On the Cover: The ethylene signaling pathway known in land plants was recently found to be conserved in *Spirogyra pratensis* (a filamentous Charophycean green alga). Ethylene treatment of *Spirogyra* induces elongation of the cells within the filament, as shown. A transcriptomic analysis of the ethylene response in *Spirogyra* by Van de Poel et al. (pages 533–545) suggests changes in cell wall metabolism, photosynthesis, and abiotic stress responses. The cover image shows confocal microscopy of two *Spirogyra* filaments, one with normal-sized cells (left) and the other with elongated cells (right). To create the image, a confocal section of DAPI-stained (blue) filaments, showing cell walls, was overlaid with the autofluorescence (red) of chlorophyll in the spiral chloroplasts. The image was produced by Dr. Bram Van de Poel.

**ON THE INSIDE**

Peter V. Minorsky

**COMMENTARY**

The Ever-Closer Union of Signals: Propagating Waves of Calcium and ROS Are Inextricably Linked.  Edgar Peiter  

Hope in Change: The Role of Root Plasticity in Crop Yield Stability.  Christopher N. Topp  

**TOPICAL REVIEW**

A Tale of Two Sugars: Trehalose 6-Phosphate and Sucrose.  Carlos M. Figueroa and John E. Lunn  

Trehalose 6-phosphate is a signal of sucrose availability in plants that influences sucrose synthesis in source leaves and the fate of imported sucrose in sink organs, thereby linking growth and development to carbon status.

**BREAKTHROUGH TECHNOLOGIES**

Long-Term Growth of Moss in Microfluidic Devices Enables Subcellular Studies in Development.  Carlisle S. Bascom Jr., Shu-Zon Wu, Katherine Nelson, John Oakey, and Magdalena Bezanilla  

Microfluidic chambers enable imaging of moss development from early to late developmental stages at cellular and subcellular resolution.

Indel Group in Genomes (IGG) Molecular Genetic Markers.  Ted W. Toal, Diana Burkart-Waco, Tyson Howell, Mily Ron, Sundaram Kuppu, Anne Britt, Roger Chetelat, and Siobhan M. Brady  

Genome-wide molecular markers are produced by a bioinformatics pipeline that analyzes pairs of genomic sequences to find primer pairs that amplify indel-containing regions having a targeted amplicon size and size difference.

Codon Optimization to Enhance Expression Yields Insights into Chloroplast Translation.  Kwang-Chul Kwon, Hui-Ting Chan, Ileana R. León, Rosalind Williams-Carrier, Alice Barkan, and Henry Daniell  

Eukaryotic genes coding for biopharmaceutical proteins expressed in chloroplasts using different codons, but identical regulatory sequences, shed light on key factors that limit or enhance protein synthesis.

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RESEARCH ARTICLES

BIOCHEMISTRY AND METABOLISM

The Structure and Catalytic Mechanism of Sorghum bicolor Caffeoyl-CoA O-Methyltransferase. Alexander M. Walker, Steven A. Sattler, Matt Regner, Jeffrey P. Jones, John Ralph, Wilfred Vermerris, Scott E. Sattler, and ChulHee Kang

The catalytic mechanism and substrate specificity of caffeoyl-CoA O-methyltransferase from Sorghum bicolor deduced from crystal structures, site-directed mutagenesis, and kinetic and thermodynamic analyses.

Suppressing Farnesyl Diphosphate Synthase Alters Chloroplast Development and Triggers Sterol-Dependent Induction of Jasmonate- and Fe-Related Responses. David Manzano, Paola Andrade, Daniel Caudepón, Teresa Altabella,Montserrat Arró, and Albert Ferrer

Suppressing FPS expression affects chloroplast development, reducing cytosolic and plastidial isoprenoid levels including sterols.

FUM2, a Cytosolic Fumarase, Is Essential for Acclimation to Low Temperature in Arabidopsis thaliana. Beth C. Dyson, Matthew A.E. Miller, Regina Feil, Nicholas Rattray, Caroline G. Bowsher, Royston Goodacre, John E. Lunn, and Giles N. Johnson

Accumulation of fumaric acid, catalyzed by a cytosolic fumarase, is essential for Arabidopsis thaliana to acclimate photosynthesis to low temperature.


CDKA phosphorylation of the RNA helicase, eIF4A, is restricted to proliferating cells and could provide a mechanism that inhibits translation and cell growth in a cell cycle-dependent manner.

Oxygen Sensing via the Ethylene Response Transcription Factor RAP2.12 Affects Plant Metabolism and Performance under Both Normoxia and Hypoxia. Melanie Verena Paul, Srignanakshi Iyer, Carmen Amerhauser, Martin Lehmman, Joost T. van Dongen, and Peter Geigenberger

Oxygen-regulated stability of the ERF-VII transcription factor RAP2.12 regulates central metabolic processes to sustain growth, development, and anoxia responses.

ACYL-ACYL CARRIER PROTEIN DESATURASE2 and 3 Are Responsible for Making Omega-7 Fatty Acids in the Arabidopsis Aleurone. Fiona M. Bryant, Olaya Munoz-Azcarate, Amélie A. Kelly, Frédéric Beaudoin, Smita Kurup, and Peter J. Eastmond

Two acyl-acyl carrier protein desaturases are responsible for the tissue-specific production of high levels of omega-7 monounsaturated fatty acids in Arabidopsis aleurone cells.

Cell Wall Invertase Promotes Fruit Set under Heat Stress by Suppressing ROS-Independent Cell Death. Yong-Hua Liu, Christina E. Offler, and Yong-Ling Ruan

Elevation of cell wall invertase activity by silencing its inhibitor improves tomato fruit set under moderate heat stress via suppressing programmed cell death in a ROS-independent manner.
Glucosinolates from Host Plants Influence Growth of the Parasitic Plant Cuscuta gronovii and Its Susceptibility to Aphid Feeding.  Jason D. Smith, Melkamu G. Woldemariam, Mark C. Mescher, Georg Inder, and Consuelo M. De Moraes

Doddle vines (Cuscuta gronovii) parasitizing Arabidopsis thaliana take up glucosinolate toxins that reduce parasite growth and modulate resistance to aphid herbivores.

Chemical Genetics Uncovers Novel Inhibitors of Lignification, Including p-Iodobenzoic Acid Targeting CINNAMATE-4-HYDROXYLASE.  Dorien Van de Wouwer, Ruben Vanholme, Raphael Decou, Geert Goeminne, Dominique Audenaert, Long Nguyen, Rene Hofer, Edward Pesquet, Bartel Vanholme, and Wout Boerjan

Chemical screening for novel inhibitors of lignification uncovered a compound processed in the plant into two such inhibitors, one of which, p-iodobenzoic acid, inhibits CINNAMATE-4-HYDROXYLASE activity.

CELL BIOLOGY

The Potyviral P3 Protein Targets Eukaryotic Elongation Factor 1A to Promote the Unfolded Protein Response and Viral Pathogenesis.  Hexiang Luan, M.B. Shine, Xiaoyan Cui, Xin Chen, Na Ma, Pradeep Kachroo, Haijan Zhi, and Aardra Kachroo

Soybean Mosaic Virus P3 targets soybean elongation factor EF1A to induce ER stress, which in turn facilitates SMV pathogenesis and this is linked to EF1A function in translation elongation.

Polypeptide Transport-Associated Domains of the Toc75 Channel Protein Are Located in the Intermembrane Space of Chloroplasts.  Yih-Lin Chen, Lih-Jen Chen, and Hsou-min Li

The transit-peptide binding domain of the chloroplast outer-membrane protein-translocating channel protrudes into the intermembrane space rather than into the cytosol.

s-Adenosylmethionine Synthetase 3 Is Important for Pollen Tube Growth.  Yuan Chen, Ting Zou, and Sheila McCormick

Arabidopsis mat3 pollen overaccumulates methionine, germinates poorly, and has short tubes.

ECOPHYSIOLOGY AND SUSTAINABILITY

Stomatal Spacing Safeguards Stomatal Dynamics by Facilitating Guard Cell Ion Transport Independent of the Epidermal Solute Reservoir.  Maria Papanatsiou, Anna Amtmann, and Michael R. Blatt

Clustering of stomata suppresses guard cell ion transport independent of ion stores in neighboring epidermal cells.

Microoxic Niches within the Thylakoid Stroma of Air-Grown Chlamydomonas reinhardtii Protect [FeFe]-Hydrogenase and Support Hydrogen Production under Fully Aerobic Environment.  Oded Liran, Rinat Semyatich, Yuval Milrad, Haviva Eilenberg, Idoo Weiner, and Iftach Yacoby

Hydrogen production catalyzed by the extremely anaerobic enzyme [FeFe]-hydrogenase in air-grown microalgae reports on microoxic niches within the thylakoid stroma.

GENES, DEVELOPMENT, AND EVOLUTION


Adaptation of seagrass to the marine environment involves modification and loss of conserved plant genes.
Evolutionary Co-Option of Floral Meristem Identity Genes for Patterning of the Flower-Like Asteraceae Inflorescence. Yafei Zhao, Teng Zhang, Suei K. Broholm, Sari Tilthiharju, Katrina Mouhu, Victor A. Albert, Teemu H. Teeri, and Paula Elomaa

Highly conserved genes that regulate the identity of single flowers in conventional plant models regulate the unique inflorescence architecture of the evolutionarily successful Asteraceae plant family.

Salt Stress Reveals a New Role for ARGONAUTE1 in miRNA Biogenesis at the Transcriptional and Posttranscriptional Levels. Jakub Dolata, Mateusz Bajczyk, Dawid Bielewicz, Katarzyna Niedojadlo, Janusz Niedojadlo, Halina Pietrykowska, Weronika Walczak, Zofia Szewykowska-Kalinska, and Artur Jarmolowski

Arabidopsis ARGONAUTE 1, in addition to its well-known role in mRNA target cleavage and miRNA-mediated translation inhibition, is involved in the cotranscriptional regulation of MIR gene expression.

The 5’ UTR Intron of Arabidopsis GGT1 Aminotransferase Enhances Promoter Activity by Recruiting RNA Polymerase II. Miriam Laxa, Kristin Müller, Natalie Lange, Lennart Doering, Jan Thomas Pruscha, and Christoph PeterhänSEL

The 5’ UTR intron of GGT1 determines maximum transcript abundance and affects RNA polymerase II binding.

eQTL Regulating Transcript Levels Associated with Diverse Biological Processes in Tomato. Aashish Ranjan, Jessica M. Budke, Steven D. Rowland, Daniel H. Chitwood, Ravi Kumar, Leonela Carriedo, Yasunori Ichihashi, Kristina Zumstein, Julin N. Maloof, and Neelima R. Sinha

Genetic mapping and coexpression highlights hot spots regulating transcripts linked to diverse biological processes.

Origin and Functional Prediction of Pollen Allergens in Plants. Miaolin Chen, Jie Xu, Deborah Devis, Jianxin Shi, Kang Ren, Iain Searle, and Dabing Zhang

Prediction and systematic analysis of pollen allergens in model plants suggest that pollen allergens evolved by gene duplication and then functional specification.

SPIKE1 Activates ROP GTPase to Modulate Petal Growth and Shape. Huibo Ren, Xie Dang, Yanqiu Yang, Dingquan Huang, Mengting Liu, Xiaowei Gao, and Deshu Lin

SPIKE1 activates ROP GTPase proteins to regulate anisotropic cell expansion and petal anisotropic growth by affecting the organization of cortical microtubule arrays in Arabidopsis.

Genome-Wide Targets Regulated by the OsMADS1 Transcription Factor Reveals Its DNA Recognition Properties. Imtiyaz Khanday, Sanjukta Das, Grace L. Chongloi, Manju Bansal, Ueli Grossniklaus, and Usha Vijayraghavan

OsMADS1 binds to many downstream target loci with distinct sequence and biophysical characteristics and likely in combination with other factors to ensure rice floret development.

Flowering Time-Regulated Genes in Maize Include the Transcription Factor ZmMADS1. Philipp Alter, Susanne Birchender, Liang-Zi Zhou, Urte Schlüter, Manfred Gahrz, Uwe Sonnewald, and Thomas Dresselhaus

ZmMADS1 is activated in leaves during shoot apical meristem transition and acts as a positive flowering time regulator in day-neutral maize.

Photoperiod-H1 (Ppd-H1) Controls Leaf Size. Benedikt Digel, Elahe Tavakol, Gabriele Verderio, Alessandro Tondelli, Xin Xu, Luigi Cattivelli, Laura Rossini, and Maria von Korff

Photoperiod-H1 controls leaf size by influencing the duration of leaf growth in barley.

Cold-regulated VRN1 and VRN3 expression is consistent with an early origin of vernalization responsiveness in the temperate Pooideae grasses.


Conservation, neofunctionalization, and specialization are main evolutionary trajectories for Arabidopsis young duplicate genes, and their relative roles change dynamically over evolutionary time.

MEMBRANES, TRANSPORT, AND BIOENERGETICS

[OPEN] Envelope K+/H+ Antiporters AtKEA1 and AtKEA2 Function in Plastid Development. María Nieves Aranda-Sicilia, Ali Aboukila, Ute Armbruster, Olivier Cagnac, Tobias Schumann, Hans-Henning Kunz, Peter Jahns, María Pilar Rodríguez-Rosales, Heven Sze, and Kees Venema

Antiporters localized to polar microdomains of dividing and developing plastids affect thylakoid membrane formation and chloroplast differentiation.

The Low Molecular Weight Protein PsaI Stabilizes the Light-Harvesting Complex II Docking Site of Photosystem I. Magdalena Plochinger, Salar Torabi, Marjana Rantala, Mikko Tikkanen, Marjana Suorsa, Poul-Erik Jensen, Eva Mari Aro, and Jörg Meurer

Loss of plant PsaI Photosystem I subunit destabilizes the binding of PsaL and PsaH subunits of this photosystem and causes nonphotochemical dark-reduction of the plastoquinone pool keeping plants in state 2 in the dark.

SIGNALING AND RESPONSE

Cytokinin Regulates the Etioplast-Chloroplast Transition through the Two-Component Signaling System and Activation of Chloroplast-Related Genes. Anne Cortleven, Inge Marg, Maria V Yamburenko, Hagen Schlicke, Kristine Hill, Bernhard Grimm, G. Eric Schaller, and Thomas Schmülling

Cytokinin regulates chloroplast development during de-etiolation through the two-component signaling system by binding of B-type ARRs to the promotors of chloroplast-related genes.

The DELLA-CONSTANS Transcription Factor Cascade Integrates Gibberellic Acid and Photoperiod Signaling to Regulate Flowering. Houping Wang, Jinjing Pan, Yang Li, Dengji Lou, Yanru Hu, and Diqiu Yu

DELLA proteins physically and genetically interact with CO to modulate flowering under long-days in Arabidopsis.

[OPEN] Cytokinins Are Initial Targets of Light in the Control of Bud Outgrowth. Hanaé Roman, Tiffanie Girault, François Barbier, Thomas Péron, Nathalie Brouard, Aleš Pencík, Ondřej Noedl, Alain Vian, Sou lainan Sakr, Jérémy Lothier, José Le Gourri erec, and Nathalie Leduc

Light perception by buds triggers a rapid cytokinin signal that controls major downstream regulators, including sugars, auxin, and strigolactones, of bud outgrowth.

[OPEN] Core Mechanisms Regulating Developmentally Timed and Environmentally Triggered Abscission. O. Rahul Patharkar and John C. Walker

A shared module of genes regulates both drought-triggered leaf abscission and developmentally timed floral organ abscission in Arabidopsis.

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Herbivory-induced auxin promotes the production of anthocyanins and phenolamides.

Transcriptome Profiling of the Green Alga *Spirogyra pratensis* (Charophyta) Suggests an Ancestral Role for Ethylene in Cell Wall Metabolism, Photosynthesis, and Abiotic Stress Responses. Bram Van de Poel, Endymion D. Cooper, Dominique Van Der Straeten, Caren Chang, and Charles F. Delwiche

The plant hormone ethylene regulates predominantly cell wall metabolism, photosynthesis, and abiotic stress responses in the charophyte green alga *Spirogyra pratensis*.

The Systemic Acquired Resistance Regulator OsNPR1 Attenuates Growth by Repressing Auxin Signaling through Promoting IAA-Amido Synthase Expression. Xiaozun Li, Dong-Lei Yang, Li Sun, Qian Li, Bizeng Mao, and Zuhua He

The regulator protein OsNPR1 inhibits rice growth by enhancing the OsGH3.8 amido synthase of rice.

A *Brachypodium* UDP-Glycosyltransferase Confers Root Tolerance to Deoxynivalenol and Resistance to Fusarium Infection. Jean-Claude Pasquet, Valentin Changenet, Catherine Macadré, Edouard Boex-Fontvieille, Camille Soulhat, Oumaya Bouchabké-Coussa, Marion Dalmais, Vessela Atanasova-Peníchon, Abdelhafid Bendahmane, Patrick Saindrenan, and Marie Dufresne

The UDP-glucosyltransferase Bradi5g03300 conjugates the Fusarium mycotoxin deoxynivalenol into deoxynivalenol-3-O-glucose and confers resistance to primary infection by Fusarium graminearum.

**SYSTEMS AND SYNTHETIC BIOLOGY**

Overexpression of the *OsERF71* Transcription Factor Alters Rice Root Structure and Drought Resistance. Dong-Keun Lee, Harin Jung, Geupil Jang, Jin Seo Jeong, Yoon Shic Kim, Sun-Hwa Ha, Yang Do Choi, and Ju-Kon Kim

*OsERF71* alters root structure to enhance drought resistance.


Genome-scale metabolic model for *Chlorella vulgaris* UTEX 395 accurately predicts phenotypes under different growth conditions.

Integrative Analyses of Nontargeted Volatile Profiling and Transcriptome Data Provide Molecular Insight into VOC Diversity in Cucumber Plants (*Cucumis sativus*). Guo Wei, Peng Tian, Fengxia Zhang, Hao Qin, Han Miao, Qingwen Chen, Zhongyi Hu, Li Cao, Meijiao Wang, Xingfang Gu, Sanwen Huang, Mingsheng Chen, and Guodong Wang

An integrated volatile detection system coupled with transcriptomic data identifies 85 compounds, including 36 terpenes, from a total of 23 cucumber tissues, and some of the genes responsible for their synthesis.

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