproteomics. *J Proteome Res*. 2025 Jul 4;24(7):3560-3568. doi: 10.1021/acs.jproteome.5c00185.

Chen CW, Lin PY, Lai YM, Lin MH, Lin SY, Hsu CC. TIMAHAC: streamlined tandem IMAC-HILIC workflow for simultaneous and high-throughput plant phosphoproteomics and N-glycoproteomics. *Mol Cell Proteomics*. 2024 May;23(5):100762. doi: 10.1016/j.mcpro.2024.100762.

Chen CW, Tsai CF, Lin MH, Lin SY, Hsu CC. Suspension trapping-based sample preparation workflow for in-depth plant phosphoproteomics. *Anal Chem*. 2023 Aug 22;95(33):12232-12239. doi: 10.1021/acs.analchem.3c00786.

Small Molecule Metabolomics Core Lab



Core Manager

Yu-Ching Wu

Core Facility Overview

#Metabolomics #LC-MS/MS #GC-MS #Phytohormones

The Small Molecule Metabolomics Core Laboratory is dedicated to providing comprehensive metabolomics analysis services. Utilizing advanced chromatographic systems including UHPLC, LC-MS/MS, GC-FID, and HPAEC, the laboratory enables precise qualitative and quantitative analysis of thousands of metabolites spanning amino acids, lipids, carbohydrates, organic acids, and plant hormones. The facility specializes in both targeted and untargeted metabolomics, supporting lipidomics and related research across diverse sample types including tissues, cells, and plant extracts. In close collaboration with the Academia Sinica Metabolomics Core Facility, the laboratory also offers high-resolution mass spectrometry analysis. Beyond core analytical services, the facility provides method development, experimental design consultation, multivariate data analysis (PCA and PLS-DA), and instrument training to support research in plant science and microbiology. Over the past five years, the laboratory has processed 1,800 LC-MS samples with more than 5,000 injections.

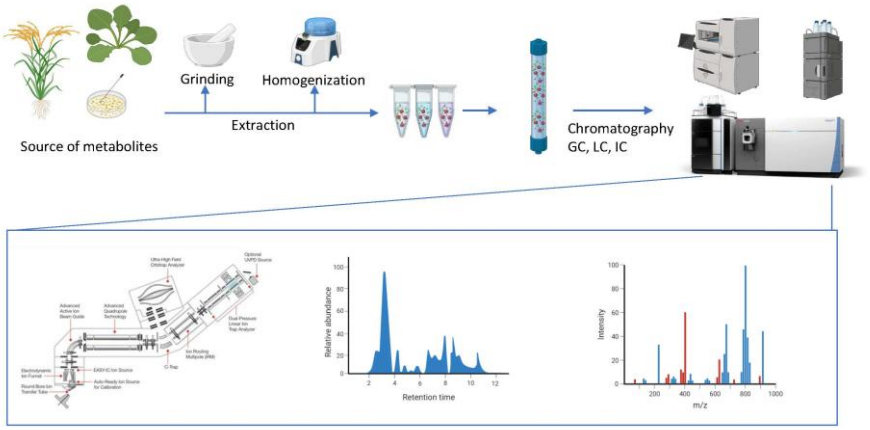


Figure: Small Molecule Metabolomics Lab workflow

Services / Capabilities

Targeted qualitative and quantitative analysis

Untargeted metabolomics analysis and principal component analysis

Compound identification

New methods development

Instruments and software training course

Experimental design and data consultation

Plant hormone extraction

Selected Publications

Hsu CC, Chen CM, Ju YM, Wu YC, Hsieh HM, Yang SH, Su CT, Fang TC, Setyaningsih W, Li SC. Effects of consuming pulsed UV light-treated *Pleurotus citrinopileatus* on Vitamin D nutritional status in healthy adults. *Foods*. 2025 Jan 15;14(2):259. doi: 10.3390/foods14020259.

Ngo AH, Wu YC, Nakamura Y. Bidirectional movement of tunicamycin in *Arabidopsis thaliana*. *New Phytol.* 2024 Jan;241(1):10-16. doi: 10.1111/nph.19306.

Tsai HH, Rodríguez-Celma J, Lan P, Wu YC, Vélez-Bermúdez IC, Schmidt W. Scopoletin 8-hydroxylase-mediated fraxetin production is crucial for iron mobilization. *Plant Physiol.* 2018 May;177(1):194-207. doi: 10.1104/pp.18.00178.

Plant Growth Facility & Experimental Farm




Core Manager

Ching-I Kuo

Core Facility Overview

#Growth Facility #Rice Field #Experimental Farm

The Plant Growth Facility & Experimental Farm provide IPMB researchers with diverse environments for plant cultivation and experiments, ranging from well-controlled indoor facilities to outdoor field sites. The facility includes plant growth rooms, tissue culture rooms, algal culture rooms, pathogen-related plant growth rooms, and more than 20 plant growth chambers, as well as paddy fields, dryland fields, and concrete troughs areas.

To support diverse experimental needs, the facility is equipped with artificial lighting, temperature and humidity control systems, and network-based environmental monitoring and alert systems. Dedicated spaces are also available for studies involving regulated plant pathogens and microorganisms, with operations conducted in accordance with biosafety and quarantine requirements.

Recent upgrades include LED lighting, improved environmental control systems, energy-efficient equipment, renovated irrigation channels, and restored field

areas. Rice harvested from spare space is also packaged into small gift bags as commemorative items for IPMB.

Through professional management and regular maintenance, the Plant Growth Facility & Experimental Farm support research from fundamental plant biology to applied agricultural and environmental studies.

Services / Capabilities

Soil media and fertilizer application

Pest and disease control

Plant Growth Facility

Facility Type	Specifications	Quantity
Growth Chambers	Standard	20 units
Plant Growth Rooms	22°C/28°C with high light	5 rooms
Tissue Culture Rooms	22°C/25°C	4 rooms
Algae Culture Room	28°C	1 room
Infectious Plant Growth Rooms	Biosafety-compliant	4 rooms

Experimental Farm

Field Type	Specifications	Quantity
Paddy field	Rice cultivation	2,000 m^2
Concrete Troughs	Outdoor / Experimental	5 sets
Dry Farmland Ridges	Field experiments	25 ridges

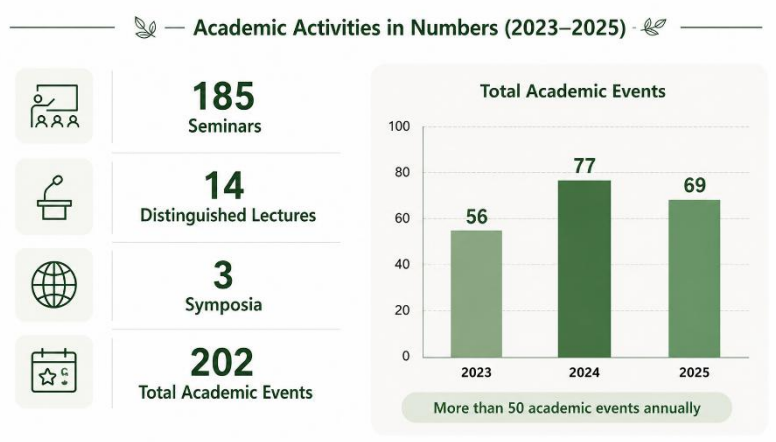
ACADEMIC ENGAGEMENT

Academic Activities

Scientific exchange is an integral part of IPMB's research culture. Throughout the year, the institute organizes a wide range of academic activities, including international symposia, seminars, distinguished lectures, and workshops. These events provide opportunities for researchers to share new discoveries, explore emerging research directions, and establish collaborations across disciplines, institutions, and international research communities. With more than 50 academic events held annually, IPMB maintains a vibrant and dynamic environment for scientific exchange and collaboration.

IPMB regularly welcomes leading scientists from Taiwan and around the world through its symposium and seminar programs. The institute also hosts several distinguished lecture series, including the IPMB Distinguished Lectures, the Hsien-Wen Li Memorial Lectures, the Shang-Fa Yang Memorial Lectures, and the Shu-Chen Grace Chen Memorial Lectures, which bring internationally recognized scholars to engage with the IPMB community.

In addition to formal academic events, faculty seminars, informal faculty chalk talks, technical workshops, and student presentation activities foster an active environment for discussion, learning, and collaboration. Collectively, these activities strengthen IPMB's connections with the global scientific community and support the continual exchange of knowledge and ideas in plant and microbial biology.



Young Investigator Association

The Young Investigator Association (YIA) was established to foster communication, collaboration, and professional development among early-career researchers at IPMB. Serving as a platform that promotes interdisciplinary interaction, YIA helps connect young scientists from diverse academic backgrounds, research fields, and cultural communities.

Through a variety of academic, professional, and networking activities, YIA promotes the exchange of knowledge, research experiences, and skills among early-career researchers. These programs support professional development, encourage cross-disciplinary collaboration, and create opportunities for interaction across research groups and scientific disciplines.

Beyond academic engagement, YIA also contributes to a welcoming and inclusive research environment by organizing community building and cultural exchange activities. By supporting both scientific growth and personal development, YIA plays an important role in strengthening the vibrant and collaborative research culture at IPMB.



Academia Sinica High School Program for Talent Cultivation in Life Sciences

Established in 1984, the Academia Sinica High School Program for Talent Cultivation in Life Sciences aims to inspire talented high school students with a strong interest in the life sciences and introduce them to scientific research at an early stage. Each year, promising first-year students from high schools across Taiwan are selected to participate in a three-year training program.

Students receive foundational training in biology, including plant biology, microbiology, molecular biology, physiology, cell biology, ecology, and biotechnology, while developing essential skills in scientific thinking, experimental design, data analysis, and problem-solving. Beginning in the summer after their first year, students select research topics based on their interests and conduct hands-on research under the guidance of Academia Sinica researchers through their senior year.

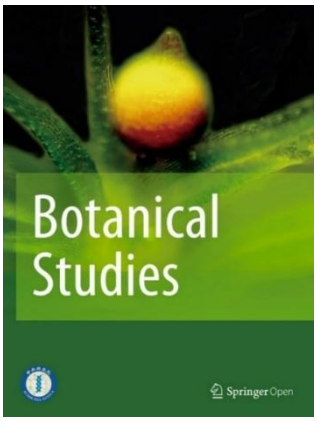
By combining classroom learning with practical research experience and access to Academia Sinica's research facilities, the program helps students build a strong foundation in the life sciences, broaden their scientific perspectives, and develop the knowledge and skills needed to pursue future studies and careers in scientific research.





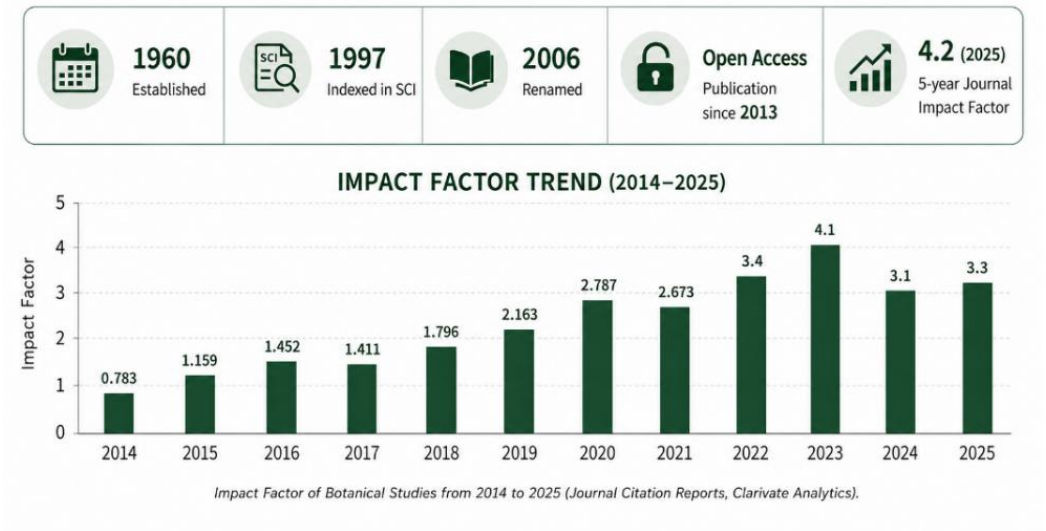


Botanical Studies



Botanical Studies is an international peer-reviewed journal published by the Institute of Plant and Microbial Biology, Academia Sinica. The journal covers a broad spectrum of plant-related research, including taxonomy, morphology, development, genetics, evolution, reproduction, systematics, and biodiversity, as well as studies on algae and fungi. It publishes original research articles and reviews that advance knowledge across the plant sciences.

Established in 1960, *Botanical Studies* has served as a platform for the communication and dissemination of plant science research for more than six decades. The journal is supported by an international Editorial Board whose members represent diverse areas of expertise in plant biology and related disciplines. Through its peer review process, the journal facilitates scientific exchange among researchers from Taiwan and around the world.
Botanical Studies has been indexed in the Science Citation Index (SCI) since 1997. According to the Journal Citation Reports (JCR), the journal achieved an Impact Factor of 4.1 in 2023 and has maintained an Impact Factor above 3.0 in recent years.



Impact Factor of Botanical Studies from 2014 to 2025 (Journal Citation Reports, Clarivate Analytics).

ACTIVITIES PHOTOS

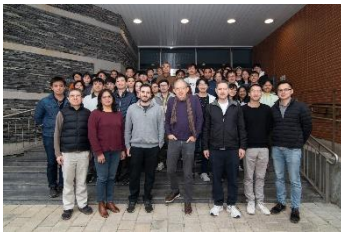

IPMB



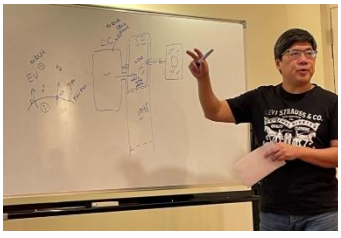

A Journey to the
Beauty of Orchids


Immune responses against SARS-CoV-2 infection
focusing on antibody responses and vaccine design


How do plants sense and distribute nitrate
to optimize utilization efficiency?







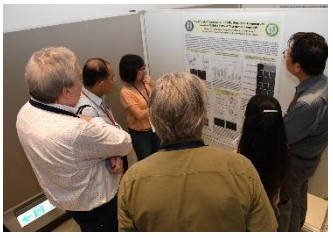





植微所80週年生日快樂!
「植」得慶祝「微」來可期
IPMB
植男植女
一起80年!




IPMB
INTERNSHIP PROGRAM



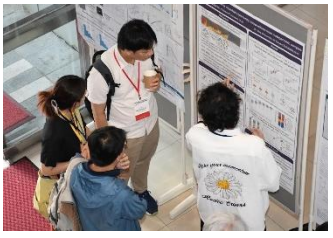



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Spring



































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