The electronic form of this issue, available as of October 11, 2007, at www.plantphysiol.org, is considered the journal of record.

On the Cover: The interactome, a complete map of all protein-protein interactions, is an invaluable tool for systems biology. As an appetizer for those awaiting the results from high-throughput experimental approaches, an interactome was predicted for the Arabidopsis (Arabidopsis thaliana) genome by identifying pairs of orthologs that interact in yeast, Drosophila, humans, and Caenorhabditis elegans. In this illustration, each circle represents an Arabidopsis protein. The color of the circle is the subcellular localization from the SUBA database, for example, dark blue = nucleus and yellow = vacuole (see article for full list). Where two proteins are connected by a line, there is a predicted interaction. The thickness of the line represents the confidence value, while the line color is the degree of gene coexpression (red = highly coexpressed, yellow = weakly). An interactome of 19,979 interactions was made for 3,617 conserved Arabidopsis proteins, and is available online at the Bio-Array Resource for Arabidopsis functional genomics and can be downloaded from The Arabidopsis Information Resource. Shown on the cover are interactions for 918 proteins where subcellular localization was known. (Illustration courtesy of Matt Geisler.)

ON THE INSIDE

Peter V. Minorsky

UPDATE

Molecular Dissection of Endosomal Compartments in Plants. Jens Müller, Ursula Mettbach, Diedrik Menzel, and Jozef Šamaj

BREAKTHROUGH TECHNOLOGIES


BIOINFORMATICS


SCIENTIFIC CORRESPONDENCE

[C]Pollen Lethality: A Phenomenon in Arabidopsis RNA Interference Plants. Shuping Xing and Sabine Zachgo

[W]Nonmotile Cellulose Synthase Subunits Repeatedly Accumulate within Localized Regions at the Plasma Membrane in Arabidopsis Hypocotyl Cells following 2,6-Dichlorobenzonitrile Treatment. Seth DeBolt, Ryan Gutierrez, David W. Ehrhardt, and Chris Somerville

Continued on next page
RESEARCH ARTICLES

BIOCHEMICAL PROCESSES AND MACROMOLECULAR STRUCTURES

Regulation of One-Carbon Metabolism in Arabidopsis: The N-Terminal Regulatory Domain of Cystathionine \( \gamma \)-Synthase Is Cleaved in Response to Folate Starvation. Karen Loizeau, Bernadette Gambonnet, Guo-Fang Zhang, Gilles Curien, Samuel Jabrin, Dominique Van Der Straeten, Willy E. Lambert, Fabrice Rébeillé, and Stéphane Ravanel 491

The Import of S-Adenosylmethionine into the Golgi Apparatus Is Required for the Methylation of Homogalacturonan. Consuelo Ibar and Ariel Orellana 504

BIOENERGETICS AND PHOTOSYNTHESIS

Optimizing the Distribution of Resources between Enzymes of Carbon Metabolism Can Dramatically Increase Photosynthetic Rate: A Numerical Simulation Using an Evolutionary Algorithm. Xin-Guang Zhu, Eric de Sturler, and Stephen P. Long 513

CELL BIOLOGY AND SIGNAL TRANSDUCTION


Golgi Regeneration after Brefeldin A Treatment in BY-2 Cells Entails Stack Enlargement and Cisternal Growth followed by Division. Markus Langhans, Chris Hawes, Stefan Hillmer, Eric Hummel, and David G. Robinson 527

DEVELOPMENT AND HORMONE ACTION

Expression of Aberrant Forms of \textit{AUXIN RESPONSE FACTOR8} Stimulates Parthenocarpy in Arabidopsis and Tomato. Marc Goetz, Lauren C. Hooper, Susan D. Johnson, Julio Carlyle Macedo Rodrigues, Adam Vivian-Smith, and Anna M. Koltunow 351

ENVIRONMENTAL STRESS AND ADAPTATION TO STRESS

Heat Suppresses Activation of an Auxin-Responsive Promoter in Cultured Guard Cell Protoplasts of Tree Tobacco. Malia A. Dong, Jennifer L. Bufford, Yutaka Oono, Kacy Church, Minh Q. Dau, Kara Michels, Michael Haughton, and Gary Tallman 367

Posttranscriptional Regulation of High-Affinity Sulfate Transporters in Arabidopsis by Sulfur Nutrition. Naoko Yoshimoto, Eri Inoue, Akiko Watanabe-Takahashi, Kazuki Saito, and Hideki Takahashi 378

Reduced Carbon Availability to Bacteroids and Elevated Ureides in Nodules, But Not in Shoots, Are Involved in the Nitrogen Fixation Response to Early Drought in Soybean. Rubén Ladrera, Daniel Marino, Estibaliz Larraznar, Esther M. González, and Cesar Arrese-Igor 539


Continued on next page
GENETICS, GENOMICS, AND MOLECULAR EVOLUTION

Transcriptional Profiling of high pigment-2dg Tomato Mutant Links Early Fruit Plastid Biogenesis with Its Overproduction of Phytonutrients. Igor Kolotilin, Hinanit Koltai, Yaakov Tadmor, Carniya Bar-Or, Moshe Reuveni, Ayala Meir, Sahadia Nahon, Havinna Shlomo, Lea Chen, and Ilan Levin 389

Ancestral Chromosomal Blocks Are Triplicated in Brassiceae Species with Varying Chromosome Number and Genome Size. Martin A. Lysak, Kwok Cheung, Michaela Kitschke, and Petr Burší 402


PLANTS INTERACTING WITH OTHER ORGANISMS

AtHIPM, an Ortholog of the Apple HrpN-Interacting Protein, Is a Negative Regulator of Plant Growth and Mediates the Growth-Enhancing Effect of HrpN in Arabidopsis. Chang-Sik Oh and Steven V. Beer 426

Medicago truncatula as a Model for Nonhost Resistance in Legume-Parasitic Plant Interactions. M. Dolores Lozano-Baena, Elena Prats, M. Teresa Moreno, Diego Rubiales, and Alejandro Pérez-de-Luque 437

Dual Regulation Role of GH3.5 in Salicylic Acid and Auxin Signaling during Arabidopsis-Pseudomonas syringae Interaction. Zhongqin Zhang, Qun Li, Zhimiao Li, Paul E. Staswick, Muyang Wang, Ying Zhu, and Zuhua He 450

Ethylene Is One of the Key Elements for Cell Death and Defense Response Control in the Arabidopsis Lesion Mimic Mutant vad1. Olivier Bouchez, Carine Huard, Séverine Lorrain, Dominique Roby, and Claudine Balague 465

WHOLE PLANT AND ECOPHYSIOLOGY

Flavonoids Are Differentially Taken Up and Transported Long Distances in Arabidopsis. Charles S. Buer, Gloria K. Muday, and Michael A. Djordjevic 478


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