

# 제1회 Global Plant Stress Research Center (GPSRC) 및 2024 한국분자세포생물학회 식물분자생물학분과 국제심포지엄

날짜 : 9월 23일(월)-24(화)

장소 : 건국대학교 새천년관 우곡국제회의장

주관 : 건국대학교, 글로벌식물스트레스센터, 한국분자세포생물학회 식물분자생물학분과



Date: September 23rd (Monday) - 24th (Tuesday)

Venue: Konkuk University, Seoul

(건국대학교 새천년관 B2층 우곡국제회의장)

### Organizer

- Korean Side: Dae-Jin Yun (Konkuk University)
- Foreign Side: Zheng-Yi Xu (Northeast Normal University, China)

### International Speaker List

- Jose M. Pardo (Spain)
- Miguel Botella (University of Malaga, Spain)
- Pradhan Sriharsa (NEB, USA)
- Takashi Hashimoto (NAIST, Japan)
- Nozomu Koizumi (Osaka Metropolitan University, Japan)
- Takeshi Nakano (Kyoto University, Japan)
- Yang Zhao (Shanghai Center for Plant Stress Biology, Chinese Academy of Sciences)
- Bao Liu (Northeast Normal University, China)
- Gao Xiang (Northeast Normal University, China)
- Zheng-Yi Xu (Northeast Normal University, China)
- Jing Bo Jin (Institute of Botany, Chinese Academy of Sciences)

### Korean Speaker List

- Tae-Wuk Kim (Hanyang University)
- Sun-Hwa Ha (Kyung Hee University)
- Choon-Tak Kwon (Kyung Hee University)
- Byeong-ha Lee (Sogang University)
- Kyuha Choi (POSTECH)
- Junghoon Park (Konkuk University)
- Lin Woo Kang (Konkuk University)
- Jaebum Kim (Konkuk University)
- Ju Dong Yeo (Konkuk University)
- Akhtar Ali (Konkuk University)

## Day 1: September 23 (Monday)

8:30-10:00 Registration

### Session 1 Chair: Doil Choi (Seoul National University)

10:00-10:25 **Takashi Hashimoto (Nara Institute of Science and Technology, Japan)**

- Acute and transient microtubule disassembly by osmotic stress: What is it good for?

10:25-10:50 **Yang Zhao (Shanghai Center for Plant Stress Biology, China)** - Plant

responses to water stress: back to the roots

10:50-11:10 **Byeong-ha Lee (Sogang University, Korea)** - RNA splicing-regulated stress tolerance in plants

11:10-11:25 Coffee Break

### Session 2 Chair: Jong-Seong Jeon (Kyung Hee University)

11:25-11:50 **Bao Liu (Northeast Normal University, China)** - Rapid formation of stable autotetraploid rice from genome-doubled F1

11:50-12:10 **Kyuha Choi (Pohang University of Science and Technology, Korea)** - Control of meiotic crossover interference in Arabidopsis

12:10-12:30 **Choon-Tak Kwon (Kyung Hee University, Korea)** - Evolutionary diversification of peptide and receptor compensation in plant stem cell control

12:30-14:30 Lunch

### Session 3 Chair: Yoo-Sun Noh (Seoul National University)

14:30-14:55 **Sriharsa Pradhan (New England Biolabs, USA)** - DNA methylation establishment and maintenance dynamics in plants

14:55-15:15 **Junghoon Park (Konkuk University, Korea)** - Cold stress-induced dynamic chromatin accessibility in Arabidopsis

15:15-15:35 **Jaebum Kim (Konkuk University, Korea)** - A computational approach for constructing a chromosome-level genome assembly

15:35-16:00 **José M. Pardo (Institute of Plant Biochemistry and Photosynthesis, CSIC, Spain)** - The vacuolar K<sup>+</sup>/H<sup>+</sup> exchangers NHX and the calmodulin-like protein CML18 constitute a pH-sensing module responding to the K<sup>+</sup> status in Arabidopsis

16:00-16:20 Coffee Break

#### **Session 4 Chair: Woe-Yeon Kim (Gyeongsang National University)**

16:20-16:45 **Takeshi Nakano (Kyoto University, Japan)** - Chemical biology research to reveal plant growth and stress resistance mechanism via brassinosteroid signaling

16:45-17:05 **Tae-Wuk Kim (Hanyang University, Korea)** - BZR1 cooperates with PAP1 of MBW complex to promote anthocyanin biosynthesis in Arabidopsis shoots

17:05-17:30 **Gao Xiang (Northeast Normal University, China)** - The biosynthesis and regulation of volatile terpenes and flavonoids in ornamental flowers

17:30-17:50 **Akhtar Ali (Konkuk University, Korea)** - Crosstalk of ABA signaling with flowering time in Arabidopsis

#### **Day 2: September 24 (Tuesday)**

#### **Session 5 Chair: Nam-Chon Paek (Seoul National University)**

9:00-9:25 **Miguel A. Botella (University of Málaga, Spain)** - From binder to bender: the dual role of SYT1 on stress-related Ca<sup>2+</sup> responses at ER-PM CS

9:25-9:50 **Sun-Hwa Ha (Kyung Hee University, Korea)** - The cytoplasmic protein trapping by a miProtein PSEUDO-ETIOLATION IN LIGHT family negatively governs photosynthesis in rice

9:50-10:15 **Zheng-Yi Xu (Northeast Normal University, China)** - The OsMPK6-OsERFA module functions in UV-B induced photomorphogenesis

10:15-10:40 **Lin Woo Kang (Konkuk University, Korea)** - Crystal structure of rice NADP-ME playing an essential role in plant immune response

10:40-11:00 Coffee Break

#### **Session 6 Chair: Sang Yeol Lee (Gyeongsang National University)**

11:00-11:25 **Nozomu Koizumi (Osaka Metropolitan University, Japan)** - Perception gap of genome-edited foods in Japan

11:25-11:50 **Jing Bo Jin (Institute of Botany, Chinese Academy of Sciences)** - A transcription factor Legume shoot branching 1 improves both yield and quality in soybean

11:50-12:15 **Ju Dong Yeo (Konkuk University, Korea)** - Creating a digital map of lipid oxidation using mass spectrometry-based metabolomics and lipidomics: An integrated system for assessing lipid oxidation of edible oil

12:15- Lunch and City Tour

## Takashi Hashimoto

Nara Institute of Science and Technology  
8916-5 Takayama, Ikoma, Nara 630-0101, Japan  
e-mail: hasimoto@bs.naist.jp



### Education

1/1988 Ph. D., Kyoto University  
3/1982 M.S., Kyoto University  
3/1980 B.S., Kyoto University

### Experience and Career

2021 – present Designated Professor, Division of Educational Development, NAIST  
2000 – 2021 Professor, NAIST  
1994 – 2000 Associate professor, Graduate School of Biological Sciences, Nara Institute of Science and Technology (NAIST)  
1985 – 1994 Assistant professor; Faculty of Agriculture, Kyoto University

### Research Interests

Functions of the microtubule cytoskeleton in plant interphase cells

### Publications (5 papers)

1. N. Yagi, T. Kato, S. Matsunaga, D.W. Ehrhardt, M. Nakamura, and T. Hashimoto (2021) An anchoring complex recruits katanin for microtubule severing at the plant cortical nucleation sites. *Nat. Commun.* 12, 3684. <https://doi.org/10.1038/s41467-021-24067-y>
2. J.H. Wong, T. Kato, S.A. Belteton, R. Shimizu, N. Kinoshita, T. Higaki, Y. Sakumura, D.B. Szymanski, and T. Hashimoto (2019) Basic Proline-rich Protein-mediated microtubules are essential for lobe growth and a flattened cell geometry. *Plant Physiol.* 181: 1535-1551. doi.org/10.1104/pp.19.00811
3. N. Yagi, S. Matsunaga, and T. Hashimoto (2018) Insights into cortical microtubule nucleation and dynamics in Arabidopsis leaf cells. *J. Cell Sci.* 131 jcs203778. doi:10.1242/jcs.203778
4. T. Hotta, S. Fujita, S. Uchimura, M. Noguchi, T. Demura, E. Muto, and T. Hashimoto (2016) Affinity purification and characterization of functional tubulin from cell suspension cultures of Arabidopsis and tobacco. *Plant Physiol.* 170: 1189-1205. Doi: 10.1104/pp.15.001173
5. S. Fujita, J. Pytela, T. Hotta, T. Kato, T. Hamada, R. Akamatsu, Y. Ishida, N. Kutsuna, S. Hasezawa, Y. Nomura, H. Nakagami, and T. Hashimoto (2013) An atypical tubulin kinase mediates stress-induced microtubule depolymerization in Arabidopsis. *Curr. Biol.* 23: 1969-1978. doi: 10.1016/j.cub.2013.08.006

# Acute and Transient Microtubule Disassembly by Osmotic Stress: What is it good for?

Takashi Hashimoto

*Nara Institute of Science and Technology*  
Correspondence: hasimoto@bs.naist.jp

## Abstract

Terrestrial colonization of land plants involves adaptation to environmental stresses, such as dehydration. While innovation of stomata and abscisic acid (ABA) pathways during land plant evolution is well studied, it is not known how green algae and seed plants utilize the ABA-independent stress response strategies. We found that hyperosmotic stress on *Arabidopsis* plants rapidly and transiently induces phosphorylation of  $\alpha$ -tubulins at the critical interdimer interface at Thr349. The phosphorylated tubulins are not incorporated into the microtubule polymer, thereby efficiently inducing disassembly of existing microtubules. The responsible plant-specific tubulin kinase Propyzamide Hypersensitive 1 (PHS1) is normally inactivated by the phosphatase activity provided by the juxtaposed phosphatase domain and its N-terminal region resembling a Kinase-Interaction Motif (KIM), but is immediately activated upon hyperosmotic and salinity stresses. Phosphatase-dead PHS1 mutants are constitutively active, and induce drastic microtubule depolymerization in planta. In vitro enzyme assays and protein structure predictions by AlphaFold suggest two distinct mechanisms for the kinase regulation: the KIM in the N-terminal extension facilitates folding of the N-terminus onto the kinase domain, thereby physically blocking the substrate (tubulin) accessibility, whereas the C-terminal phosphatase domain dephosphorylates (putative) critical residues in the kinase catalytic site. Acute and transient tubulin phosphorylation and subsequent microtubule disassembly by osmotic stress are highly conserved in *Arabidopsis*, liverwort, and *Chlamydomonas*, demonstrating its ancient origin in fresh-water green algae, prior to evolution of the ABA pathway. Physiological significance is largely unclear, however, possibly due to its highly transient nature.

**Key words:** microtubule, tubulin, phosphorylation, protein kinase, hyperosmotic stress

## Zhao, Yang



Professor,  
CAS Center for Excellence in Molecular Plant Sciences,  
Chinese Academy of Sciences  
E-mail, [zhaoyang@cemps.ac.cn](mailto:zhaoyang@cemps.ac.cn)

### EDUCATION

2000-2004 China Agricultural University (CAU), BS  
2004-2009 CAU & National Institute of Biological Sciences (NIBS), *Ph.D.*  
2009-2012 NIBS & CAU, *Postdoc.*  
2012-2016 Purdue University, *Postdoc.*

### EXPERIENCE AND CAREER

2016-present Professor, Shanghai Center for Plant Stress Biology, CAS Center for Excellence in Molecular Plant Sciences, Chinese Academy of Sciences

### RESEARCH INTERESTS

Osmotic Stress Signaling in Plant

### PUBLICATIONS (5 papers)

1. Yu B, et al. (2024). How plants sense and respond to osmotic stress. *Journal of Integrative Plant Biology* 66, 394-423.
2. Yu B, et al. (2022). Root twisting drives halotropism via stress-induced microtubule reorientation. *Developmental Cell* 57, 2412-2425.e2416.
3. Chen Q, et al. (2022). Phosphorylation of SWEET sucrose transporters regulates plant root:shoot ratio under drought. *Nature Plants* 8, 68-77.
4. Chen K, et al. (2020). BONZAI proteins control global osmotic stress responses in plants. *Current Biology* 30, 4815-4825 e4814.
5. Chen K, et al. (2020). Abscisic acid dynamics, signaling, and functions in plants. *Journal of Integrative Plant Biology* 62(1):25-54.

# Plant responses to water stress: back to the roots

Yang Zhao

*<sup>1</sup>Shanghai Center for Plant Stress Biology, and CAS Center for Excellence in Molecular Plant Sciences, Chinese Academy of Sciences, Shanghai 200032, China*  
Correspondence: [zhaoyang@cemps.ac.cn](mailto:zhaoyang@cemps.ac.cn)

## Abstract

My research aims to decipher the stress-induced stimuli, identify sensors and core signaling components, and illustrate growth regulation mechanisms, ultimately improving plant drought and salt stress tolerance. We have established scientific models and research systems for osmotic and salt stress signaling. In past years, we discovered the plasma membrane-localized protein OSMO1/BON1 controls early osmotic stress signaling (Current Biology, 2020). We have also found that ABA-activated SnRK2s phosphorylate SWEET sucrose transporters and microtubule-binding protein SP2L, which mediates root growth and halotropism under stressed conditions (Nature Plants, 2022; Developmental Cell, 2022). I will present these discoveries, especially the cellular and molecular mechanisms of root halotropism and hydrotropism, and our recent findings on early osmotic stress signaling.

**Key words:** Osmotic stress signaling; hydrotropism; halotropism; SnRK2s; abscisic acid.



## Pardo, José M.

Professor,  
Institute of Plant Biochemistry and Photosynthesis  
CSIC – University of Seville, Spain  
E-mail: jose.pardo@csic.es



### EDUCATION

1976-1981 University of Seville, B.S.  
1981-1987 Universidad Autonoma de Madrid, *Ph.D.*  
1987-1989 European Molecular Biology Lab (EMBL), Germany, *Postdoc.*

### EXPERIENCE AND CAREER

2016-present Professor, Institute of Plant Biochemistry and Photosynthesis (IBVF-CSIC), Seville, Spain  
2010-2014 Director, Institute of Natural Resources and Agrobiology (IRNAS-CSIC), Seville, Spain.  
2010-2011 Visiting Professor, Plant Stress Genomics Research Center, King Abdullah University of Science and Technology, Saudi Arabia.  
2007-2016 Professor, IRNAS-CSIC, Seville, Spain  
2005-2010 Program Manager, Biotechnology Section, Ministry of Science and Innovation, Spain.  
2002-2010 Research Scientist, IRNAS-CSIC, Seville, Spain  
1998-2005 Head, Plant Biology Dpt. IRNAS-CSIC, Seville, Spain  
1993-1994 Visiting Scientist Center for Plant Stress Physiology, Purdue University, Indiana, USA.  
1995-1997 University, Indiana, USA.  
1989-2002 Scientist IRNAS-CSIC, Seville, Spain

### RESEARCH INTERESTS

Nutrition and Plant Stress Physiology

### PUBLICATIONS (5 papers)

1. Gamez-Arjona F et al. (2024). Inverse regulation of SOS1 and HKT1 protein localization and stability by SOS3/CBL4 in *Arabidopsis thaliana*. *Proc. Natl. Acad. Sci. USA* 121: e2320657121
2. Park HJ et al. (2023) S-acylated and nucleus-localized SALT OVERLY SENSITIVE3/CALCINEURIN B-LIKE4 stabilizes GIGANTEA to regulate Arabidopsis flowering time under salt stress. *Plant Cell* 35,298-317
3. Chen C et al. (2023). A salt stress-activated GSO1-SOS2-SOS1 module protects the Arabidopsis root stem cell niche by enhancing sodium ion extrusion. *The EMBO Journal*, 42: e113004.
4. Cha JY et al (2022). The Na<sup>+</sup>/H<sup>+</sup> antiporter SALT OVERLY SENSITIVE 1 regulates salt compensation of circadian rhythms by stabilizing GIGANTEA in Arabidopsis. *Proc. Natl. Acad. Sci. USA* 119: e2207275119
5. Morales de los Ríos L et al. (2021). The Arabidopsis protein NPF6.2/NRT1.4 is a plasma membrane nitrate transporter and a target of protein kinase CIPK23. *Plant Physiology and Biochemistry* **168**: 239-251.

# The vacuolar K<sup>+</sup>/H<sup>+</sup> exchangers NHX and the calmodulin-like protein CML18 constitute a pH-sensing module responding to the K<sup>+</sup> status in *Arabidopsis*

José M. Pardo

*Institute of Plant Biochemistry and Photosynthesis, Consejo Superior de Investigaciones Científicas and University of Seville, Seville 41092, Spain*

Correspondence: [jose.pardo@csic.es](mailto:jose.pardo@csic.es)

## Abstract

Mounting evidence supports the interdependence between H<sup>+</sup> and Ca<sup>2+</sup> signaling in eukaryotic cells. Shifts in cytosolic pH have been recognized as key signaling events that might precede Ca<sup>2+</sup> spikes. Vacuolar K<sup>+</sup>/H<sup>+</sup> exchangers of the NHX family control luminal pH and, together with K<sup>+</sup> and H<sup>+</sup> transporters at the plasma membrane, have been suggested to regulate cytoplasmic pH. We will show the regulation of vacuolar K<sup>+</sup>/H<sup>+</sup> exchange by cytoplasmic pH and the calmodulin-like protein CML18 in *Arabidopsis*. We have determined the crystal structure of CML18 and found that this atypical Ca<sup>2+</sup>-binding protein has greater pH-sensing ability than Ca<sup>2+</sup>-sensing. Interaction of CML18 with tonoplast exchangers was favored at acidic pH, a physiological condition elicited by K<sup>+</sup> starvation in *Arabidopsis* roots, whereas surplus K<sup>+</sup> produced cytoplasmic alkalinization. Acidic conditions favored CML18 binding and inhibition of K<sup>+</sup>/H<sup>+</sup> exchange at the tonoplast to prevent further ionic imbalance. We conclude that the pH-responsive NHX-CML18 module is an essential component of the cellular K<sup>+</sup>- and pH-stats at the interface between pH- and Ca<sup>2+</sup> signaling.

Funding: Agencia Estatal de Investigación, Spanish Ministry of Science and Innovation (MCIN/AEI/10.13039/501100011033), grants PID2020-119805RB-I00 and PID2021-126863NB-I00, co-financed by “ERDF A way of making Europe”.

**Key words:** K<sup>+</sup> nutrition, pH- and Ca<sup>2+</sup>-signaling, NHX, CML18, *Arabidopsis*

## **Bao Liu**

Distinguished professor

School of Life Sciences, Northeast Normal University, Changchun, China.

E-mail, [baoliu@nenu.edu.cn](mailto:baoliu@nenu.edu.cn)

### **EDUCATION**

1985 BS, Jilin Agricultural University, Changchun China;

1988: MS, Jilin Agricultural University, Changchun China;

1992: PhD, Nanjing Agricultural University, Nanjing, China;

1995-1997□Postdoc, The Weizmann Institute of Science, Israel

2000-2001□Postdoc, Iowa State University, USA

2002-present: Professor, Northeast Normal University, China (distinguished professor since 2006).

### **EXPERIENCE AND CAREER**

2002-present: Professor, Northeast Normal University, China

2006 : distinguished professor

2007 : Head, Key Laboratory of Molecular Epigenetics of the Ministry of Education

2014: Head, the University Natural Science Committee, Northeast Normal University, China

Member, Discipline Appraisal Committee, The State Council of China

### **RESEARCH INTERESTS**

Major research interest include genome evolution, plant polyploidy, plant epigenetics, plant genomics, and crop genetic improvement. Authored or coauthored > 250 peer-reviewed publications.

### **TEACHING**

Five major courses for under and graduate students including international students. Have advised > 150 graduate students who obtained MSc or PhD degrees.

# Rapid formation of stable autotetraploid rice from genome-doubled F1

Bao Liu

Key Laboratory of Molecular Epigenetics of the Ministry of Education (MOE), Northeast Normal University, Changchun 130024, China

Correspondence: [baoliu@nenu.edu.cn](mailto:baoliu@nenu.edu.cn)

Theory predicts that in the absence of selection, a newly formed segmental allopolyploid will rapidly become ‘autopolyploidized’ if duplicated (homoeologous) chromosomes freely recombine by homoeologous exchange (HE). Because selection against meiotic abnormalities is expected to be strong in the initial generations following hybridization and chromosome doubling, we would thus anticipate that rampant genome-wide HEs are uncommon in newly formed segmental allopolyploids. Here we analyzed the whole-genome composition of 202 phenotypically homogeneous and stable rice tetraploid recombinant inbred lines (TRILs) derived from *Oryza sativa* subsp. *japonica* × subsp. *indica* hybridization and whole-genome doubling. We measured functional traits related to growth, development, and reproductive fitness, and analyzed meiotic chromosomal behavior of the TRILs. We uncover factors that constrain the genomic composition of the TRILs, including asymmetric parental contribution and exclusive uniparental segment retention. Intriguingly, some TRILs that have high fertility and grain yield, as well as enhanced resistance or resilience to abiotic stresses, also demonstrate largely stabilized meiosis. These findings have implications for the evolutionary possibility of HE-catalyzed ‘allo-to-auto’ polyploidy transitions in nature. In addition, this study suggests that new polyploid crops may be feasibly created using domesticated congeneric diploid (sub)species as the initial hybridizing parents.

**Keywords:** hybridization, genome doubling, homoeologous exchange, meiotic stability, evolution, polyploid crop

## Choi, Kyuha

Associate Professor,  
*Department of Life Sciences, Pohang University of Science  
and Technology (POSTECH)*  
E-mail, [kyuha@postech.ac.kr](mailto:kyuha@postech.ac.kr)



### EDUCATION

1993-2000 Seoul National University, BS  
2000-2002 Seoul National University, MS  
2002-2007 Seoul National University, *Ph.D.*  
2007-2010 Seoul National University, *Postdoc.*  
2010-2016 University of Cambridge, *Postdoc.*

### EXPERIENCE AND CAREER

2017-present Professor, POSTECH  
2016-2017 Research Professor, Gyeongsang National University  
2017-2022 Suh kyugbae foundation (SUHF) Young Investigator Fellow  
2010-2012 EMBO Long-Term Research Fellow

### RESEARCH INTERESTS

Genetic and Epigenetic Control of Meiotic Crossovers in Plants

### PUBLICATIONS (5 papers)

1. Kim H, et al. (2024) Control of meiotic crossover interference by a proteolytic chaperone network. *Nature Plants* 10, 453-468
2. Kim J et al. (2022) Arabidopsis HEAT SHOCK FACTOR BINDING PROTEIN is required to limit meiotic crossovers and *HEI10* transcription. *EMBO Journal* 41, e109958
3. Nageswaran DC et al. (2021) *HIGH CROSSOVER RATE1* encodes PROTEIN PHOSPHATASE X1 and restricts meiotic crossovers in Arabidopsis. *Nature Plants* 7, 452-467
4. Lim E et al. (2020) DeepTetrad: high-throughput image analysis of meiotic tetrads by deep learning in *Arabidopsis thaliana*. *Plant Journal* 101,473-483
5. Choi K et al. (2018) Nucleosomes and DNA methylation shape meiotic DSB frequency in Arabidopsis transposons and gene regulatory regions. *Genome Research* 28, 532-546

# Control of meiotic crossover interference in *Arabidopsis*

Kyuha Choi

<sup>1</sup>*Department of Life Sciences, Pohang University of Science and Technology, Pohang, Gyeongbuk, Republic of Korea*

Correspondence: [kyuha@postech.ac.kr](mailto:kyuha@postech.ac.kr)

## Abstract

Meiotic crossovers are tightly regulated, with one obligate exchange forming per a pair of homologous chromosomes, and multiple crossovers on the same chromosome pair are rarely formed and widely spaced by crossover interference. In *Arabidopsis thaliana*, crossover number and positioning can be explained by a diffusion-mediated coarsening model. In the model, large, approximately evenly-spaced foci of the pro-crossover E3 ligase HEI10 grow at the expense of smaller, closely-spaced clusters and eventually concentrate at crossover sites. However, the molecular mechanisms that regulate the abundance and dynamics of HEI10 remain unexplored. We performed a forward genetic screen in *Arabidopsis* to identify new regulators of crossover patterning using fluorescence-tagged recombination reporters. We isolated and characterized three *high crossover rate (hcr)* mutants, *hcr1*, *hcr2*, *hcr3*, that increase meiotic crossovers genome-wide and reduce crossover interference. Using a comprehensive array of cytogenetic, genetic, genomic, biochemical and modeling approaches, we demonstrated that HCR1/PPX1 and HCR3/J3 facilitates the proteolysis of HEI10, while HCR2/HSBP represses the transcription of *HEI10*. Our findings provide new insights into how HCR1, HCR2, and HCR3 anti-crossover factors mediate crossover interference through transcriptional and post-translational control of HEI10. In addition, I will also present our ongoing research on how we can increase meiotic crossovers in heterochromatic regions to unlock genetic diversity for plant breeding.

**Key words:** meiosis, crossover, HEI10, HCR3, *Arabidopsis*

## Kwon, Choon-Tak

Assistant Professor,  
Department of Smart Farm Science  
Graduate School of Green-Bio Science  
Kyung Hee University  
E-mail, [ctkwon@khu.ac.kr](mailto:ctkwon@khu.ac.kr)



### EDUCATION

2004-2010 Seoul National University, BS  
2010-2012 Seoul National University, MS  
2012-2015 Seoul National University, *Ph.D.*  
2015-2016 Seoul National University, *Postdoc.*  
2016-2020 Cold Spring Harbor Laboratory, *Postdoc.*

### EXPERIENCE AND CAREER

2021-present Assistant Professor, Kyung Hee University

### RESEARCH INTERESTS

1. Controlling plant architecture for urban agriculture and vertical farming.
2. Dissecting redundancy and compensation of ligands and receptors for plant development.
3. Improving plant tolerance to abiotic stresses by CRISPR technology

### PUBLICATIONS (5 papers)

1. Seo MG, et al. (2024) Evolutionary conservation of receptor compensation for stem cell homeostasis in Solanaceae plants. *Horticulture Research* 11:uhae126
2. Jeong HY et al. (2024) Tomato arabinosyltransferase prevents precocious senescence. *Horticultural Plant Journal*. <https://doi.org/10.1016/j.hpj.2023.11.006>
3. Lim YS, et al. (2024) Comparative yield evaluation of mini-Tomato cultivar in two hydroponic systems. *Horticulture, Environment, and Biotechnology* 65:239-250.
4. Kwon CT, et al. (2022) Dynamic evolution of small signalling peptide compensation in plant stem cell control. *Nature Plants* 8:346-355.
5. Kwon CT, et al. (2020) Rapid customization of Solanaceae fruit crops for urban agriculture. *Nature Biotechnology* 38:182-188.

# Evolutionary diversification of peptide and receptor compensation in plant stem cell control

Choon-Tak Kwon<sup>1,2</sup>

<sup>1</sup>*Department of Smart Farm Science, Kyung Hee University, Yongin 17104, Republic of Korea*

<sup>2</sup>*Graduate School of Green-Bio Science, Kyung Hee University, Yongin 17104, Republic of Korea*

Correspondence: [ctkwon@khu.ac.kr](mailto:ctkwon@khu.ac.kr)

## Abstract

Stem cell homeostasis is crucial for the continuous and programmed formation of organs in plants. This process is regulated by evolutionarily conserved signaling pathways that involve complex interactions among multiple peptide ligands and their receptor-like kinases. Here, we identified compensation mechanisms involving the CLAVATA3 (CLV3) peptide, CLV1 receptor, and their paralogs that support stem cell proliferation in tomato and groundcherry. We examined the evolutionary pathways of these duplicates and their transcriptional compensation, as evidenced by phenotypic comparisons among CRISPR-Cas9-generated plants. Our findings suggest that peptide compensation is maintained by the presence of the closest paralogs, which are directly linked to the fates of these paralogs. Moreover, we found that expression and sequence variations of the peptides affect their compensatory potencies. Unlike the transcriptional compensation mechanism between peptides, we observed that receptor compensation functions effectively even without transcriptional upregulation. This study provides further insights into the evolutionary dynamics of small peptide signaling and how genetic compensation evolves across diverse developmental processes.

**Key words:** Plant stem cell, CLV3 peptide, CLV1 receptor, paralog compensation, Solanaceae



## Sriharsa Pradhan

Distinguished Scientist,  
Division of Molecular Genetics and Genomics,  
New England Biolabs, Inc  
E-mail: [pradhan@neb.com](mailto:pradhan@neb.com)



### EDUCATION

- 1990 Hyderabad Central University, M.Phil.
- 1995 University of Glasgow, *Ph.D*
- 1999 New England Biolabs, Inc Postdoc (Sir Richard J. Roberts (1993 Nobel Laureate in Physiology or Medicine))

### EXPERIENCE AND CAREER

- 2016-present Distinguished Scientist, New England Biolabs, Inc
- 2016-2022 Adjunct Professor, Boston University
- 2007-2014 Associate Director, RNA Division, New England Biolabs, Inc.
- 2002-2016 Group leader, New England Biolabs, Inc.
- 1999-2001 Staff scientist, New England Biolabs, Inc.
- 2000-present Board of directors, Epigenetics Society, USA

### RESEARCH INTERESTS

Epigenetics mechanism and epigenome structure in eukaryotes

### PUBLICATIONS (5 papers); h index: 58

1. Spracklin, G., Abdennur, N., Imakaev, M. et al. (2023) Diverse silent chromatin states modulate genome compartmentalization and loop extrusion barriers. *Nat Struct Mol Biol* 30, 38–51.
2. Estève, PO, et al. (2011) Methylation and phosphorylation switch between adjacent lysine and serine determines human DNMT1 stability. *Nat. Struct. Mol. Biol.* 18: 42-48
3. Cokus, SJ. et al., (2008) Shotgun bisulphite sequencing of the Arabidopsis genome reveals DNA methylation patterning. *Nature* 452: 215-219.
4. Bostick, M. et al. (2007) UHRF1 Plays a Role in Maintaining DNA Methylation in Mammalian Cells. *Science* 317: 1760-1764.
5. Evans, TC., Jr., Xu, MQ. and Pradhan, S. (2005) Protein splicing elements and plants: from transgene containment to protein purification. *Annual Review of Plant Biol.* 56: 375-392.

# DNA methylation establishment and maintenance dynamics in plants

Sriharsa Pradhan

*Division of Molecular Genetics and Genomics, New England Biolabs, 240 County Road, Ipswich, Massachusetts 01938, USA.*

Correspondence: [pradhan@neb.com](mailto:pradhan@neb.com)

## Abstract

DNA methylation is an epigenetic mark that regulates multiple biological processes, including gene expression, development and genome stability. In plants, DNA methylation is found in the CG, CHG and CHH sequence context (where H is A, C or T), and it is highly enriched over repeats and transposable elements (TEs), as it plays a prominent role in Transcriptional Gene Silencing (TGS). Both de novo and maintenance DNA methylation in plants have two different sets of machinery. In plants, de novo DNA methylation is mediated through the RNA-directed DNA methylation (RdDM) pathway, which involves small interfering RNAs (siRNAs) and scaffold RNAs in addition to an array of proteins along with DNA methyltransferase DOMAINS REARRANGED METHYLASE 2 (DRM2). However, the maintenance of plant DNA methylation depends on the cytosine sequence context (CG or CHG) and is catalyzed by DNA methyltransferases that are regulated by different mechanisms. Canonical dinucleotide CG methylation is maintained by METHYLTRANSFERASE 1 (MET1), an orthologue of the mammalian DNA (cytosine-5)-methyltransferase 1 (DNMT1), which recognizes hemi-methylated CG dinucleotides following DNA replication and methylates the unmodified cytosine in the daughter strand. Maintenance of CHG methylation in *A. thaliana* is catalyzed by the DNA methyltransferase CHROMOMETHYLASE 3 (CMT3) and to a much lesser extent by CMT2. Similarly, CHH methylation is maintained by DRM2 or CMT2, depending on the genomic region. Although, during development DNA methylation dynamics plays a role in development, more evidence of environmental stress impact on DNA methylation are being reported.

**Key Words:** DNA methylation, DRM2, MET1, CMT3, environmental stress, Epigenetic mark

## Park, Junghoon



Research professor,  
Institute of Global Disease Control, Konkuk University, 05029,  
Republic of Korea  
E-mail, [p6259l@konkuk.ac.kr](mailto:p6259l@konkuk.ac.kr)

### EDUCATION

2001-2008 Gyeongsang National University, *BS*  
2008-2016 Gyeongsang National University, *MS & Ph.D*

### EXPERIENCE AND CAREER

2011-2013 Visiting scholar. Purdue University.  
2016-2018 Postdoc, Gyeongsang National University.  
2018–2021 Postdoc, Konkuk University.  
2021-present Research professor, Konkuk University

### RESEARCH INTERESTS

Abiotic Stress signaling, Epigenetics.

### PUBLICATIONS (5 papers)

1. Ali A, et al. (2024) ABA INSENSITIVE 2 promotes flowering by inhibiting OST1/ABI5-dependent *FLOWERING LOCUS C* transcription in Arabidopsis, *Journal of Experimental Botany*, 15;75(8):2481-2493
2. Park J, et al. (2023) The HIGH EXPRESSION OF OSMOTICALLY RESPONSIVE GENE15–HISTONE DEACETYLASE9 complex associates with HYPONASTIC LEAVES 1 to modulate microRNA expression in response to abscisic acid signaling. *Plant Cell* 35, 2910-2928
3. Shen M et al. (2020) HOS15 is a transcriptional corepressor of NPR1-mediated gene activation of plant immunity. *Proc Natl Acad Sci USA*. 117,30805-30815.
4. Lim C et al. (2020) The Histone-Modifying Complex PWR/HOS15/HD2C Epigenetically Regulates Cold Tolerance, *Plant Physiology*, 184(2):1097-1111
5. Park J et al. (2018) Epigenetic switch from repressive to permissive chromatin in response to cold stress. *Proc. Natl. Acad. Sci. USA* 115,E5400-E5409

# **Cold stress induced dynamic chromatin accessibility facilitates histone reorganization and transcription factor recruitment in *Arabidopsis*.**

Junghoon Park

*Institute of Global Disease Control, Konkuk University, Seoul, Korea*

E-mail, [p6259l@konkuk.ac.kr](mailto:p6259l@konkuk.ac.kr)

## **Abstract**

Plants exposed to various environmental stresses, including cold temperature, undergo differential gene expression, and activate stress response pathways by various molecular mechanisms including chromatin remodeling. Here, we used genome wide chromatin accessibility studies to investigate the dynamic changes on chromosomes in *Arabidopsis*. We show the heterochromatin structure was lost in the nucleus upon cold exposure. There was gain in chromatin accessibility throughout the genome and that this was associated with histone reorganization in response to cold stress. In addition, we observed differential gene expression that did not correspond with gain in chromatin accessibility upon cold stress. The differential gene expression was mediated by positional CBFs/DREB1 (C-repeat Binding Factors/Dehydration-Responsive Element-Binding) transcription factor recruitment. Binding of CBFs on H2A.X.5 promoter led to its upregulation upon cold exposure. In contrast, binding of CBFs to H2A.W.12 enhancer led to its downregulation. Therefore, in response to increased chromatin accessibility under cold stress, transcription factor CBFs plays a critical role in regulating gene expression depending on its binding locations in the *Arabidopsis* genome.

**Key words:** Cold stress, Epigenetic, Chromatin accessibility, Histone reorganization

## Lee, Byeong-ha

Professor,  
*Department of Life Science, Sogang University*  
E-mail, [byeongha@konkuk.ac.kr](mailto:byeongha@konkuk.ac.kr)



### EDUCATION

May 2004      University of Arizona, Ph.D.  
Feb 1997      Seoul National University, M.S.  
Feb 1993      Seoul National University, B.S.

### EXPERIENCE AND CAREER

2007-present    Asst. Assoc. and Professor, Sogang University  
2004-2007      Postdoctoral Fellow, Cold Spring Harbor Laboratory

### RESEARCH INTERESTS

Abiotic Stress Tolerance in Plants

### PUBLICATIONS (5 papers)

1. Yun, J.-Y., et al. (2022) Identification of CRISPR-Induced Mutations in Plants: with a Focus on the Next-Generation Sequencing Assay. *J Plant Biol.* 65: 435-443.
2. Yolcu, S., et al. (2020) Natural Genetic Resources from Diverse Plants to Improve Abiotic Stress Tolerance in Plants. *Int J Mol Sci.* 21(22):8567.
3. Kim, H., et al. (2019) The F-box Protein SAGL1 and ECERIFERUM3 Regulate Cuticular Wax Biosynthesis in Response to Changes in Humidity in Arabidopsis. *Plant Cell* 31: 2223-2240.
4. Yu, S.-i., et al. (2019) Post-translational and transcriptional regulation of phenylpropanoid biosynthesis pathway by Kelch repeat F-box protein SAGL1. *Plant Molecular Biology* 99: 135-148.
5. Alavilli, H., et al. (2018). Enhanced multiple stress tolerance in Arabidopsis by overexpression of the polar moss peptidyl prolyl isomerase FKBP12 gene. *Plant Cell Reports* 37: 453-465.

# RNA Splicing-Regulated Stress Tolerance in Plants

Byeong-ha Lee

Department of Life Science, Sogang University, Seoul, Korea

Correspondence: [byeongha@sogang.ac.kr](mailto:byeongha@sogang.ac.kr)

## Abstract

The *Arabidopsis* *STABILIZED1* (*STA1*) gene encodes a putative pre-mRNA processing factor. It is homologous to the human U5 snRNP-associated 102-kDa protein (PRPF6) and the yeast pre-mRNA splicing factors PRP1p (fission yeast) and Prp6p (budding yeast). Originally, the *Arabidopsis* mutant defective in the *STA1* gene was isolated during a genetic screen for stress-responsive gene deregulation mutants. The *sta1-1* mutant showed pleiotropic developmental defects and temperature sensitivity. Consistently, *STA1* was expressed in all tissues and is induced by temperature stress. The *sta1-1* mutant also showed a reduced accumulation of miRNAs and defects in pre-mRNA splicing and transcript stability. We overexpressed *STA1* in *Arabidopsis thaliana* and its close relatives *Brassica napus* and *Brassica rapa*, resulting in increased heat tolerance. In addition, we performed a genetic modifier screen of *sta1-1*. Our efforts to understand the function of *STA1* through the *sta1-1* modifier will be presented and discussed.

**Key words:** RNA processing, RNA splicing, STA1, modifier screening

## Kim, Jaebum



Professor,  
*Department of Biomedical Science and Engineering*  
*Konkuk University*  
E-mail: jbkim@konkuk.ac.kr

### EDUCATION

1995-1999 Seoul National University, BS  
1999-2001 Seoul National University, MS  
2004-2010 University of Illinois at Urbana-Champaign, Ph.D.

### EXPERIENCE AND CAREER

2012-present Professor, Konkuk University  
2010-2012 Postdoctoral Fellow, Institute for Genomic Biology

### RESEARCH INTERESTS

Bioinformatics, Computational Biology

### PUBLICATIONS (5 papers)

1. Park N, et al. (2024) PAPIpe: a pipeline for comprehensive population genetic analysis, *Molecular Biology and Evolution*, 41:3
2. Kwon D, et al. (2023) A chromosome-level genome assembly of the Korean crossbred pig Nanchukmacdon (*Sus scrofa*), *Scientific Data*, 10, 761
3. Wy S, et al. (2022) DLEB: a web application for building deep learning models in biological research, *Nucleic Acids Research*, 50(W1):W254-W260
4. Kwon D, et al. (2018) INTERSPIA: a web application for exploring the dynamics of protein-protein interactions among multiple species, *Nucleic Acids Research*, 46(W1): W89-W94
5. Kim J, et al. (2017) Reconstruction and evolutionary history of eutherian chromosomes, *PNAS*, 114(27), E5379-E5388, doi:10.1073/pnas.1702012114

# A computational approach for constructing a chromosome-level genome assembly

Jaebum Kim

*Department of Biomedical Science and Engineering  
Konkuk University, Seoul, Korea*

Correspondence: jbkim@konkuk.ac.kr

## Abstract

Genome assembly is the process of concatenating short DNA sequences generated by DNA sequencing to reconstruct the original chromosome sequences. The recent advances in DNA sequencing technologies and genome assembly algorithms have enabled the construction of high-quality genome assemblies in terms of contiguity and completeness. However, generating a chromosome-level genome assembly is still difficult and requires repeated manual intervention. To alleviate this difficulty, we developed a novel computational method for genome assembly by utilizing Hi-C sequencing data. The goal of our method is to construct chromosome-level DNA sequences by using a draft-level genome assembly as input. In this process, the adjacencies of short DNA sequences in the draft-level genome assembly are predicted by probabilistic modeling and application of the patterns of chromosome contacts using the Hi-C sequencing data. The inferred adjacencies of short DNA sequences are then used to finally organize them to construct chromosome sequences. The superior performance of our method was confirmed by comparing with similar existing methods using simulated and real data. Our method will contribute to developing an end-to-end computational method for accurately constructing a chromosome-level genome assembly.

**Keywords:** genome, assembly, computational method, sequencing



## Takeshi Nakano

Professor  
Laboratory of Plant Chemical Biology,  
Graduate School of Biostudies,  
Kyoto University.  
E-mail: nakano.takeshi.6x@kyoto-u.ac.jp



### Education

1985-1989 Kyoto University, BS  
1989-1991 Kyoto University, MS  
1991-1994 Kyoto University, Ph. D. (D. Agriculture)

### Research Experience

1994 Research Fellow, The Japan Society for the Promotion of Science

1995 Special Postdoctoral Researcher, RIKEN

1996 Research Scientist, Plant Functions Lab, RIKEN

2000 Research Fellow, Plant Molecular Biology-Chory Lab, Salk Institute.CA, USA

2003 Senior Research Scientist, Plant Functions Lab, RIKEN Advanced Science Institute.

2007 Unit Leader, Plant Chemical Biology Research Unit RIKEN Advanced Science Institute.

2007 PRESTO researcher, Japan Science and Technology Agency

2010 Senior Research Scientist, Molecular Membrane Biochemistry Lab, RIKEN Advanced Science Institute.

2012 Senior Research Scientist, Antibiotic Lab., RIKEN.

2013- Part-time Lecturer, Graduate School of Medical and Dental Sciences and Research Institute, Tokyo Medical and Dental Univ.

2014, 2018 Part-time Lecturer, Fac. Science, Ochanomizu Univ.

2015-2019 Senior Research Scientist, Gene Discovery Research Group., Center for Sustainable Resource Science, RIKEN

2016- Visiting Professor, School of Engineering and Applied Sciences, National University of Mongolia

2019- Professor, Graduate School of Biostudies, Kyoto University

### RESEARCH INTERESTS

Plant chemical biology, Plant hormone signaling, Plant biotechnology.

## **PUBLICATIONS (5 papers)**

1. Tachibana, R., Abe, S., Marugami, M., Yamagami, A., Akema, R., Ohashi, T., Nishida, K., Nosaki, S., Miyakawa, T., Tanokura, M., Kim, J., Seki, M., Inaba, T., Matsui, M., Ifuku, K., Kushiro, T., Asami, T., Nakano, T. BPG4 regulates chloroplast development and homeostasis by suppressing GLK transcription factors and involving light and brassinosteroid signaling. ***Nature Communications***. 15, Article number:370 (2024)
2. Chagan, Z., Nakata, G., Suzuki, S., Yamagami, A., Tachibana, R., Surina, S., Fujioka, S., Matsui, M., Kushiro, T., Miyakawa, T., Asami, T., Nakano, T. BRZ-INSENSITIVE-LONG HYPOCOTYL8 inhibits kinase-mediated phosphorylation to regulate brassinosteroid signaling. ***Plant Physiology***, kiae191, doi.org/10.1093/plphys/kiae191, (2024)
3. Nosaki, S., Mitsuda, N., Sakamoto, S., Kusubayashi, K., Yamagami, A., Xu, Y., Bao, T., Bui, C., Terada, T., Miura, K., Nakano, T., Tanokura, M., Miyakawa, T. Brassinosteroid-induced gene repression requires specific and tight promoter binding of BIL1/BZR1 via DNA shape readout. ***Nature Plants***, 8(12), 1440–1452. (2022). DOI: 10.1038/s41477-022-01289-6
4. Nosaki, S., Miyakawa, T., Xu, Y., Nakamura, A., Hirabayashi, K., Asami, T., Nakano, T., Tanokura, M. Structural basis for brassinosteroid response by BIL1/BZR1. ***Nature Plants***, 4, 771-776 (2018)
5. Yamagami, A., Saito, C., Nakazawa, M., Fujioka, S., Uemura, T., Matsui, M., Sakuta, M., Osada, H., Nakano, A., Asami, T., Nakano, T. Evolutionarily conserved BIL4 interacts with the brassinosteroid receptor BRI1 and regulates cell elongation. ***Scientific Reports*** 7(1) Article number 5739 (2017)

# Chemical biology research to reveal plant growth and stress resistance mechanism via brassinosteroid signaling.

Takeshi Nakano<sup>1</sup>

<sup>1</sup>Laboratory of Plant Chemical Biology, Graduate School of Biostudies, Kyoto University

Correspondence: [nakano.takeshi.6x@kyoto-u.ac.jp](mailto:nakano.takeshi.6x@kyoto-u.ac.jp)

## Abstract

In higher organisms, several compounds are known to have a similar chemical structure or steroid skeleton; these include testosterone (a male sex hormone controlling differentiation of reproductive organs), estrogens and progesterone (female sex hormones regulating pregnancy), and corticosterone (adrenal cortex hormone) in mammals and ecdysone (a hormone that controls molting) in insects and crustaceans. In plant, brassinosteroids is identified as plant steroid hormone, and also belong to a class of chemical compounds called plant hormones. Thus, steroid hormones are bioactive substances conserved widely across species. These steroid hormones have bioactivity in specific organs in an individual species, e.g., functional regulation of chloroplasts in plants, regulation of pregnancy in mammals, and regulation of molting in insects. Additionally, these hormones have universal roles, such as stimulation of growth, that are common across species. This parallel existence of universality and specificity of steroid hormone bioactivity is of interest in steroid hormone research.

Brassinosteroids (BRs), plant steroid hormones, have crucial effects on not only plant growth but also chloroplast development. Chloroplast development adapts to the environment for performing suitable photosynthesis, but the detailed molecular mechanisms of BR signaling in chloroplast development remain unclear. Here, we identify a novel regulator of chloroplast development, BPG4, involved in light and BR signaling. BPG4 interacts with GOLDEN2-LIKE (GLK) transcription factors that promote the expression of photosynthesis-associated nuclear genes (*PhANGs*), and suppresses their activities, thereby causing a decrease in the amounts of chlorophylls and the size of light-harvesting complexes. *BPG4* expression is induced by BR deficiency and light, and is regulated by the circadian rhythm. *BPG4* deficiency causes increased reactive oxygen species (ROS) generation and damage to photosynthetic activity under excessive high-light conditions. Our findings suggest that BPG4 acts as a chloroplast homeostasis factor by fine-tuning the expression of *PhANGs*, optimizing chloroplast development, and avoiding ROS generation.

1) *Nature Communications*. (2024) Jan 8;15(1):370. doi: 10.1038/s41467-023-44492-5.

- MEMO

## Kim, Tae-Wuk

Professor,  
Department of Life Science, Hanyang University  
E-mail, [twgibio@hanyang.ac.kr](mailto:twgibio@hanyang.ac.kr)



### EDUCATION

1992-1998 Chung-Ang University, BS  
1998-2000 Chung-Ang University, MS  
2000-2003 Chung-Ang University, *Ph.D.*  
1994-1998 Carnegie Institution for Science, Stanford University, *Postdoc.*

### EXPERIENCE AND CAREER

2011-present Professor, Hanyang University  
2015-2017 Chair, Department of Life Science, Hanyang University  
2020-2022 Vice Dean, College of Natural Science, Hanyang University  
2024- present Director, Brain Korea (BK21) Four program

### RESEARCH INTERESTS

Molecular mechanism of brassinosteroid-mediated plant growth, development, and physiological responses

### PUBLICATIONS (5 papers)

1. Lee S et al. (2024) Transcription factors BZR1 and PAP1 cooperate to promote anthocyanin biosynthesis in *Arabidopsis* shoots. *Plant Cell*, *in press*, <https://doi.org/10.1093/plcell/koae172>.
2. Kim S et al. (2024) Comparative analysis of BZR1/BES1 family transcription factors in *Arabidopsis*. *Plant Journal*, *117*(3); 747-765
3. Kim T et al. (2023) Mapping the signaling network of BIN2 kinase using TurboID-mediated biotin labeling and phosphoproteomics. *Plant Cell*, *35*; 975-993
4. Park C et al. (2022) Deconvoluting signals downstream of growth and immune receptor kinases by phosphocodes of the BSU1 family phosphatases. *Nature Plants*. *8*, 646-655
5. Kim Y et al. (2022) Brassinosteroids enhance salicylic acid-mediated immune responses by inhibiting BIN2 phosphorylation of clade I TGA transcription factors in *Arabidopsis*. *Molecular Plant*. *15*, 991-1007

# **BZR1 Cooperates with PAP1 of MBW Complex to Promote Anthocyanin Biosynthesis in Arabidopsis shoots**

Tae-Wuk Kim

*Department of Life Science, Hanyang University, Seoul 04763, Republic of Korea*  
Correspondence: [twgibio@hanyang.ac.kr](mailto:twgibio@hanyang.ac.kr)

## **Abstract**

Anthocyanins play critical roles in the protection of plant tissues against diverse stresses. The complicated regulatory networks induced by various environmental factors modulate the homeostatic level of anthocyanins. Here we show anthocyanin accumulation induced by brassinosteroid (BR) in Arabidopsis shoots and its regulatory mechanism. We observed that anthocyanin levels are altered considerably in BR-related mutants and BR induces anthocyanin accumulation by up-regulating the expression of anthocyanin biosynthetic genes. Our genetic analysis indicated that Brassinazole Resistant 1 (BZR1) and Production of Anthocyanin Pigment 1 (PAP1) are essential for BR-induced anthocyanin accumulation. The BR-responsive BZR1 transcription factor directly binds to the promoter of PAP1, regulating its expression. In addition, we found that intense anthocyanin accumulation caused by the pap1-D dominant mutation is significantly reduced in BR mutants, implying that BR activity is required for PAP1 function after transcription of the PAP1 gene. We further demonstrated that BZR1 physically interacts with PAP1 to cooperatively regulate the expression of PAP1-target genes, such as TT8, DFR, and LDOX. Our findings indicate that BZR1 functions as an integral component of the PAP1-containing transcription complex, contributing to the promotion of anthocyanin biosynthesis. Notably, we also show that functional interaction of BZR1 with PAP1 is required for anthocyanin accumulation induced by low nitrogen stress.

**Key words:** Anthocyanin, Brassinosteroid, BZR1, MBW complex, Transcriptional Regulation, Arabidopsis, Low Nitrogen

# Xiang Gao



Professor

Key Laboratory of Molecular Epigenetics of MOE and Institute of Genetics & Cytology, Northeast Normal University.

Correspondence: [gaoxiang424@163.com](mailto:gaoxiang424@163.com)

## EDUCATION

2001 - 2005, Linyi University, China, BS.

2005 - 2010, Northeast Normal University, China, Ph.D.

## EXPERIENCE AND CAREER :

2010 - 2013, Northeast Normal University, China, Assistant Professor.

2014 - 2020, Northeast Normal University, China, Associate Professor.

2016 - 2017, [The University of British Columbia](#), Vancouver, Canada, Visiting scholar.

2021 - Present, Northeast Normal University, China, Professor.

## RESEARCH INTERESTS

- Biosynthesis and regulation of flower pigments
- Biosynthesis and regulation of flower volatile terpenes
- Transcriptional regulation of flavonoids biosynthesis in soybean seeds

## PUBLICATIONS (5 papers)

1. Hongjie Li, et al. (2024), The Complexity of Volatile Terpene Biosynthesis in Roses: Particular Insights into  $\beta$ -Citronellol Production, *Plant Physiology*. in press.
2. Tingting Bao, et al. (2023), Allelic Variation of Terpene Synthases Drives Terpene Diversity in the Wild Species of *Freesia* Genus. *Plant Physiology*. 192(3):2419-2435.
3. Xiaotong Shan, et al. (2020), The spatio-temporal biosynthesis of floral flavonols is controlled by differential phylogenetic MYB regulators in *Freesia hybrida*. *New Phytologist*, 228: 1864–1879.
4. Yang, Z, et al. (2020). MYB21 interacts with MYC2 to control the expression of terpene synthase genes in flowers of *F. hybrida* and *A. thaliana*. *Journal of Experimental Botany*, 71(14): 4140–4158.
5. Gao F, et al. (2018), Identification and Characterization of Terpene Synthase Genes Accounting for the Volatile Terpene Emissions in Flowers of *Freesia*  $\times$  *hybrida*, *Journal of Experimental Botany*, 69(18): 4249–4265.

# The biosynthesis and regulation of volatile terpenes and flavonoids in ornamental flowers

Xiang Gao

<sup>1</sup>Key Laboratory of Molecular Epigenetics of MOE, Northeast Normal University, Changchun 130024, China

Presenting author(s) e-mail gaoxiang424@163.com

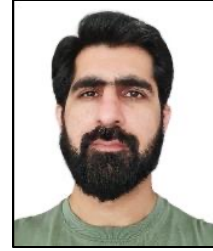
## Abstract

Color and fragrance are important flower characters, determining the ornamental and economic values of flower crops, however, they are not equally selected in domestication and unbiasedly investigated. As fragrant flowers are more and more prevalent in the current market, horticulturist are aiming to breed cultivars with both colorful and fragrant flowers. In our recent studies, we mainly focused on three questions using flower plants from *Freesia*, *Rosa*, *Aquilegia* and *Clivia* genus, 1. How do *TPS* genes determine floral scents? 2. How do allelic variants of *TPS* genes evolve? 3. How are *TPS* genes co-regulated with flower pigments biosynthesis related genes? We found that the majority of floral volatile terpenes were controlled by a small set of *TPS* genes and almost all *TPS* proteins from *TPS*-a, b, g subgroups could utilize four kinds of substrates to yield multiple products. Allelic variant of *TPS* genes could drive the emission of both intra- and inter-species specific floral scents, several amino acids substitutions or insertions not only affected the catalytic ability of the *TPS* allelic variants, but also affected their products specificity. In addition to the enzyme encoding genes mentioned above, our group is also interested in the transcriptional regulation of these genes. We discovered a MYB-bHLH module controlled the biosynthesis of linalool through activation the expression of *FhTPS1* gene in *Freesia hybrida*. Interestingly, we also found that FhMYB21L2 could control the biosynthesis of floral flavonols, the co-pigment of anthocyanins. Moreover, after comparative analysis of the roles of MBW complex in *Freesia hybrida* and soybean, we found that the transcriptional regulation model of anthocyanin biosynthesis might be conserved in angiosperms. After we deciphered the biosynthesis pathway of the major floral scents and pigments, obtained the candidate genes and their stronger allelic variants and dissected the regulation networks of these specialized metabolites, we are aiming to breed new varieties with desired phenotypes, such as colorful and scented *Clivia miniata*, rose flowers with recovered fragrance and rose scented tomato fruits.



## Akhtar Ali

Research Professor,  
*Department of Biomedical Science & Engineering,*  
*Konkuk University, Seoul, Korea*  
E-mail, [aali@konkuk.ac.kr](mailto:aali@konkuk.ac.kr)



### EDUCATION

2005-2009 BSc, University of Malakand, Pakistan  
2010-2012 MS, Gyeongsang National University, Korea  
2012-2016 PhD, Gyeongsang National University, Korea

### EXPERIENCE AND CAREER

2021-present Research Professor, Konkuk University, Korea  
2017-2021 Postdoc, Konkuk University, Korea  
2016-2017 Postdoc, Gyeongsang National University, Korea  
2022-present Senior Research Scientist (Visiting), CPSBB, Bulgaria

### RESEARCH INTERESTS

Abiotic Stress Signaling in Plant

### PUBLICATIONS (5 papers)

1. Ali A, et al. (2024) ABA INSENSITIVE 2 promotes flowering by inhibiting OST1/ABI5-dependent *FLOWERING LOCUS C* transcription in Arabidopsis. *Journal of Experimental Botany*. 75, 2481–2493
2. Zareen et al. (2022) The Transcriptional Corepressor HOS15 Mediates Dark-Induced Leaf Senescence in Arabidopsis. *Frontiers in Plant Sci.* 13,828264
3. Ali A et al. (2019) Rheostatic control of ABA signaling through HOS15-mediated OST1 degradation. *Molecular Plant* 12,1447-1462
4. Ali A et al. (2018) The High-affinity potassium transporter EpHKT1;2 from the extremophile *Eutrema parvula* mediates salt tolerance. *Frontiers in Plant Sci.* 9,1108
5. Ali A et al. (2016) A single amino-acid substitution in the sodium transporter HKT1 associated with plant salt tolerance. *Plant Physiology* 171, 2112–2126.

# Crosstalk of ABA signaling with flowering time in *Arabidopsis*

Akhtar Ali

<sup>1</sup>*Department of Biomedical Science and Engineering, Konkuk University, Seoul, Korea*

Correspondence: [aali@konkuk.ac.kr](mailto:aali@konkuk.ac.kr)

## Abstract

The plant hormone abscisic acid (ABA) is an important regulator of plant growth and development and plays a crucial role in both biotic and abiotic stress responses. The involvement of ABA in the regulation of flowering time however remains elusive. Here we report ABI2 (ABA Insensitive2), as the only phosphatase from ABA-signaling core that positively regulates the transition to flowering in *Arabidopsis*. Loss-of-function *abi2-2* mutant shows significantly delayed flowering both under long day (LD) and short day (SD) conditions. Expression of floral repressor genes such as *FLC* and *CDF1* was significantly up-regulated in *abi2-2* plants while that of the flowering promoting genes *FT* and *SOC1* was down-regulated. Through genetic interactions we further found that *ost1-3* and *abi5-1* mutations are epistatic to *abi2-2*, as both of them individually rescued the late flowering phenotype of *abi2-2*. Interestingly, ABI5 phosphorylation and protein stability were enhanced in *abi2-2* plants suggesting that ABI2 dephosphorylates ABI5, thereby reducing protein stability and the capacity to induce *FLC* expression. Our findings therefore uncovered the unexpected role of ABI2 to promote flowering by inhibiting ABI5-mediated FLC activation in *Arabidopsis*.

**Key words:** Flowering time, ABI2, ABI5, FLC, SnRK2, ABA-signaling.

## Miguel A. Botella



Professor,

Instituto de Hortofruticultura Subtropical y Mediterránea (IHSM)

Universidad de Málaga

E-mail, [mabotella@uma.es](mailto:mabotella@uma.es)

### EDUCATION

1982-1987 University of Málaga, BS

1988-1990 University of Málaga, MS

1991-1994 University of Málaga/Purdue University, Ph.D.

1994-1995 Purdue University, USA, Postdoc.

1995-1998 John Innes Centre, UK, Postdoc.

### EXPERIENCE AND CAREER

2012 – present Full Professor, University of Málaga

2001 - 2012 Assistant Professor, University of Málaga

1999 - 2001 EU Returning Grant/Universidad de Málaga/Spain

2022 - Present Vice Director, IHSM

### RESEARCH INTERESTS

Environmental Stress Perception and Signaling in Plants

### PUBLICATIONS (5 papers)

1. C. Kesten, A. et al. (2022). Peripheral membrane proteins modulate stress tolerance by safeguarding cellulose synthases. *Science Advances* 8, eabq6971. DOI:10.1126/sciadv.abq6971
2. N. Ruiz-Lopez, et al. (2021). Synaptotagmins Maintain Diacylglycerol Homeostasis at Endoplasmic Reticulum-Plasma Membrane Contact Sites during Abiotic Stress. *The Plant Cell*. 33, 2431–2453. DOI:1093/plcell/koab122
3. E. Lee, S. et al. (2019). Ionic stress enhances ER-PM connectivity via phosphoinositide-associated SYT1 contact site expansion in Arabidopsis. *PNAS*: 116: 1420–1429. DOI:10.1073/pnas.1818099116
4. V. Amorim-Silva, et al., (2019). TTL Proteins Scaffold Brassinosteroid Signaling Components at the Plasma Membrane to Optimize Signal Transduction in Arabidopsis. *The Plant Cell*. 31: 1807–1828. DOI:10.1105/tpc.19.00150
5. J. Perez-Sancho, S. et al. (2015). The Arabidopsis synaptotagmin1 is enriched in endoplasmic reticulum-plasma membrane contact sites and confers cellular resistance to mechanical stresses. *Plant physiology*. 168: 132–143.

# From binder to bender: the dual role of SYT1 on stress-related Ca<sup>2+</sup> responses at ER-PM CS

Miguel A. Botella

Instituto de Hortofruticultura Subtropical y Mediterránea “La Mayora”. Universidad de Málaga

Correspondence: [mabotella@uma.es](mailto:mabotella@uma.es)

## Abstract

Endoplasmic Reticulum-Plasma Membrane Contact Sites (ER-PM CS) are specialized microdomains where the ER and the PM come into close proximity without membrane fusion. These membrane microdomains mediate the interaction of proteins and the exchange of lipids and ions, including calcium, a second messenger that modulates downstream events in response to environmental changes such as salt stress. Our group identified Arabidopsis Synaptotagmin1 (SYT1) as a tethering protein of ER-PM CS in screening for mutants showing high sensitivity to NaCl. We have also uncovered a new role of SYT1 in biotic stress signaling, as the *syt1* mutant shows decreased generation of reactive oxygen species (ROS) upon flagellin 22 (*flg22*) application. To further analyze whether this response is due to a defect in Ca<sup>2+</sup> signaling, we have tested Ca<sup>2+</sup> responses of wild type (WT) and *syt1* expressing a cytosolic Ca<sup>2+</sup> reporter upon *flg22* treatment. Our results show differences in the Ca<sup>2+</sup> wave of *syt1* compared to WT when treated with *flg22*, suggesting that SYT1-enriched ER-PM CS is involved in the Ca<sup>2+</sup> response that triggers ROS generation. SYT1 proteomic data reveal the ER-localized Ca<sup>2+</sup>-ATPases ECA1 and ECA4 as SYT1 interactors. To further study their role in Ca<sup>2+</sup> signaling at plant ER-PM CS, we generated an *eca1eca4* double mutant using CRISPR/Cas9 since these genes are linked. The *eca1eca4* double mutant does not present any apparent phenotype in vegetative development but exhibits a substantial defect in silique formation, resulting in low seed yield. We are investigating the responses of *eca1eca4* and *syt1* under NaCl stress in the presence of different concentrations of extracellular Ca<sup>2+</sup> to determine the role of ECA1/ECA4 and SYT1 in Ca<sup>2+</sup>-modulated salt stress responses. These studies aim to elucidate the molecular mechanisms by which ER-PM CS contribute to the plant's ability to respond to and manage environmental stresses.

**Key words:** ER-PM CS, SYT1, ECA1ECA4, Ca<sup>2+</sup> signaling, Arabidopsis

## Ha, Sun-Hwa



Professor,  
*Department of Genetics and Biotechnology,*  
*Kyung Hee University,*  
E-mail, [sunhwa@khu.ac.kr](mailto:sunhwa@khu.ac.kr)

### EDUCATION

1987-1991 Kyungpook National University, BS  
1991-1993 Kyungpook National University, MS  
1993-1999 Kyungpook National University, *Ph.D.*  
1999-2000 Hohenheim University, *Visiting Scientist*  
2004-2005 Michigan State University, *Postdoc.*

### EXPERIENCE AND CAREER

1992-2009 Researcher, National Academy of Agricultural Science, RDA  
2009-2013 Principal Researcher, National Academy of Agricultural Science, RDA  
2013-2018 Associate Professor, Kyung Hee University  
2018-present Professor, Kyung Hee University

### RESEARCH INTERESTS

Plant Metabolic Engineering

### PUBLICATIONS (5 papers)

1. Choi H, et al. (2024) Molecular Action of GOLDEN2-LIKE Transcription Factor Family with Diverse Interacting Promoters and Proteins. *Physiol. Plant.* 176, e14164
2. Yu JS, et al. (2023) Stepwise protein targeting into plastoglobules are facilitated by three hydrophobic regions of rice phytoene synthase 2. *Front. Plant Sci.* 14, 1181311
3. Jeong YS, (2022) Overexpression of OsMYBR22/OsRVE1 Transcription Factor Simultaneously Enhances Chloroplast-Dependent Metabolites in Rice Grains. *Metab. Eng.* 70, 89-101
4. You MK, et al. (2020) The organ-specific differential roles of rice DXS and DXR, the first two enzymes of the MEP pathway, in carotenoid metabolism in *Oryza sativa* leaves and seeds. *BMC Plant Biol.* 20, 167
5. Ha SH, et al. (2019) Stepwise pathway engineering to the biosynthesis of zeaxanthin, astaxanthin and capsanthin in rice endosperm. *Metab. Eng.* 52, 178-189

# The Cytoplasmic Protein Trapping by a miProtein PSEUDO-ETIOLATION IN LIGHT family Negatively Governs Photosynthesis in Rice

Sun-Hwa Ha

<sup>1</sup> Department of Genetics and Biotechnology, Kyung Hee University, Yongin, Korea

\*Correspondence: [sunhwa@khu.ac.kr](mailto:sunhwa@khu.ac.kr)

## Abstract

The autotrophic life of plants depends on photosynthesis. Improving photosynthetic efficiency has long been a challenge for better net primary production in agriculture. To join this effort in rice, we identified three PSEUDO-ETIOLATION IN LIGHT (PEL) proteins, OsPEL1, 2, 3, which belong to a land plant-specific microProtein family. They redundantly function as negative regulators for plant greening traits when individually overexpressed. Triple knock-out of OsPEL family, *ospel1/2/3*, enhanced chloroplast development with anatomical innovation forming C4-like Kranz structure. The morphological change was correlated with an increase of CO<sub>2</sub> assimilation and yield. To elucidate the molecular mechanism, we performed Y2H library screening with OsPEL1 and proposed eleven candidates as binding partners including photosynthesis-associate proteins such as GOLDEN2-LIKE (GLK) transcription factors and PHOTOSYSTEM 1 ASSEMBLY 2 (PSA2) DnaJ E1-type chaperon. For protein-protein interaction structure with OsPEL1, the crucial domains were elucidated and AI-based 3D models were predicted. The molecular action of OsPEL1 traps OsGLK1 and OsPSA2 in the cytoplasm, preventing their subcellular localization into the nucleus and chloroplast, respectively. We uncover the PEL-related mechanism for effectively controlling overall photosynthesis and propose the PEL family as a promising target for crop improvement through genome editing.

**Key words:** miProtein, PEL family, GLKs, PSA2, Rice (*Oryza sativa*)

## Xu, Zheng-Yi

Professor,  
Department of Life Science, Northeast Normal University  
E-mail, xuzhy100@nenu.edu.cn



### EDUCATION

2003-2007 Shandong University, BS  
2007-2012 POSTECH, *Ph.D.*  
2012-2015 Harvard University/MGH, *Postdoc.*

### EXPERIENCE AND CAREER

2015-present Professor, Northeast Normal University

### RESEARCH INTERESTS

Abiotic Stress Signaling in Plant

### PUBLICATIONS (5 papers)

1. Wang J, et al. (2020). A DNA Methylation Reader-Chaperone Regulator-Transcription Factor Complex Activates OsHKT1;5 Expression during Salinity Stress. *Plant Cell*. 32(11):3535-3558.
2. Liu Y, et al. (2021). SET DOMAIN GROUP 721 protein functions in saline-alkaline stress tolerance in the model rice variety Kitaake. *Plant Biotechnology Journal*. 19(12):2576-2588.
3. Nan N, et al. (2020). Rice plastidial NAD-dependent malate dehydrogenase 1 negatively regulates salt stress response by reducing the vitamin B6 content. *Plant Biotechnology Journal*. 18(1):172-184.
4. Liu Y, et al. (2023). Plasma membrane-localized Hsp40/DNAJ chaperone protein facilitates OsSUVH7-OsBAG4-OsMYB106 transcriptional complex formation for OsHKT1;5 activation. *Journal of Integrative Plant Biology*. 65(1): 265-279.
5. Liu Y, et al. (2023). Type-B response regulator OsRR22 forms a transcriptional activation complex with OsSLR1 to modulate OsHKT2;1 expression in rice. *SCIENCE CHINA Life Sciences*. 66(12): 2922-2934

# The OsMPK6-OsERFA module functions in UV-B induced photomorphogenesis

Zheng-Yi Xu

<sup>1</sup>Department of Life Science, Northeast Normal University, Changchun, China

Correspondence: [xuzy100@nenu.edu.cn](mailto:xuzy100@nenu.edu.cn)

## Abstract

Plants are exposed to UV-B irradiation, which has been increasing due to ozone depletion over the past few decades. Rice subspecies *japonica* normally showed higher sensitivities in terms of coleoptile inhibition and anthocyanin accumulation compared to *indica* under UV-B; however, the underlying genetic basis and molecular mechanism remain unknown. By using the activation tagging mutant pool generated in the Kitaake background, we found *oserfa* gain-of-function mutant displayed higher sensitivity during UV-B induced photomorphogenesis. Natural variation in the *OsERFA* gene contributes to the divergence in UV-B induced photomorphogenesis between rice subspecies *indica* and *japonica*. *OsERFA* activates the expression of genes involved in anthocyanin accumulation and flavonoid biosynthesis under UV-B. Yeast one-hybrid screening identified that NAC domain transcription factor *OsNAC3* and the core component of FACT complex *OsSSRP1A* can make the transcriptional complex to directly bind to the promoter region of *OsERFA* to activate its expression. Intriguingly, differential transcriptional activity mediated by *OsNAC3*-*OsSSRP1A* complex shapes distinguished UV-B sensitivity between *japonica* and *indica*. Furthermore, we observed UV-B activates the *OsMPK6* to induce *OsERFA* phosphorylation, thereby mediating rapid degradation of *OsERFA*, which possibly attenuates the *OsERFA* functionality under UV-B. Taken together, we established *OsERFA* participates in the determination of differential photomorphogenesis induced by UV-B between *japonica* and *indica* subspecies.

**Key words:** Photomorphogenesis, UV-B, transcriptional regulation, MAPK, rice



## Kang, Lin-Woo



Professor/director  
Department of Biological Sciences  
Konkuk University, Seoul, Korea  
E-mail : lkang@konkuk.ac.kr

### EDUCATION

1991 – 1995 Pohang Univ. of Sci. & Tech, BS  
1995 – 1997 Pohang Univ. of Sci. & Tech, MS  
2000 – 2004 Johns Hopkins University, PhD

### EXPERIENCE AND CAREER

2015.3-Present Professor, Konkuk University  
2012.3-2015.2 Associate professor, Konkuk University  
2010- 2015 Director, Center for Biotechnology Research in UBITA,  
2006 – 2009 Assistant professor, Konkuk University  
2004 – 2005 Postdoc, Stanford University  
1997 – 1998 Hansol Institute of Science and Technology

### RESEARCH INTERESTS

protein structure and gene expression study for the pathogenicity

### PUBLICATIONS (5 papers)

1. Yun Y, et al. (2022), Structural Insights for Core Scaffold and Substrate Specificity of B1, B2, and B3 Metallo-beta-Lactamases, *Frontiers in Microbiology*, 13,12,752535.
2. Kim S, et al. (2021), Combined analysis of the time-resolved transcriptome and proteome of plant pathogen *Xanthomonas oryzae pv.oryzae*, *Frontiers in Microbiology*, 2,12,664857
3. Shin KC, et al. (2020), Development of Tagaturonate 3-Epimerase into Tagatose 4-Epimerase with a Biocatalytic Route from Fructose to Tagatose, *ACS Catalysis*, 10, 20, 12212–12222
4. Choi MY, et al. (2020), Fructuronate-tagaturonate epimerase UxaE from *Cohnella laeviribosi* has a versatile TIM-barrel scaffold suitable for a sugar metabolizing biocatalyst, *International Journal of Biological Macromolecules*, 0141-8130
5. Lee JH, et al. (2019), Nashimoto MK & Lee SH, Dual activity of PNGM-1 pinpoints the evolutionary origin of subclass B3 metallo-β-lactamases: a molecular and evolutionary study, *Emerging Microbes & Infections*, 8 , 1688-1700

# Crystal structure of rice NADP-ME, playing an essential role in plant immune response

Lin-Woo Kang

<sup>1</sup>Department of Biological Sciences, Konkuk University, Seoul, Korea, <sup>2</sup>Department of Integrative Bioscience and Biotechnology, Sejong University, Seoul, Korea

## Abstract

NADP-MEs are ubiquitous enzymes in all living organisms. NADP-ME have drawn attention because it is important in producing CO<sub>2</sub> as carbon resources are metabolized in C<sub>4</sub> plants by oxidative decarboxylation of malate into pyruvate. In C<sub>3</sub> plants, it has multiple roles in regulation of cellular processes including stomatal movement, cellular pH and ionic balance. Rice NADP-ME family consists of one plastidic and three cytosolic members. Sequence analysis indicated that rice NADP-MEs have been evolved from two distinct origins. Probably they have been evolved as tissues are developed specifically to cope with essential cellular needs. We focused on one of the rice cytosolic NADP-ME member, NADP-ME2. It is recently suggested that it plays an essential role in plant immune response by supplying NADPHs to plasma membrane bound NADPH-oxidase upon pathogen infection. This process is relatively similar to mammalian neutrophil immune responses. In spite of its important role in plant immunity, the structural aspect in active form is not well understood. Herein, we determined the 3D structure of rice NADP-ME2.

**Key words:** NADP-ME (NADP-Malic Enzyme), Rice, Plant Immunity

## Nozomu Koizumi

Professor,  
*Department of Agricultural Biology, Osaka Metropolitan University*  
E-mail, [nkoizumi@omu.ac.jp](mailto:nkoizumi@omu.ac.jp)



### EDUCATION

1981-1985 Kyoto University, BS  
1985-1987 Kyoto University, MS  
1987-1991 Kyoto University, *Ph.D.*

### EXPERIENCE AND CAREER

2022-present Professor, Osaka Metropolitan University  
2009-2022 Professor, Osaka Prefecture University  
2007-2009 Associate Professor, Osaka Prefecture University  
2001-2007 Associate Professor, Nara Institute of Science and Technology  
1993-2001 Assistant Professor, Nara Institute of Science and Technology  
1991-1993 Research Fellow of Japan Society for the Promotion of Science  
2021-2022 President, Japanese Society for Plant Biotechnology

### RESEARCH INTERESTS

ER stress response in plants, Plant Molecular Breeding and its ELSI

### PUBLICATIONS (5 papers)

1. Shineha R., Takeda K.F., Yamaguchi Y. & Koizumi N. (2024) A comparative analysis of attitudes towards genome-edited food among Japanese public and scientific community. *PLoS ONE*, 19, e0300107
2. Yamamoto R., Higuchi S., Iwata, Y., Takeda, S., Koizumi, N. & Mishiba K-I. (2024) High  $\beta$ -carotene accumulation in transgenic eggplant fruits grown under artificial light. *Plant Biotechnology*, 41, 77-81
3. Takeda, K.F., Yazawa, A., Yamaguchi, Y., Koizumi, N., & Shineha, R. (2023) Comparison of public attitudes toward five alternative proteins in Japan. *Food Quality and Preference*, 105, 104787
4. Mishiba, K.-I., Nishida, K., Inoue, N., Fujiwara, T., Teranishi, S., Iwata, Y., Takeda, S., & Koizumi, N. (2020). Genetic engineering of eggplant accumulating  $\beta$ -carotene in fruit. *Plant Cell Reports*, 39, 1029-1039.
5. Mishiba, K.-I., Iwata, Y., Mochizuki, T., Matsumura, A., Nishioka, N., Hirata, R., & Koizumi, N. (2019). Unfolded protein-independent IRE1 activation contributes to multifaceted developmental processes in Arabidopsis. *Life Sci Alliance*, 2, e201900459.

# Perception gap of genome edited foods in Japan

Nozomu Koizumi

*Department of Agricultural Biology, Osaka Metropolitan University, Osaka, Japan*

Correspondence: [nkoizumi@omu.ac.jp](mailto:nkoizumi@omu.ac.jp)

## Abstract

The emergence of CRISPR-Cas9 has resulted in a significant advancement in genome editing, impacting crop and livestock breeding, including fish. In Japan, genome-edited organisms like high-GABA tomatoes and fleshier sea bream are already being commercialized. To bring these products to market, addressing three key issues is crucial: intellectual property, regulation, and public acceptance. Intellectual property considerations seem to vary case by case. In Japan, three regulatory frameworks were established in 2019, outlining rules for the cultivation or aquaculture, food use, and feed use of genome edited organisms. These rules are exempt from GMO regulations and are voluntary since distinguishing their DNA sequence from that of conventionally bred organisms is impossible. However, some argue that safety assessments should be mandatory for genome edited foods among media and consumers. In 2019, a survey was conducted among 4,000 consumers and 398 scientists to gauge public attitudes. The results revealed perceptual differences between consumers and scientists. We are currently trying to clarify the relationship of these perception gaps among stakeholders.

**Key words:** genome edited food, perception gap

## Jin, Jing Bo



Professor,

*Key Laboratory of Plant Molecular Physiology, Institute of Botany, Chinese Academy of Sciences*

E-mail, jinjb@ibcas.ac.cn

### EDUCATION

1992-1996 China Agricultural University, BS

1997-1999 Gyeongsang National University, MS

1999-2002 Gyeongsang National University, *Ph.D.*

2002-2004 Pohang University of Science and Technology, *Postdoc.*

2004-2008 Purdue University, *Postdoc.*

### EXPERIENCE AND CAREER

2008-present Professor, Institute of Botany, Chinese Academy of Sciences

### RESEARCH INTERESTS

1. SUMOylation and histone demethylation in plants
2. Molecular design breeding of soybeans and alfalfa

### PUBLICATIONS (5 papers)

1. Wang Q, et al. (2021) JMJ27-mediated histone H3K9 demethylation positively regulates drought-stress responses in Arabidopsis. *New Phytologist* 232, 221-236
2. Qu GP et al. (2020) Reversible SUMOylation of FHY1 regulates phytochrome a signaling in Arabidopsis. *Molecular Plant* 13, 879-893
3. Liu P et al. (2019) The histone H3K4 demethylase JMJ16 represses leaf senescence in Arabidopsis. *Plant Cell* 31, 430-443
4. Niu D et al. (2019) SIZ1-mediated SUMOylation of TPR1 suppresses plant immunity in Arabidopsis. *Molecular Plant* 12, 215-228
5. Feng XJ et al. (2016) Light affects salt stress-induced transcriptional memory of *P5CS1* in Arabidopsis. *Proc. Natl. Acad. Sci. USA* 113, E8335-E8343

# A Transcription Factor Legume Shoot Branching 1 Improves Both Yield and Quality in Soybean

Jing Bo Jin

<sup>1</sup>Key Laboratory of Plant Molecular Physiology, Institute of Botany, Chinese Academy of Sciences, Beijing, China

Correspondence: [jinjb@ibcas.ac.cn](mailto:jinjib@ibcas.ac.cn)

## Abstract

The strong negative correlation between yield and protein content restricts breeding of high yield and high protein soybean cultivars. Here, we demonstrate that a transcription factor LSB1 (Legume shoot branching 1) regulates both yield and protein content in soybean. Through QTL fine mapping, we identified *LSB1* as a negative regulator of shoot branching in soybean. Interestingly, mutations in *LSB1* led to more branches with increased yield and protein content but slightly decreased oil content. *LSB1* associates with promoters of cytokinin oxidases/dehydrogenases and activates their transcription, consequently reduces cytokinins levels in axillary meristem, which may cause reduced shoot branching number. Sequence diversity analysis identified four major haplotypes of *LSB1*. *LSB1<sup>Hap1</sup>* encodes a functional full-length protein, accessions carrying *LSB1<sup>Hap1</sup>* exhibited the fewest branches, lowest protein content and highest oil content, and mainly distributed in northeast China and the United States. By contrast, *LSB1<sup>Hap2-4</sup>* encode non-functional proteins, accessions carrying *LSB1<sup>Hap2-4</sup>* tend to develop more branches, higher protein content and lower oil content, and mainly distributed in southern area of China. The introduction of non-functional alleles of *LSB1* to an elite soybean cultivar Hefeng 55 significantly enhanced both yield and protein content. Therefore, *LSB1* offers an ideal target for molecular breeding by natural allele introgression or by genome editing to improve both yield and quality in soybean.

**Key words:** Shoot branching, cytokinin, yield, quality, soybean

## Yeo, JuDong



Assistant professor,  
*Department of Food Science and Biotechnology of Animal  
Resources, Konkuk University*  
E-mail, [jyeo@konkuk.ac.kr](mailto:jyeo@konkuk.ac.kr)

### EDUCATION

2003-2009 Seoul National University of Science and Technology, *BS*  
2009-2011 Seoul National University of Science and Technology, *MS*  
2013-2018 Memorial University of Newfoundland, *Ph.D.*

### EXPERIENCE AND CAREER

2018-2020 Memorial University of Newfoundland, *Postdoc.*  
2021–2021 University of Ottawa, *Postdoc.*  
2022-present Assistant professor, Konkuk University

### RESEARCH INTERESTS

Food omics, metabolomics, lipidomics

### PUBLICATIONS (5 papers)

1. JuDong Yeo, et al. (2021). Liberation of insoluble-bound phenolics from lentil hull matrices as affected by *Rhizopus oryzae* fermentation: Alteration in phenolic profiles and their inhibitory capacities against low-density lipoprotein (LDL) and DNA oxidation. *Food Chemistry*, 363, 130275
2. JuDong Yeo et al. (2021). Riboflavin sensitized photooxidation of low-density lipoprotein (LDL) cholesterol: A culprit in the development of cardiovascular diseases (CVDs). *Journal of Agricultural and Food Chemistry*, 69, 4204–4209
3. JuDong Yeo et al. (2021). Mass spectrometry-based lipidomics in the characterization of individual triacylglycerols (TAGs) and phospholipids (PLs) species in marine sources and their beneficial health effects. *Reviews in Fisheries Science & Aquaculture*
4. JuDong Yeo et al. (2020). Evaluation of triacylglycerol (TAG) profiles and their contents in salmon tissue using ESI-MS-MS spectrometry with multiple neutral loss scans. *Food Chemistry*, 126816
5. JuDong Yeo, et al. (2020). Identification and quantification of soluble and insoluble-bound phenolics in lentil hulls using HPLC-ESI-MS/MS and their antioxidant potential. *Food Chemistry*, 315, 126202.

# Creating digital map of lipid oxidation using mass spectrometry-based metabolomics and lipidomics: An integrated system for assessing lipid oxidation of edible oil

JuDong Yeo

<sup>1</sup> *Department of Food Science and Biotechnology of Animal Resources, Konkuk University*

E-mail, [jyeo@konkuk.ac.kr](mailto:jyeo@konkuk.ac.kr)

## Abstract

We describe the application of advanced technology, metabolomics and lipidomics, to address the limitations of classical methodologies for measuring lipid oxidation. Despite usefulness of current methodologies for measuring lipid oxidation (i.e., colorimetric assay, chromatography approach, targeted mass spectrometry analysis), significant challenges still remain owing to its low sensitivity, narrow spectrum of markers, and labor-intensive performance. Here, we propose a novel approach, mass spectrometry-based mapping of lipid oxidation, which integrates comprehensive information including the depletion of antioxidants, extensive lipidome profiling and distinct alterations in complex lipid subclasses and discriminating oxidized oils using statistical tools upon lipid oxidation of oils. Metabolomics data displayed sensitive responses at the initial stage of lipid oxidation by showing the drastic depletion in the level of metabolites/antioxidants to retard radical chain reactions, which was not observed in the classical methods such as conjugated dienes (CDs) and p-Anisidine value (p-AV) measurements in olive oil model. Lipidomics showed the global changes in both subclasses and individual lipids, used as the indicator for lipid oxidation determination. PCA and PLS-DA were efficient for discriminating oxidized lipids in the oxidation-time dependent manner. Our dataset based on comprehensive metabolite and lipidome profiling provides insights into sensitive and precise determination of lipid oxidation, potentially guiding future monitoring strategies in wide research area.

**Key words:** mapping lipid oxidation, lipidomics, metabolomics



- MEMO

- MEMO

- MEMO

- MEMO

- MEMO