

On the Cover: Leaf angle is an important agricultural trait determining leaf erectness and, hence, the photosynthesis efficiency and grain yield. Rice leaf angle is determined by lamina joint, and elucidation of the regulatory network of lamina joint development will contribute to molecular breeding of ideal architecture of rice. However, the understanding of morphological changes, cytological transitions, and underlying transcriptional programming is still limited. In this issue, studies by Zhou et al. (pp. 1728–1746) reveal a dynamic and a common—but distinct—development of lamina joint at successive stages accompanying sequential cell division and expansion of parenchyma cells, differentiation of sclerenchyma cells, cell wall thickening, and programmed cell death (PCD). The increased leaf angle results from the asymmetric cell proliferation and elongation at the adaxial or abaxial sides. Analysis of the transcriptome at four developmental stages ranging from initiation to senescence indicate that dynamic cytology is fine-regulated by multiple processes, including phytohormone signaling, transcription, and protein phosphorylation. Furthermore, phytohormones may regulate the lamina joint development synergistically and antagonistically. The image shows the rice lamina joint anatomies at stage 4, and the vascular bundles, sclerenchyma cells (newly formed), and parenchyma cells are highlighted with purple, green, or blue shade colors, respectively. Cover art by Li-Juan Zhou.

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Repression of CYSTATHIONINE γ -SYNTHASE in Seeds Recruits the S-Methylmethionine Cycle. *Hagai Cohen, Yael Hacham, Irina Panizel, Ilana Rogachev, Asaph Aharoni, and Rachel Amir*

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LNK1 and LNK2 Corepressors Interact with the MYB3 Transcription Factor in Phenylpropanoid Biosynthesis. Meiliang Zhou, Kaixuan Zhang, Zhanmin Sun, Mingli Yan, Cheng Chen, Xinquan Zhang, Yixiong Tang, and Yanmin Wu

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^[OPEN]An R2R3-MYB Transcription Factor Regulates Capsaicinoid Biosynthesis. Magda L. Arce-Rodríguez and Neftalí Ochoa-Alejo

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^[OPEN]Impaired Mitochondrial Transcription Termination Disrupts the Stromal Redox Poise in *Chlamydomonas*. Andreas Uhmeyer, Michela Cecchin, Matteo Ballottari, and Lutz Wobbe

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^[OPEN]Acyl-CoA-Binding Protein ACBP1 Modulates Sterol Synthesis during Embryogenesis. Shiu-Cheung Lung, Pan Liao, Edward C. Yeung, An-Shan Hsiao, Yan Xue, and Mee-Len Chye

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^[OPEN]NADPH Thioredoxin Reductase C and Thioredoxins Act Concertedly in Seedling Development. Valle Ojeda, Juan Manuel Pérez-Ruiz, Maricruz González, Victoria A. Nájera, Mariam Sahrawy, Antonio J. Serrato, Peter Geigenberger, and Francisco Javier Cejudo

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The redox state of the apoplast has a profound influence on cellular metabolism.

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[OPEN] Structure of eIF4E in Complex with an eIF4G Peptide Supports a Universal Bipartite Binding Mode for Protein Translation. *Manuel Miras, Verónica Truniger, Cristina Silva, Núria Verdaguer, Miguel A. Aranda, and Jordi Querol-Audí*

The first structure of a plant eIF4E bound to an eIF4G interacting peptide supports a universal mechanism of regulation of translation initiation in higher eukaryotes.

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[OPEN] A Novel N-Methyltransferase in Arabidopsis Appears to Feed a Conserved Pathway for Nicotinate Detoxification among Land Plants and Is Associated with Lignin Biosynthesis. *Wei Li, Fengxia Zhang, Ranran Wu, Lijia Jia, Guosheng Li, Yalong Guo, Cuimin Liu, and Guodong Wang*

N-Methylated nicotinate, produced by NANMT and COMT, is a conserved nicotinate detoxification in land plants.

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[OPEN] In Vitro Characterization of Thermostable CAM Rubisco Activase Reveals a Rubisco Interacting Surface Loop. *Devendra Shivhare and Oliver Mueller-Cajar*

In vitro characterization of a thermostable Rubisco activase from Agave tequilana reveals a surface loop involved in the interaction between Rubisco activase and its substrate.

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[OPEN] A Central Role for Triacylglycerol in Membrane Lipid Breakdown, Fatty Acid β -Oxidation, and Plant Survival under Extended Darkness. *Jilian Fan, Linhui Yu, and Changcheng Xu*

Triacylglycerol is a key intermediate in membrane lipid breakdown and fatty acid β -oxidation, and blocking triacylglycerol hydrolysis reduces oxidative stress and enhances plant survival under extended darkness.

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[OPEN] Stearoyl-Acyl Carrier Protein Desaturase Mutations Uncover an Impact of Stearic Acid in Leaf and Nodule Structure. *Naoufal Lakhssassi, Vincent Colantonio, Nicholas D. Flowers, Zhou Zhou, Jason Henry, Shiming Liu, and Khalid Meksem*

Mutational analysis of SACPD-C reveals an impact of stearic acid accumulation in leaf and nodule structure and morphology.

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[OPEN] Vesicle Dynamics during Plant Cell Cytokinesis Reveals Distinct Developmental Phases. *Chloë van Oostende-Triplet, Dominique Guillet, Thomas Triplet, Elvis Pandzic, Paul W. Wiseman, and Anja Geitmann*

Cell plate formation in dividing plant cells follows a highly consistent pattern involving precisely choreographed vesicle motion and functionally distinct stages.

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[OPEN] Similarities between Reproductive and Immune Pistil Transcriptomes of Arabidopsis Species. *Mariana Mondragón-Palomino, Ajay John-Arputharaj, Maria Pallmann, and Thomas Dresselhaus*

Pistil transcriptomes of Arabidopsis species show a clear overlap between responses to fungal infection and pollination and suggest novel roles for cysteine-rich peptides in fertilization.

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The Prenylated Rab GTPase Receptor PRA1.F4 Contributes to Protein Exit from the Golgi Apparatus. *Myoung Hui Lee, Yun-Joo Yoo, Dae Heon Kim, Nguyen Hong Hanh, Yun Kwon, and Inhwan Hwang*

AtPRA1.F4, an isoform of Arabidopsis prenylated Rab acceptor1 protein, regulates the exit of post-Golgi proteins from the Golgi apparatus. 1576

Rice Sucrose Partitioning Mediated by a Putative Pectin Methyltransferase and Homogalacturonan Methylesterification. *Yonghan Xu, Julien Sechet, Yingbao Wu, Yaping Fu, Longfei Zhu, Jincan Li, Yinping Zhang, Emilie Gineau, Cyril Gaertner, Jian Zhou, Xiaorong Fan, Yu Liu, Li Zhou, Grégory Mouille, and Xinchun Lin*

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[^{OPEN}] Adaptor Protein-3-Dependent Vacuolar Trafficking Involves a Subpopulation of COPII and HOPS Tethering Proteins. *Qiang-Nan Feng, Shi-Jian Song, Shi-Xia Yu, Jia-Gang Wang, Sha Li, and Yan Zhang*

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[^{OPEN}] Primitive Auxin Response without TIR1 and Aux/IAA in the Charophyte Alga *Klebsormidium nitens*. *Kinuka Ohtaka, Koichi Hori, Yuri Kanno, Mitsunori Seo, and Hiroyuki Ohta*

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ECOPHYSIOLOGY AND SUSTAINABILITY

[^{OPEN}] Metal Tolerance Protein 8 Mediates Manganese Homeostasis and Iron Reallocation during Seed Development and Germination. *Seckin Eroglu, Ricardo F. H. Giehl, Bastian Meier, Michiko Takahashi, Yasuko Terada, Konstantin Ignatyev, Elisa Andresen, Hendrik Küpper, Edgar Peiter, and Nicolaus von Wirén*

MTP8 mediates metal homeostasis and seed vigor by cell type-specific vacuolar loading of Mn and Fe in developing embryos and during seed imbibition. 1633

[^{OPEN}] Heavy Metals Induce Iron Deficiency Responses at Different Hierarchic and Regulatory Levels. *Alexandra Lešková, Ricardo F. H. Giehl, Anja Hartmann, Agáta Fargašová, and Nicolaus von Wirén*

A comparative physiological, regulatory, and morphological examination shows that individual heavy metals affect iron deficiency-related responses at different regulatory and mechanistic levels. 1648

[^{OPEN}] Quantifying Wheat Sensitivities to Environmental Constraints to Dissect Genotype × Environment Interactions in the Field. *Boris Parent, Julien Bonneau, Lance Maphosa, Alex Kovalchuk, Peter Langridge, and Delphine Fleury*

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A reproductive barrier causes female gamete abortion of indica-japonica rice hybrids by damaging cell wall integrity, inducing massive biotic and abiotic stresses resulting in ER stress leading to premature PCD.

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[OPEN]Diversification of Root Hair Development Genes in Vascular Plants. Ling Huang, Xinhui Shi, Wenjia Wang, Kook Hui Ryu, and John Schiefelbein

A combined phylogenetic and transcriptomic analysis of root hair development genes in seven vascular plant species reveals unexpected diversification in gene structure and expression.

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[OPEN]Trimethylguanosine Synthase1 (TGS1) Is Essential for Chilling Tolerance. Jinpeng Gao, James G. Wallis, Jeremy B. Jewell, and John Browse

Arabidopsis trimethylguanosine synthase 1, identified from a novel forward screen under chilling conditions, is a functional ortholog of yeast TGS1 and essential for chilling tolerance.

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[OPEN]Dynamic Cytology and Transcriptional Regulation of Rice Lamina Joint Development. Li-Juan Zhou, Lang-Tao Xiao, and Hong-Wei Xue

A systemic study of dynamic morphology, cytology, and transcriptome reveals the cytological basis and fine-regulation by multiple factors, especially phytohormones, of rice lamina joint.

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[OPEN]A Rice NAC Transcription Factor Promotes Leaf Senescence via ABA Biosynthesis. Chanjuan Mao, Songchong Lu, Bo Lv, Bin Zhang, Jiabin Shen, Jianmei He, Liqiong Luo, Dandan Xi, Xu Chen, and Feng Ming

The NAC transcription factor OsNAC2 plays an important role in ABA-dependent leaf senescence by targeting both abscisic acid biosynthetic and senescence-associated genes.

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[OPEN]Target RNA Secondary Structure Is a Major Determinant of miR159 Efficacy. Zihui Zheng, Marlene Reichel, Ira Deveson, Gigi Wong, Junyan Li, and Anthony A. Millar

In addition to high miR159-target gene complementarity, conserved RNA secondary structures abutting the miR159 binding sites are required for strong miR159-mediated silencing of MYB target genes in Arabidopsis.

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[OPEN]Transcriptome Profiling of Wheat Inflorescence Development from Spikelet Initiation to Floral Patterning Identified Stage-Specific Regulatory Genes. Nan Feng, Gaoyuan Song, Jiantao Guan, Kai Chen, Meiling Jia, Dehua Huang, Jiajie Wu, Lichao Zhang, Xiuying Kong, Shuai Feng Geng, Jun Liu, Aili Li, and Long Mao

Transcriptome analyses of key stages in wheat inflorescence development uncover molecular pathways and candidate genes that may be essential for final seed setting and yield improvement in wheat.

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[CC-BY]ATX3, ATX4, and ATX5 Encode Putative H3K4 Methyltransferases and Are Critical for Plant Development. Li-Qun Chen, Jin-Hong Luo, Zhen-Hai Cui, Ming Xue, Li Wang, Xiao-Yu Zhang, Wojciech P. Pawlowski, and Yan He

Characterization of ATX3/4/5 completes elucidation of Arabidopsis Throrax homologs and enhances the understanding of the occurrence, distribution, and function of H3K4me2 and H3K4me3 in plants.

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^[OPEN]The DnaJ-Like Zinc-Finger Protein HCF222 Is Required for Thylakoid Membrane Biogenesis in Plants.

Stephanie Hartings, Susanne Paradies, Bianca Karnuth, Sabrina Eisfeld, Jasmin Mehning, Christian Wolff, Tatjana Levey, Peter Westhoff, and Karin Meierhoff

The chloroplast-located DnaJ-like protein HCF222 is indispensable for accumulation of the cytochrome b₆f complex and to a lesser extent necessary for wild-type levels of PSI and PSII.

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MEMBRANES, TRANSPORT, AND BIOENERGETICS

^[OPEN]Flavodiiron Proteins Promote Fast and Transient O₂ Photoreduction in *Chlamydomonas*.

Frédéric Chaux, Adrien Burlacot, Malika Mekhalfi, Pascaline Auroy, Stéphanie Blangy, Pierre Richaud, and Gilles Peltier

Chlamydomonas flavodiiron proteins FlvA and FlvB massively drive the photosynthetic electron flow to O₂ during the induction of photosynthesis and are critical for growth in fluctuating light.

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^[OPEN]A Magnesium Transporter OsMGT1 Plays a Critical Role in Salt Tolerance in Rice.

Zhi Chang Chen, Naoki Yamaji, Tomoaki Horie, Jing Che, Jian Li, Gynheung An, and Jian Feng Ma

Magnesium transported by OsMGT1 in rice roots is required for enhancing transport activity of OsHKT1;5, which confers salt tolerance through retrieval of Na from xylem vessels.

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^[OPEN]PSA3, a Protein on the Stromal Face of the Thylakoid Membrane, Promotes Photosystem I Accumulation in Cooperation with the Assembly Factor PYG7. Jie Shen, Rosalind Williams-Carrier, and Alice Barkan

PSA3 cooperates with the tetratricopeptide repeat protein PYG7 to promote PSI biogenesis in angiosperms.

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^[OPEN]Role of Type 2 NAD(P)H Dehydrogenase NdbC in Redox Regulation of Carbon Allocation in *Synechocystis*. Tuomas Huokko, Dorota Muth-Pawlak, Natalia Battchikova, Yagut Allahverdiyeva, and Eva-Mari Aro

NdbC has a significant function in regulating carbon allocation between storage and the biosynthesis pathways but also affects cell division.

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Scanning for New BRI1 Mutations via TILLING Analysis. Chao Sun, Kan Yan, Jian-Ting Han, Liang Tao, Ming-Hui Lv, Tao Shi, Yong-Xing He, Michael Wierzba, Frans E. Tax, and Jia Li

Nine morphologically altered new BRI1 mutants were identified from 83 independent TILLING mutations in Arabidopsis.

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^[OPEN]Cooperative Regulatory Functions of miR858 and MYB83 during Cyst Nematode Parasitism.

Sarbottam Piya, Christina Kihm, J. Hollis Rice, Thomas J. Baum, and Tarek Hevezi

The miR858-MYB83 regulatory system regulates a substantial number of genes encoding key etiological factors mediating cyst nematode parasitism of Arabidopsis.

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[OPEN] Stress-Related Gene Expression Reflects Morphophysiological Responses to Water Deficit. Wojciech Rymaszewski, Denis Vile, Alexis Bediee, Myriam Dauzat, Nathalie Luchaire, Dominika Kamrowska, Christine Granier, and Jacek Hennig

Morphophysiological acclimation to long-term water deficit is linked to the transcriptional response and reflected by gene expression levels measured in intact Arabidopsis.

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miR156-Targeted SBP-Box Transcription Factors Interact with DWARF53 to Regulate TEOSINTE BRANCHED1 and BARREN STALK1 Expression in Bread Wheat. Jie Liu, Xiliu Cheng, Pan Liu, and Jiaqiang Sun

miR156-regulated SBP-box transcription factors function antagonistically with DWARF53 to affect TEOSINTE BRANCHED1 and BARREN STALK1 expression during bread wheat tillering and spikelet development.

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[OPEN] Circadian, Carbon, and Light Control of Expansion Growth and Leaf Movement. Federico Apelt, David Breuer, Justyna Jadwiga Olas, Maria Grazia Annunziata, Anna Flis, Zoran Nikoloski, Friedrich Kragler, and Mark Stitt

A 3D imaging platform was used to analyze the contribution of clock and light signaling to the regulation of diurnal changes in rosette expansion rate and leaf angles in Arabidopsis.

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SYSTEMS AND SYNTHETIC BIOLOGY

[OPEN] Root Cell-Specific Regulators of Phosphate-Dependent Growth. Joshua Linn, Meiyang Ren, Oliver Berkowitz, Wona Ding, Margaretha J. van der Merwe, James Whelan, and Ricarda Jost

In silico analysis of iterative coexpression and protein interaction identifies root cell-enriched regulators of the phosphate starvation response in Arabidopsis with impact on phosphate status, transcriptome, and growth.

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