

On the Cover: The Cover photomicrograph is of a cross section of the outermost growth ring of a 40-year-old Norway spruce tree cut during the active growth period. The section is stained red with Safranin O for lignified tissues, and blue with Alcian blue for acidic polysaccharides in non-lignified cell walls. Note the thick tracheid cell walls in the previous year's xylem (on the bottom), and lignification starting in the current year's growth ring in the cell corners and middle lamellae (red). Parenchymatous rays (blue) run through the xylem. Bordered pits between tracheids are clearly visible. Newly formed tracheids are not yet lignified (blue, on the top). The photomicrograph was taken by Olga Blokhina.

ON THE INSIDE

Peter V. Minorsky 1394

NEWS AND VIEWS

Keep it Steamy: Improved Quantification of the Humidity within the Leaf. *Magdalena M. Julkowska* 1396

Restriction Release: Improved Maize Transformation Efficiency. *Magdalena M. Julkowska* 1397

A Novel Upstream Regulator of Trichome Development Inhibitors. *Naomi Cox and Lisa M. Smith* 1398

Enhanced Metabolic Degradation: The Last Evolved Glyphosate Resistance Mechanism of Weeds?
Stephen O. Duke 1401

BREAKTHROUGH TECHNOLOGIES

^[OPEN]A Sequence-Indexed *Mutator* Insertional Library for Maize Functional Genomics Study.
Lei Liang, Ling Zhou, Yuanping Tang, Niankui Li, Teng Song, Wen Shao, Ziru Zhang, Peng Cai, Fan Feng, Yafei Ma, Dongsheng Yao, Yang Feng, Zeyang Ma, Han Zhao, and Rentao Song

A newly developed maize Mutator insertional library named ChinaMu represents the largest sequence-indexed insertional resource for maize to date. 1404

A Deep Learning-Based Approach for High-Throughput Hypocotyl Phenotyping. *Orsolya Dobos, Peter Horvath, Ferenc Nagy, Tivadar Danka, and András Viczián*

A deep learning-based algorithm provides an adaptable tool for determining hypocotyl or coleoptile length of different plant species. 1415

^[OPEN]Machine Learning Approaches to Improve Three Basic Plant Phenotyping Tasks Using Three-Dimensional Point Clouds. *Illia Ziamtsov and Saket Navlakha*

Machine learning tools can improve plant phenotyping (e.g. lamina identification, stem skeletonization) using 3D point clouds. 1425

^[OPEN]A Novel Ternary Vector System United with Morphogenic Genes Enhances CRISPR/Cas Delivery in Maize. *Qiang Zhang, Yu Zhang, Min-Hui Lu, Yi-Ping Chai, Yuan-Yuan Jiang, Yun Zhou, Xue-Chen Wang, and Qi-Jun Chen*

High-throughput genome editing is achieved in recalcitrant plant species using a ternary vector system in combination with morphogenic regulators and CRISPR/Cas modules. 1441

Continued on next page

RESEARCH REPORT

Identification of the Arabidopsis Calmodulin-Dependent NAD⁺ Kinase That Sustains the Elicitor-Induced Oxidative Burst. *Elisa Dell'Aglio, Cécile Giustini, Alexandra Kraut, Yohann Couté, Alex Costa, Guillaume Decros, Yves Gibon, Christian Mazars, Michel Matringe, Giovanni Finazzi, and Gilles Curien*

A long-sought calmodulin- and Ca²⁺-dependent NAD kinase that is conserved in the plant lineage is the missing link between Ca²⁺ signaling, metabolism, and the oxidative burst. 1449

[OPEN] Plant Cell-Cell Transport via Plasmodesmata Is Regulated by Light and the Circadian Clock. *Jacob O. Brunkard and Patricia Zambryski*

Molecular movement through plasmodesmata, which connect plant cells to each other, is dynamically regulated by light and the circadian clock to promote intercellular transport during the day. 1459

RESEARCH ARTICLES

BIOCHEMISTRY AND METABOLISM

Isoforms of Acyl-CoA:Diacylglycerol Acyltransferase2 Differ Substantially in Their Specificities toward Erucic Acid. *Kamil Demski, Simon Jeppson, Ida Lager, Agnieszka Misztak, Katarzyna Jasieniecka-Gazarkiewicz, Małgorzata Waleron, Sten Stymne, and Antoni Banaś*

Despite highly similar amino acid sequences, isoforms of Acyl-CoA:Diacylglycerol Acyltransferase2 from Brassica napus form two distinct groups according to their affinity toward erucic acid. 1468

[OPEN] The *Chlamydomonas deg1c* Mutant Accumulates Proteins Involved in High Light Acclimation. *Jasmine Theis, Julia Lang, Benjamin Spaniol, Suzanne Ferté, Justus Niemeyer, Frederik Sommer, David Zimmer, Benedikt Venn, Shima Farazandeh Mehr, Timo Mühlhaus, Francis-André Wollman, and Michael Schroda*

The depletion of a highly active protease located to the stroma and at the stromal side of thylakoid membranes triggers the upregulation of proteins normally involved in high light responses. 1480

Natural Variation Reveals a Key Role for Rhamnogalacturonan I in Seed Outer Mucilage and Underlying Genes. *Isabelle Fabrissin, Gwendal Cueff, Adeline Berger, Fabienne Granier, Christine Sallé, Damien Poulain, Marie-Christine Ralet, and Helen M. North*

Analysis of natural variation in Arabidopsis provides insight into adaptive constraints and underlying gene functions influencing the composition and properties of outer seed mucilage. 1498

Aldo-keto Reductase Metabolizes Glyphosate and Confers Glyphosate Resistance in *Echinochloa colona*. *Lang Pan, Qin Yu, Heping Han, Lingfeng Mao, Alex Nyporko, Longjiang Fan, Liyang Bai, and Stephen Powles*

The plant metabolic enzyme aldo-keto reductase has evolved to metabolize glyphosate in a glyphosate-resistant weed species 1519

CELL BIOLOGY

Basic Proline-Rich Protein-Mediated Microtubules Are Essential for Lobe Growth and Flattened Cell Geometry. *Jeh Haur Wong, Takehide Kato, Samuel A. Belton, Rie Shimizu, Nene Kinoshita, Takumi Higaki, Yuichi Sakumura, Daniel B. Szymanski, and Takashi Hashimoto*

In early lobe formation, basic proline-rich proteins associated with microtubules organize distinct microtubule arrays that are essential for lobe growth and a flattened cell shape in pavement cells. 1535

[^{OPEN}] Ray Parenchymal Cells Contribute to Lignification of Tracheids in Developing Xylem of Norway Spruce. *Olga Blokhina, Teresa Laitinen, Yuto Hatakeyama, Nicolas Delhomme, Tanja Paasela, Lei Zhao, Nathaniel R. Street, Hiroshi Wada, Anna Kärkönen, and Kurt Fagerstedt*

Transcriptomics combined with single-cell metabolomics give new information on the role of rays in lignification of developing xylem in Norway spruce.

1552

ECOPHYSIOLOGY AND SUSTAINABILITY

[^{OPEN}] Effect of Vapor Pressure Deficit on Gas Exchange in Wild-Type and Abscisic Acid–Insensitive Plants. *Lucas A. Cernusak, Gregory R. Goldsmith, Matthias Arend, and Rolf T. W. Siegwolf*

Altered gas exchange and isotope discrimination in ABA-insensitive poplar with impaired stomata is consistent with unsaturated leaf intercellular vapor pressure at low air vapor pressure deficits.

1573

GENES, DEVELOPMENT AND EVOLUTION

[^{OPEN}] The TCP4 Transcription Factor Directly Activates *TRICHOMELESS1* and 2 and Suppresses Trichome Initiation. *Batthula Vijaya Lakshmi Vadde, Krishna Reddy Challa, Preethi Sunkara, Anjana S. Hegde, and Utpal Nath*

The class II TEOSINTE BRANCHED1/CYCLOIDEA/PROLIFERATING CELL FACTOR group of proteins suppresses trichome initiation on leaf surface.

1587

RETINOBLASTOMA-RELATED Genes Specifically Control Inner Floral Organ Morphogenesis and Pollen Development in Rice. *Yuanlin Duan, Yaguang Chen, Wengiang Li, Meizhen Pan, Xiaojie Qu, Xiaoqing Shi, Zhengzheng Cai, Huaqing Liu, Fen Zhao, Lan Kong, Yanfang Ye, Feng Wang, Yongbiao Xue, and Weiren Wu*

Members of a cell-cycle-related gene family maintain floral meristem function to ensure floral organ origination and regulate tapetum degradation to promote pollen formation in rice.

1600

MEMBRANES, TRANSPORT AND BIOENERGETICS

[^{OPEN}] The Role of Phosphorylation Dynamics of CURVATURE THYLAKOID 1B in Plant Thylakoid Membranes. *Andrea Trotta, Azfar Ali Bajwa, Ilaria Mancini, Virpi Paakkarinen, Mathias Pribil, and Eva-Mari Aro*

Phosphorylation dynamics of CURVATURE THYLAKOID 1B, PSII core, and Light-harvesting II complex proteins cooperate in regulation of thylakoid lateral heterogeneity under fluctuating light.

1615

[^{OPEN}] A Mitochondrial LYR Protein Is Required for Complex I Assembly. *Aneta Ivanova, Mabel Gill-Hille, Shaobai Huang, Rui M. Branca, Beata Kmiec, Pedro F. Teixeira, Janne Lehtiö, James Whelan, and Monika W. Murcha*

A mitochondrial LYR protein is involved in the biogenesis of a matrix arm domain subunit of Complex I.

1632

SIGNALLING AND RESPONSE

Alternative Splicing Provides a Mechanism to Regulate LIHSA3 Function in Response to Heat Stress in Lily. *Ze Wu, Jiahui Liang, Chengpeng Wang, Liping Ding, Xin Zhao, Xing Cao, Sujuan Xu, Nianjun Teng, and Mingfang Yi*

A genetic buffering mechanism of lily through alternative splicing counteracts the side effect of LIHSA3 in response to heat stress.

1651

[OPEN] Jasmonic Acid Is Required for Plant Acclimation to a Combination of High Light and Heat Stress. *Damián Balfagón, Soham Sengupta, Aurelio Gómez-Cadenas, Felix B. Fritschi, Rajeev K. Azad, Ron Mittler, and Sara I. Zandalinas*

The phytohormone jasmonic acid is required for plant acclimation to combined high light and heat stress in Arabidopsis.

1668

[OPEN] Transcription Factor bHLH2 Represses CYSTEINE PROTEASE77 to Negatively Regulate Nodule Senescence. *Jie Deng, Fugui Zhu, Jiaying Liu, Yafei Zhao, Jiangqi Wen, Tao Wang, and Jiangli Dong*

A transcription factor-cysteine protease regulatory module is associated with programmed cell death and reactive oxygen species accumulation in nodule senescence.

1683

[OPEN] PECTIN ACETYLESTERASE9 Affects the Transcriptome and Metabolome and Delays Aphid Feeding. *Karen J. Kloth, Ilka N. Abreu, Nicolas Delhomme, Ivan Petřík, Cloé Villard, Cecilia Ström, Fariba Amini, Ondřej Novák, Thomas Moritz, and Benedicte R. Albrechtsen*

PECTIN ACETYLESTERASE9 is involved in the accumulation of jasmonic acid, camalexin and antioxidants, and delays establishment of aphid phloem feeding, but is not required for aphid-induced defenses.

1704

SYSTEMS AND SYNTHETIC BIOLOGY

[CC-BY] Proteome Mapping of a Cyanobacterium Reveals Distinct Compartment Organization and Cell-Dispersed Metabolism. *Laura L. Baers, Lisa M. Breckels, Lauren A. Mills, Laurent Gatto, Michael J. Deery, Tim J. Stevens, Christopher J. Howe, Kathryn S. Lilley, and David J. Lea-Smith*

The most extensive proteome map of an entire cyanobacterial cell demonstrates that thylakoid and plasma membrane proteins have distinct functions and that metabolic pathways are dispersed throughout the cell.

1721

[OPEN] Cis-Regulatory Code for Predicting Plant Cell-Type Transcriptional Response to High Salinity. *Sahra Uygun, Christina B. Azodi, and Shin-Han Shiu*

Machine learning models uncover cis-regulatory sequences regulating gene expression in response to high-salinity stress at the cell-type level.

1739

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