

The electronic form of this issue, available as of January 7, 2014, at www.plantphysiol.org, is considered the journal of record.

On the Cover: Natural variation in grape leaf morphology is immense. Before the advent of genetics, the science of ampelography (*αμπελος*, “vine” and *γραφος*, “writing”) would distinguish grapevine varieties by their phenotypes. Leaves are one of the most distinctive, variable features of grapevines, and ampelographers quantified leaves to an unprecedented degree. In this issue, Chitwood et al. (pp. 259–272) describe modern morphometric techniques, such as generalized Procrustes analysis and elliptical Fourier descriptors, to quantify the complex shapes of grape leaves. These results are compared to previous ampelographic measurements, and heritabilities are calculated to demonstrate a strong genetic basis underlying grape leaf shape. The cover shows a small selection of the over 9,500 leaves from more than 1,200 *Vitis vinifera* accessions sampled. Cover design: Daniel Chitwood. Leaf sampling and photography: Aashish Ranjan, Ciera Martinez, Lauren Headland, and Think Thiem.

THANK YOU TO REVIEWERS

Acknowledgment of *Plant Physiology* Reviewers. 1

ON THE INSIDE

Peter V. Minorsky 10

EDITORIAL

Plant Physiology Sees the Light. *John Christie and Mike Blatt* 12

FOUNDER’S REVIEW

Phototropism: Some History, Some Puzzles, and a Look Ahead. *Winslow R. Briggs*

After over a century of progress, phototropism research still presents some fascinating challenges. 13

BREAKTHROUGH TECHNOLOGIES

[C][W][OPEN] Recovering Root System Traits Using Image Analysis Exemplified by Two-Dimensional Neutron Radiography Images of Lupine. *Daniel Leitner, Bernd Felderer, Peter Vontobel, and Andrea Schnepf*

Image-based parameterization of root architectural models is advanced by a new approach for the analysis of image sequences of plant root systems. 24

[C][W][OPEN] Virus-Based MicroRNA Silencing in Plants. *Aihua Sha, Jinping Zhao, Kangquan Yin, Yang Tang, Yan Wang, Xiang Wei, Yiguo Hong, and Yule Liu*

Virus-based microRNA silencing can be used for functional analysis of endogenous microRNAs in plants. 36

RESEARCH REPORTS

[W] Peroxisomal ATP-Binding Cassette Transporter COMATOSE and the Multifunctional Protein ABNORMAL INFLORESCENCE MERISTEM Are Required for the Production of Benzoylated Metabolites in Arabidopsis Seeds. *John D. Bussell, Michael Reichelt, Andrew A.G. Wiszniewski, Jonathan Gershenzon, and Steven M. Smith*

A peroxisomal substrate transporter and β -oxidation provide benzoic acid for the accumulation of benzoylated secondary metabolites during Arabidopsis seed development. 48

BIOCHEMISTRY AND METABOLISM

[C][W][OPEN] Conserved Changes in the Dynamics of Metabolic Processes during Fruit Development and Ripening across Species. *Sebastian Klie, Sonia Osorio, Takayuki Tohge, Maria F. Drincovich, Aaron Fait, James J. Giovannoni, Alisdair R. Fernie, and Zoran Nikoloski*

STATIS analysis of metabolic profiles discerns conserved metabolic processes during development and ripening across fruits. 55

Continued on next page

- [C][W][OPEN] Unusual Small Subunit That Is Not Expressed in Photosynthetic Cells Alters the Catalytic Properties of Rubisco in Rice. *Koichi Morita, Tomoko Hatanaka, Shuji Misoo, and Hiroshi Fukayama*
Rice utilizes different type of Rubisco small subunit in nonphotosynthetic cells. 69
- [W][OPEN] Determination of Residues Responsible for Substrate and Product Specificity of *Solanum habrochaites* Short-Chain cis-Prenyltransferases. *Jin-Ho Kang, Eliana Gonzales-Vigil, Yuki Matsuba, Eran Pichersky, and Cornelius S. Barry*
The relative positions of aromatic amino acids and adjacent residues within domain II of short-chain cis-prenyltransferases contributes to the evolution of volatile terpene biosynthesis in Solanum species trichomes. 80
- [C][W][OPEN] Deciphering the Role of Aspartate and Prephenate Aminotransferase Activities in Plastid Nitrogen Metabolism. *Fernando de la Torre, Jorge El-Azaz, Concepción Ávila, and Francisco M. Cánovas*
Molecular and metabolic analysis in tobacco plants after virus-induced gene silencing uncovers different pathways of amino acid biosynthesis within the plastids. 92
- CELL BIOLOGY**
- [W] Leaf Oil Body Functions as a Subcellular Factory for the Production of a Phytoalexin in Arabidopsis. *Takashi L. Shimada, Yoshitaka Takano, Tomoo Shimada, Masayuki Fujiwara, Yoichiro Fukao, Masashi Mori, Yozo Okazaki, Kazuki Saito, Ryosuke Sasaki, Koh Aoki, and Ikuko Hara-Nishimura*
Leaf oil bodies are the source of a novel phytoalexin produced in response to fungal infection and senescence. 105
- [C][W][OPEN] Deletion Mutagenesis Identifies a Haploinsufficient Role for γ -Zein in *opaque2* Endosperm Modification. *Lingling Yuan, Yongchao Dou, Shahryar F. Kianian, Chi Zhang, and David R. Holding*
A haploinsufficient role is identified for γ -zein in maize mutant endosperm modification. 119
- ECOPHYSIOLOGY AND SUSTAINABILITY**
- [W] Stable Carbon Isotope Discrimination Is under Genetic Control in the C_4 Species Maize with Several Genomic Regions Influencing Trait Expression. *Sebastian Gresset, Peter Westemeier, Svenja Rademacher, Milena Ouzunova, Thomas Presterl, Peter Westhoff, and Chris-Carolin Schön*
Multiplatform-based phenotyping and high-density genotyping uncovers multiple genomic regions controlling stable carbon isotope discrimination in a maize introgression library. 131
- [W][OPEN] Genome-Wide Association Mapping Combined with Reverse Genetics Identifies New Effectors of Low Water Potential-Induced Proline Accumulation in Arabidopsis. *Paul E. Verslues, Jesse R. Lasky, Thomas E. Juenger, Tzu-Wen Liu, and M. Nagaraj Kumar*
Genome-wide association analysis and spatial patterning of single-nucleotide polymorphism data guide reverse genetics to identify new genes linking stress-induced proline accumulation with cellular redox and energy status. 144
- [C][W][OPEN] Feruloyl-CoA 6'-Hydroxylase1-Dependent Coumarins Mediate Iron Acquisition from Alkaline Substrates in Arabidopsis. *Nicole B. Schmid, Ricardo F.H. Giehl, Stefanie Döll, Hans-Peter Mock, Nadine Strehmel, Dierk Scheel, Xiaole Kong, Robert C. Hider, and Nicolaus von Wirén*
The release of F coumarins is a component of the reduction-based iron acquisition machinery that helps plants to mobilize iron under alkaline conditions. 160
- [C][W][OPEN] Estimates of Leaf Vein Density Are Scale Dependent. *Charles A. Price, Peter R.T. Munro, and Joshua S. Weitz*
Best practice minimizes complications arising in estimates of leaf vein density that depend strongly and systematically on the scale of inquiry and the tradeoff between field of view, magnification, lattice effects, and vein hierarchical effects. 173

GENES, DEVELOPMENT, AND EVOLUTION

[W][OPEN] Characterization and Identification of cis-Regulatory Elements in Arabidopsis Based on Single-Nucleotide Polymorphism Information. *Paula Korcuć, Jos H.M. Schippers, and Dirk Walther*

Information on genomic variation provided by novel sequencing technologies offers new and powerful approaches to identify regulatory elements and characterize gene promoter sequences.

181

[W] RBF1, a Plant Homolog of the Bacterial Ribosome-Binding Factor RbfA, Acts in Processing of the Chloroplast 16S Ribosomal RNA. *Rikard Fristedt, Lars B. Scharff, Cornelia A. Clarke, Qin Wang, Chentao Lin, Sabeeha S. Merchant, and Ralph Bock*

A plant homolog of a bacterial ribosome biogenesis factor functions in chloroplasts, associates with thylakoid membranes, and is involved in maturation of ribosomal RNA.

201

[C][W][OPEN] Regulation of Compound Leaf Development by PHANTASTICA in *Medicago truncatula*. *Liangfa Ge, Jianling Peng, Ana Berbel, Francisco Madueño, and Rujin Chen*

*A MYB domain protein maintains petiole identity by repressing expression of a motor organ identity gene and promoting petiole and stipule development in *Medicago truncatula*.*

216

[C][W][OPEN] Unequal Redundancy in Maize *knotted1* homeobox Genes. *Nathalie Bolduc, Randall G. Tyers, Michael Freeling, and Sarah Hake*

*A homeobox gene plays a critical, dosage-dependent role in shoot apical meristem establishment and maintenance, stem elongation, and inflorescence development that is only uncovered in a *knotted1* mutant background.*

229

[W][OPEN] A Major Role for the Plastid-Encoded RNA Polymerase Complex in the Expression of Plastid Transfer RNAs. *Rosalind Williams-Carrier, Reimo Zoschke, Susan Belcher, Jeannette Pfalz, and Alice Barkan*

Proteins that associate with the plastid-encoded RNA polymerase are required for robust expression of numerous plastid tRNAs.

239

[W] Molecular Mechanism of microRNA396 Mediating Pistil Development in Arabidopsis. *Gang Liang, Hua He, Yang Li, Fang Wang, and Diqiu Yu*

miR396 affects pistil development by suppressing its target genes and cotranscription complex.

249

[C][W][OPEN] A Modern Ampelography: A Genetic Basis for Leaf Shape and Venation Patterning in Grape.

Daniel H. Chitwood, Aashish Ranjan, Ciera C. Martinez, Lauren R. Headland, Thinh Thiem, Ravi Kumar, Michael F. Covington, Tommy Hatcher, Daniel T. Naylor, Sharon Zimmerman, Nora Downs, Nataly Raymundo, Edward S. Buckler, Julin N. Maloof, Mallikarjuna Aradhya, Bernard Prins, Lin Li, Sean Myles, and Neelima R. Sinha

Statistical methods can globally describe the complex shapes of grape leaves, permitting the evaluation of not only the genetic basis of leaf shape but its correlation with traits of economic interest.

259

MEMBRANES, TRANSPORT, AND BIOENERGETICS

[W] Modification of Plasma Membrane Organization in Tobacco Cells Elicited by Cryptogein. *Patricia Gerbeau-Pissot, Christophe Der, Dominique Thomas, Iulia-Andra Anca, Kevin Grosjean, Yann Roche, Jean-Marie Perrier-Cornet, Sébastien Mongrand, and Françoise Simon-Plas*

The ordering and organization of the plasma membrane of tobacco suspension cells as well as membrane fluidity, is modified during the early steps of the signaling cascade induced by an elicitor of defense reactions.

273

[C][W][OPEN] Do Plants Contain G Protein-Coupled Receptors? *Bruck Taddese, Graham J.G. Upton, Gregory R. Bailey, Siân R.D. Jordan, Nuradin Y. Abdulla, Philip J. Reeves, and Christopher A. Reynolds*

GCR1 shares the fold and key functional motifs of class A, class B, and class E G protein-coupled receptors.

287

Continued on next page

[W][OPEN]Glucose Elevates NITRATE TRANSPORTER2.1 Protein Levels and Nitrate Transport Activity Independently of Its HEXOKINASE1-Mediated Stimulation of NITRATE TRANSPORTER2.1 Expression. *Femke de Jong, Kate Thodey, Laurence V. Lejay, and Michael W. Bevan*

Independent mechanisms link photosynthate availability with nitrate uptake and assimilation into amino acids. 308

SIGNALING AND RESPONSE

[W]Terpene Down-Regulation Triggers Defense Responses in Transgenic Orange Leading to Resistance against Fungal Pathogens. *Ana Rodríguez, Takehiko Shimada, Magdalena Cervera, Berta Alquézar, José Gadea, Aurelio Gómez-Cadenas, Carlos José De Ollas, María Jesús Rodrigo, Lorenzo Zacarías, and Leandro Peña*

Down-regulation of a D-limonene synthase gene in orange fruit triggers defense cascades linked to isoprenoid metabolism and resistance to necrotroph pathogens. 321

[W][OPEN]Recognition of the Protein Kinase AVRPPHB SUSCEPTIBLE1 by the Disease Resistance Protein RESISTANCE TO PSEUDOMONAS SYRINGAE5 Is Dependent on S-Acylation and an Exposed Loop in AVRPPHB SUSCEPTIBLE1. *Dong Qi, Ullrich Dubiella, Sang Hee Kim, D. Isaiah Sloss, Robert H. Downen, Jack E. Dixon, and Roger W. Innes*

A nucleotide-binding protein distinguishes among closely related protein kinases based on plasma membrane localization and an exposed loop in the C-terminal third of the kinase domain. 340

[W]Fungal Endopolygalacturonases Are Recognized as Microbe-Associated Molecular Patterns by the Arabidopsis Receptor-Like Protein RESPONSIVENESS TO BOTRYTIS POLYGALACTURONASES1. *Lisha Zhang, Ilona Kars, Bert Essenstam, Thomas W.H. Liebrand, Lia Wagemakers, Joyce Elberse, Panagiota Tagkalaki, Devlin Tjoitang, Guido van den Ackerveken, and Jan A.L. van Kan*

Fungal pectin-degrading enzymes act as microbe-associated molecular patterns that are recognized by a pattern recognition receptor from Arabidopsis. 352

[W][OPEN]The Basic Leucine Zipper Transcription Factor ABSCISIC ACID RESPONSE ELEMENT-BINDING FACTOR2 Is an Important Transcriptional Regulator of Abscisic Acid-Dependent Grape Berry Ripening Processes. *Philippe Nicolas, David Lecourieux, Christian Kappel, Stéphanie Cluzet, Grant Cramer, Serge Delrot, and Fatma Lecourieux*

A basic leucine zipper family transcription factor is an important transcriptional regulator of abscisic acid-dependent grape berry ripening. 365

[W][OPEN]Reciprocal Responses in the Interaction between Arabidopsis and the Cell-Content-Feeding Chelicerate Herbivore Spider Mite. *Vladimir Zhurov, Marie Navarro, Kristie A. Bruinsma, Vicent Arbona, M. Estrella Santamaria, Marc Cazaux, Nicky Wybouw, Edward J. Osborne, Cherise Ens, Cristina Rioja, Vanessa Vermeirssen, Ignacio Rubio-Somoza, Priti Krishna, Isabel Diaz, Markus Schmid, Aurelio Gómez-Cadenas, Yves Van de Peer, Miodrag Grbic, Richard M. Clark, Thomas Van Leeuwen, and Vojislava Grbic*

Analysis of genome-wide Arabidopsis responses to spider mite identifies the secondary metabolites that limit the mite's ability to use Arabidopsis as a host. 384

[C][W][OPEN]Regulation of Drought Tolerance by the F-Box Protein MAX2 in Arabidopsis. *Qingyun Bu, Tianxiao Lv, Hui Shen, Phi Luong, Jimmy Wang, Zhenyu Wang, Zhigang Huang, Langtao Xiao, Cawas Engineer, Tae Houn Kim, Julian I. Schroeder, and Enamul Huq*

An F-box protein regulates drought and osmotic stress responses in a strigolactone-independent manner in Arabidopsis. 424

[W][OPEN]Sensitivity to Flg22 Is Modulated by Ligand-Induced Degradation and de Novo Synthesis of the Endogenous Flagellin-Receptor FLAGELLIN-SENSING2. *John M. Smith, Daniel J. Salamango, Michelle E. Leslie, Carina A. Collins, and Antje Heese*

Ligand-induced degradation of endogenous flagellin receptor desensitizes cells to its stimulus, likely to remove ligand-bound receptors from the site of perception, and subsequent de novo receptor synthesis resensitizes cells for a new round of stimulus perception. 440

Continued on next page

SYSTEMS AND SYNTHETIC BIOLOGY

^[W]An RNA Sequencing Transcriptome Analysis Reveals Novel Insights into Molecular Aspects of the Nitrate Impact on the Nodule Activity of *Medicago truncatula*. Ricardo Cabeza, Beke Koester, Rebecca Liese, Annika Lingner, Vanessa Baumgarten, Jan Dirks, Gabriela Salinas-Riester, Claudia Pommerenke, Klaus Dittert, and Joachim Schulze

A nitrate-induced decline in nitrogenase activity in Medicago truncatula nodules is connected with a strong down-regulation of genes for nodule-specific cysteine-rich peptides and leghemoglobins, changes in inner cell iron allocation, and a decline in nodule respiration efficiency.

400

^{[W][OPEN]}A Sequence-Ready Physical Map of Barley Anchored Genetically by Two Million Single-Nucleotide Polymorphisms. Ruwini Ariyadasa, Martin Mascher, Thomas Nussbaumer, Daniela Schulte, Zeev Frenkel, Naser Poursarebani, Ruonan Zhou, Burkhard Steuernagel, Heidrun Gundlach, Stefan Taudien, Marius Felder, Matthias Platzer, Axel Himmelbach, Thomas Schmutzer, Pete E. Hedley, Gary J. Muehlbauer, Uwe Scholz, Abraham Korol, Klaus F.X. Mayer, Robbie Waugh, Peter Langridge, Andreas Graner, and Nils Stein

A genome-wide physical map of barley was constructed and anchored genetically by a novel method involving whole-genome resequencing of a mapping population.

412

^{[W][OPEN]}Coexpressing *Escherichia coli* Cyclopropane Synthase with *Sterculia foetida* Lysophosphatidic Acid Acyltransferase Enhances Cyclopropane Fatty Acid Accumulation. Xiao-Hong Yu, Richa Rawat Prakash, Marie Sweet, and John Shanklin

Heterologous expression in plant seeds of two lipid-modifying enzymes enables a synthetic cycle that enriches for the accumulation of cyclopropane fatty acids at both sn-1 and sn-2 positions of phosphatidylcholine.

455

^[W]The Operation of Two Decarboxylases, Transamination, and Partitioning of C₄ Metabolic Processes between Mesophyll and Bundle Sheath Cells Allows Light Capture To Be Balanced for the Maize C₄ Pathway. Chandra Bellasio and Howard Griffiths

Light quality was used to manipulate ATP supply and demand between C₄ pathway mesophyll and bundle sheath, and the results are consistent with a metabolic model that explains the requirement for two decarboxylases and the partitioning of metabolic activities in maize.

466

^{[C][W][OPEN]}Machine Learning Approaches Distinguish Multiple Stress Conditions using Stress-Responsive Genes and Identify Candidate Genes for Broad Resistance in Rice. Rafi Shaik and Wusirika Ramakrishna

Meta-analysis of differentially expressed rice genes under different stress conditions accurately classified them using machine learning approaches and identified genes likely to confer broad resistance to multiple abiotic and biotic stresses.

481

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