On the Cover: Natural variation in grape leaf morphology is immense. Before the advent of genetics, the science of ampelography (αμπελόγος, “vine” and γραφός, “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

Acknowledgment of Plant Physiology Reviewers.

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

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

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.

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

BIOCHEMISTRY AND METABOLISM

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STATIS analysis of metabolic profiles discerns conserved metabolic processes during development and ripening across fruits.
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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Determination of Residues Responsible for Substrate and Product Specificity of Solanum habrochaites Short-Chain cis-Prenyltransferases. Jin-Ho Kang, Eliana Gonzales-Vigil, Yuki Matsuda, 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.

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.

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 Saiio, 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.

Deletion Mutagenesis Identifies a Haploinsufficient Role for γ-Zein in opaque2 Endosperm Modification. Lingling Yuan, Yongchao Dou, Shahraray F. Kianian, Chi Zhang, and David R. Holding

A haploinsufficient role is identified for γ-zein in maize mutant endosperm modification.

Stable Carbon Isotope Discrimination Is under Genetic Control in the C₄ Species Maize with Several Genomic Regions Influencing Trait Expression. Sebastian Gresset, Peter Westermeier, 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.


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.

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.

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.

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

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, Subeeha 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.

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.

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.

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.

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.


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.

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.


GCR1 shares the fold and key functional motifs of class A, class B, and class E G protein-coupled receptors.
Independent mechanisms link photosynthetic availability with nitrate uptake and assimilation into amino acids.

**SIGNALLING AND RESPONSE**

**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

**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, Deolin Tjoitang, Guido van den Ackerveken, and Jan A.L. van Kan

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.

**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. Dooven, 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.


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.

**Regulation of Drought Tolerance by the F-Box Protein MAX2 in Arabidopsis.** Qingsyun Bu, Tianxiao Lv, Hui Shen, phi Luong, Jimmy Wang, Zhenyu Wang, Zhigang Huang, Langzhao Xiao, Cauvas 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.

**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.
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.

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

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.

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.