On the Cover: Image of sorghum (Sorghum bicolor) crops. A targeted control of the monolignol pathway promises to reduce plant lignin content, which is a major obstacle for biofuel production. Sorghum is a good candidate for this process due to its drought tolerance and high sugar yields, as compared with maize (Zea mays). Globally, the United States is the third-largest producer of sorghum. See Walker et al. in this issue (pp. 640–651). Photo courtesy of Patrick O’Neill.

ON THE INSIDE
Peter V. Minorsky

BREAKTHROUGH TECHNOLOGIES


An exploratory data-analysis method describes changes in gene expression profiles across multiple tissues between species.


A novel genetical genomics analysis of metabolites in four developmental stages of Arabidopsis germination unravels both genetic and genetic × environment loci controlling these metabolites.

RESEARCH ARTICLES

Arabidopsis 3-Ketoacyl-Coenzyme A Synthase9 Is Involved in the Synthesis of Tetracosanoic Acids as Precursors of Cuticular Waxes, Suberins, Sphingolipids, and Phospholipids.  Juyoung Kim, Jin Hee Jung, Saet Buyl Lee, Young Sam Go, Hae Jin Kim, Rebecca Cahoon, Jonathan E. Markham, Edgar B. Cahoon, and Mi Chung Suh

KCS9 is involved in the elongation of C22 to C24 fatty acids, which are essential precursors for the biosynthesis of cuticular waxes, aliphatic suberins, and membrane lipids, including sphingolipids and phospholipids.


Coenzyme A made in the cytosol is imported into plant mitochondria by twin transporters from the mitochondrial carrier family that are cognates of coenzyme A transporters of animals and yeast and can functionally replace the yeast transporter.

Functional Redundancy and Divergence within the Arabidopsis RETICULATA-RELATED Gene Family.  José Manuel Pérez-Pérez, David Estève-Bruna, Rebeca González-Bayón, Saijalisa Kangasjärvi, Camila Caldana, Matthew A. Hannah, Lothar Willmitzer, María Rosa Ponce, and José Luis Micol

Proteins of the RETICULATA-RELATED family functionally link photoperiodic growth, amino acid homeostasis, and reactive oxygen species metabolism during Arabidopsis leaf growth.

Genetic Analysis of the Biosynthesis of 2-Methoxy-3-Isobutylpyrazine, a Major Grape-Derived Aroma Compound Impacting Wine Quality.  Sabine Guillaumie, Andrea Ilg, Stéphane Réty, Maxime Brette, Claudine Trossat-Magnin, Stéphane Decroocq, Céline Léon, Céline Keime, Tao Ye, Raymond Balentweck-Gayot, Patricia Claudel, Louis Bordenave, Sandra Vanbrabant, Eric Duchêne, Serge Delrot, Philippe Darriet, Philippe Hugueney, and Eric Gomes

Genetic and candidate gene approaches are combined to identify an O-methyltransferase with a major role in methoxyypyrazine biosynthesis in grapevine.
Enzymes involved in the biosynthesis of sporopollenin, the main constituent of pollen exine, likely form a metabolon in the endoplasmic reticulum of the anther tapetal cells.

Enzymes involved in the biosynthesis of sporopollenin, the main constituent of pollen exine, likely form a metabolon in the endoplasmic reticulum of the anther tapetal cells.

The coexpression of a uniquely stabilized plant structural protein (Cys-oleosin) and diacylglycerol O-acyltransferase in Arabidopsis led to a 24% increase in the CO₂ assimilation rate and a 50% increase in leaf biomass as well as oil accumulation in the leaves and roots.

The catalytic mechanism and exact specificity for hydroxycinnamoyltransferase from sorghum were determined by comprehensive approaches with crystal structures of apo-form and ternary product complex, site-directed mutagenesis, and kinetic and thermodynamic analyses.

The chloroplast ABC1-like kinase ABC1K3 affects the accumulation of VTE1-dependent metabolites, α-tocopherol quinone and plastochromanol, most likely via phosphorylation of VTE1.

Nannochloropsis oceanica IMET1 has the ability to recover from long periods of nitrate deprivation without apparent detriment to the culture.

GLUP6/GEF is the activator of Rab5 GTPase, and the cycling of GTP- and GDP-bound forms of this regulatory protein is essential for the intracellular transport of proglutelin and α-globulin from the Golgi to PSV and in the maintenance of the general structural organization of the endomembrane system in rice seeds.

The rate of insertion and lifetime of cellulose-synthesizing complexes at the plasma membrane is dependent on the organization of the actin cytoskeleton.

In Arabidopsis leaf pavement cells and trichomes, the ER is a reservoir for W/SRC signaling and may have a key role in the early steps of W/SRC activation.
The involvement of the sieve element cytoskeleton in electrical responses to cold shocks is described.

The isolation and characterization of the arf17 mutant uncovers potential roles for auxin in pollen wall pattern formation and pollen tube growth.

Complex transcriptional response of AtALMT1 malate transporter could account for its contribution to pleiotropic traits.

There is a phase of diversifying selection of duplicated genes following function relaxation after whole-genome duplication.

Identification of novel loci that regulate root cellular and morphological development that may be useful for breeding programs.

Identification of novel loci regulating interspecific variation in root morphology and cellular development in tomato.

The cyp78a8 cyp78a9 loss-of-function mutant has reduced seed set due to outer integument development arrest leading to female sterility.

Knowledge and assays from Arabidopsis axillary meristem biology can be successfully applied to Salix spp. and can increase the understanding of a fundamental aspect of SRC biomass production, allowing more targeted breeding.

The ATM-dependent DNA damage response acts as an upstream trigger for compensation, an enhanced cell expansion caused by defective cell proliferation, during Arabidopsis leaf development.
WEBE, an AP2/ERF Transcription Factor Highly Expressed in Proliferating Cells, Affects Shoot Architecture in Arabidopsis. Mohammad Mehrnia, Salma Balazadeh, María-Inés Zanor, and Bernd Mueller-Roeber

A transcription factor is expressed in proliferating cells and affects shoot architecture.

COLLAPSED ABNORMAL POLLEN1 Gene Encoding the Arabinokinase-Like Protein Is Involved in Pollen Development in Rice. Kenji Ueda, Fumiaki Yoshimura, Akio Miyao, Hirohiko Hirochika, Ken-Ichi Nonomura, and Hirotsu Wabiko

Pollen-expressed arabinokinase-like protein gene CAP1 is important for rice pollen development, and its related genes are conserved in both monocotyledonous and dicotyledonous plants.

MULTI-FLORET SPIKELET1, Which Encodes an AP2/ERF Protein, Determines Spikelet Meristem Fate and Sterile Lemma Identity in Rice. Deyong Ren, Yunfeng Li, Fangming Zhao, Xianchun Sang, Junqiong Shi, Nan Wang, Shuang Guo, Yinghua Ling, Changwei Zhang, Zhenglin Yang, and Guanghua He

MULTI-FLORET SPIKELET1 determines spikelet meristem fate and sterile lemma identity in rice.

The Methylation of the PcMYB10 Promoter Is Associated with Green-Skinned Sport in Max Red Bartlett Pear. Zhigang Wang, Dong Meng, Aide Wang, Tianlai Li, Shuling Jiang, Peihua Cong, and Tianzhong Li

In MRB-G fruits, the expression of PcMYB10 was reduced by the methylation of regions −604 to −911 bp and −1,218 to −1,649 bp in its promoter. As a result, the expression of PcUFGT, a key gene involved in anthocyanin biosynthesis and regulated by PcMYB10, was also reduced. This might cause the inhibition of anthocyanin biosynthesis and the formation of green-skinned sport.

Ubiquitin-Specific Proteases UBP12 and UBP13 Act in Circadian Clock and Photoperiodic Flowering Regulation in Arabidopsis. Xia Cui, Falong Lu, Yue Li, Yongming Xue, Yanyuan Kang, Qi Qiu, Xiekui Cui, Shuzhi Zheng, Bin Liu, Xiaodong Xu, and Xiaofeng Cao

Deubiquitination plays a role in daylength measurement to regulate flowering time.

A Change in SHATTERPROOF Protein Lies at the Origin of a Fruit Morphological Novelty and a New Strategy for Seed Dispersal in Medicago Genus. Chloé Fourquin, Carolina del Cerro, Filipe C. Victoria, Aurélie Viallette-Guiraud, Antonio C. de Oliveira, and Cristina Ferrándiz

The evolutionary origin of a novel fruit morphology in legumes and the importance of changes in coding regions of master genes to generate diversity.

Genome-Wide Prediction of Nucleosome Occupancy in Maize Reveals Plant Chromatin Structural Features at Genes and Other Elements at Multiple Scales. Justin A. Fincher, Daniel L. Vera, Diana D. Hughes, Karen M. McGinnis, Jonathan H. Dennis, and Hank W. Bass

Genome-wide prediction of nucleosome occupancy in maize was performed using a computational approach, and the predictions were validated using biochemical data and reveal novel features of maize promoters.

MEMBRANES, TRANSPORT, AND BIOENERGETICS


Differentiating xylem tissues of both hybrid poplar and Japanese cypress exhibit almost identical transport properties of coniferin, a monolignol glucoside, suggesting the involvement of a common endomembrane H+/-coniferin antiport mechanism in the lignifying tissues of woody plants.

Preferential Delivery of Zinc to Developing Tissues in Rice Is Mediated by P-Type Heavy Metal ATPase OsHMA2. Naoki Yamaji, Jixing Xia, Namiki Mitani-Ueno, Kengo Yokosho, and Jian Feng Ma

OsHMA2 is a plasma membrane-localized transporter for zinc and cadmium in rice that mainly expresses at the phloem region of developed vascular tissues in the nodes and mediates exclusive zinc and cadmium delivery to upper nodes and finally to the panicle.
Reduced Tonoplast Fast-Activating and Slow-Activating Channel Activity Is Essential for Conferring Salinity Tolerance in a Facultative Halophyte, Quinoa. Edgar Bonales-Alatorre, Sergey Shabala, Zhong-Hua Chen, and Igor Pottosin

The negative control of SV and FV tonoplast channel activity in quinoa leaves reduces Na⁺ leak. This improves the efficiency of Na⁺ sequestration in leaf vacuoles, thus enabling optimal photosynthetic performance and conferring salinity tolerance in this halophyte species.

Functional Characterization and Determination of the Physiological Role of a Calcium-Dependent Potassium Channel from Cyanobacteria. Vanessa Checchetto, Elide Formentin, Luca Carraretto, Anna Segalla, Giorgio Mario Giacometti, Ildiko Szabo, and Elisabetta Bergantino

Lack of a calcium-activated potassium channel confers increased resistance to zinc in cyanobacteria.

ROOT ULTRAVIOLET B-SENSITIVE1/WEAK AUXIN RESPONSE3 Is Essential for Polar Auxin Transport in Arabidopsis. Hong Yu, Michael Karampelias, Stephanie Robert, Wendy Ann Peer, Ranjan Swarup, Songqing Ye, Lei Ge, Jerry Cohen, Angus Murphy, Jiri Friml, and Mark Estelle

The growth phenotype of the rus1/wwx3 mutant is related to a defect in auxin transport caused by decreased accumulation of auxin transporters.

Quantification of Extracellular Carbonic Anhydrase Activity in Two Marine Diatoms and Investigation of Its Role. Brian M. Hopkinson, Christof Meile, and Chen Shen

eCA enhances CO₂ supply for photosynthesis in two marine diatoms.

Deletion of the Transcriptional Regulator cyAbrB2 Deregulates Primary Carbon Metabolism in Synechocystis sp. PCC 6803. Yuki Kaniya, Ayumi Kizawa, Atsuko Miyagi, Maki Kawai-Yamada, Hirofumi Uchimiya, Yasuko Kaneko, Yoshikata Nishiyama, and Yukako Hihara

The transcriptional regulator cyAbrB2 in Synechocystis sp. PCC 6803 is indispensable for coordination of cellular metabolism upon the changes in trophic conditions.

A Regulatory Cascade Involving Class II ETHYLENE RESPONSE FACTOR Transcriptional Repressors Operates in the Progression of Leaf Senescence. Tomotsugu Koyama, Haruka Nii, Nobutaka Mitsuda, Masaru Ohta, Sakihito Kitajima, Masaru Ohme-Takagi, and Fumihiko Sato

The proteasome-mediated regulation of class II ERF transcriptional repressors is involved in the progression of leaf senescence.

A transcriptional regulator generated by alternative splicing uses a cryptic binding site to negatively regulate bHLH-type transcription factors that promote jasmonate responses.

The bacterial effector AvrRpt2 promotes pathogen virulence via stimulating the turnover of Arabidopsis auxin regulators AXR2 and AXR3.
CYCLIN H;1 regulates reactive oxygen species-dependent but abscisic acid-independent inhibition of blue light-induced stomatal aperture required for drought stress responses.

ASF1A and ASF1B genes are regulated by cell cycle progression and are involved in DNA repair after UV-B irradiation.

A bHLH gene (PtrbHLH) confers cold tolerance and modulates peroxidase-mediated scavenging of H$_2$O$_2$.

DNA Pol λ participates in the repair of double strand breaks induced by high salinity and DNA cross-linking agent in Arabidopsis seedlings, demonstrating the importance of Pol λ in the double strand break repair signaling network in higher plant genome.

SYSTEMS AND SYNTHETIC BIOLOGY

Deciphering Herbivory-Induced Gene-to-Metabolite Dynamics in Nicotiana attenuata Tissues Using a Multifactorial Approach.  

A multifactorial SOM-based approach can be used to investigate the time and spatial dimensions of induced changes in gene and metabolite expression following herbivory in shoot and root tissues of a wild tobacco, Nicotiana attenuata.

Responses to Light Intensity in a Genome-Scale Model of Rice Metabolism.  

Analysis of a genome-scale metabolic of rice shows numerous coordinated changes between chloroplast and mitochondrial reactions in response to alteration in available light.

Gene Discovery of Modular Diterpene Metabolism in Nonmodel Systems.  

Metabolite-guided transcriptome sequencing of nonmodel species, custom reference databases of terpene synthases and cytochrome P450s, and phylogenetic and enzymatic analyses identified new gene family members for modular biosynthesis of diterpenes with applications as bioproducts.

RNA-Seq of Arabidopsis Pollen Uncovers Novel Transcription and Alternative Splicing.  

High-throughput sequencing of Arabidopsis pollen cDNA uncovers novel transcription and alternative splicing.

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