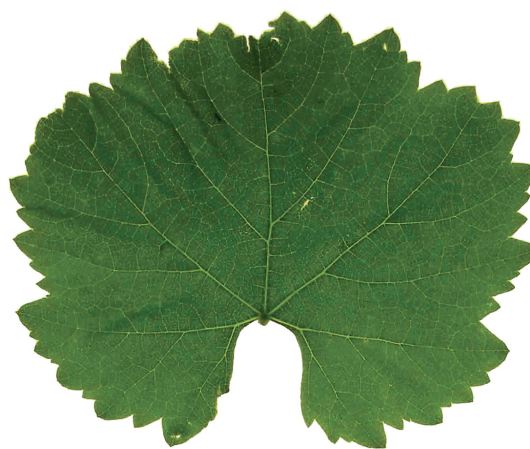
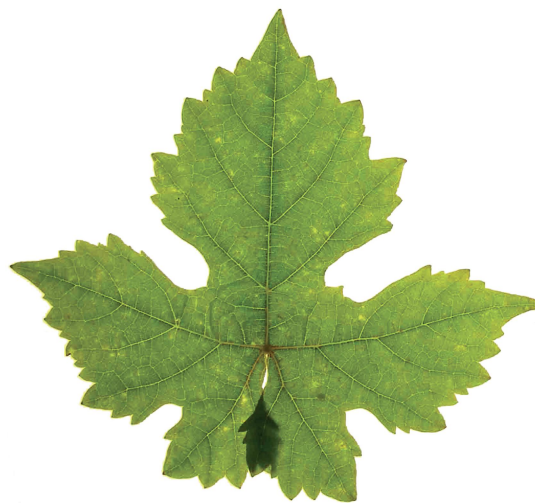
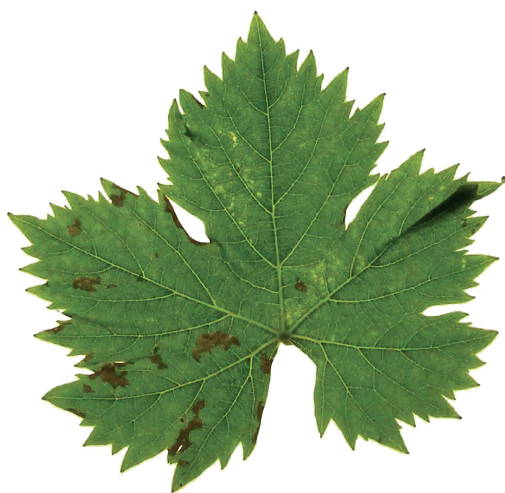


# *Plant Physiology*<sup>®</sup>

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**Morphometric Analysis Reveals a Genetic Basis for  
Leaf Shape in Grape**

The electronic form of this issue, available as of January 7, 2014, at [www.plantphysiol.org](http://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.

## THANK YOU TO REVIEWERS

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*A peroxisomal substrate transporter and  $\beta$ -oxidation provide benzoic acid for the accumulation of benzoylated secondary metabolites during Arabidopsis seed development.*

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[C][W][OPEN]Conserved Changes in the Dynamics of Metabolic Processes during Fruit Development and Ripening across Species. Sebastian Klie, Sonia Osorio, Takayuki Tohge, María 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.*

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

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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

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

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[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.*

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*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

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

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*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

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

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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. Immes

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

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[W][OPEN]The Basic Leucine Zipper Transcription Factor ABSCISIC ACID RESPONSE ELEMENT-BINDING FACTOR2 Is an Important Transcriptional Regulator of Absciscic 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

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

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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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[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

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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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*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  $C_4$  Metabolic Processes between Mesophyll and Bundle Sheath Cells Allows Light Capture To Be Balanced for the Maize  $C_4$  Pathway. Chandra Bellasio and Howard Griffiths

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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

*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.*

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