

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 Thinh Thiem.

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

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

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[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*

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

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

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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.

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[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*

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[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.

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[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*

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[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.

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[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*

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[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*

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[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.

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[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*

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[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.

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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.

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[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

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[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.

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[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.

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[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

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