On the Cover: Cellulose is the major structural component of plant cell walls and has great potential as a renewable source of energy. The plant cellulose synthesis complex (CSC), also called a ‘rosette’ because of its hexameric appearance in transmission electron microscope (TEM) images, is a large multi-subunit transmembrane protein complex responsible for synthesis of cellulose chains and their assembly into microfibrils. Despite the importance of cellulose, fundamental properties of the CSC remain unclear. The number of cellulose synthase (CESA) proteins in the CSC and the number of cellulose chains in a microfibril have been debated for years. Vandavasi et al report a solution structure of the catalytic domain of CESA1 from Arabidopsis thaliana determined by small-angle scattering that provides experimental evidence for the self-assembly of CESA into a stable trimer. This study strongly supports the ‘hexamer of trimers’ model for the rosette CSC that synthesizes an 18-chain cellulose microfibril as its primary product. The cover shows ab initio structures of CESA trimers calculated from small-angle scattering data represented by semi-transparent grey surface envelopes, superposed with the computational atomic models in orange. The trimer models are arranged in a hexameric configuration consistent with the rosette shape observed in TEM images. The view is from the cytoplasmic side of the membrane. Cellulose microfibrils are visible in the apoplastic space. Cover image credits: Thomas Splettstoesser, scistyle.com, Berlin, Germany.
RESEARCH ARTICLES

BIOCHEMISTRY AND METABOLISM

[OPEN] Regulation of Primary Metabolism in Response to Low Oxygen Availability as Revealed by Carbon and Nitrogen Isotope Redistribution. Carla António, Carola Päpke, Marcio Rocha, Houssein Diab, Anis M. Limami, Toshihiro Obata, Alisdair R. Fernie, and Joost T. van Dongen

During low-oxygen stress, activation of Ala and GABA metabolism and bifurcation of the tricarboxylic acid cycle explains the down-regulation of respiratory oxygen consumption.


Transcriptomic profiling of the paddy weed Echinochloa glabrescens identifies its C₄ molecular signature and genes important for paddy growth.

[OPEN] Redox-Dependent Modulation of Anthocyanin Biosynthesis by the TCP Transcription Factor TCP15 during Exposure to High Light Intensity Conditions in Arabidopsis. Ivana L. Viola, Alejandra Camoirano, and Daniel H. Gonzalez

The transcription factor TCP15 represses anthocyanin biosynthesis in a redox-dependent manner during high-light intensity conditions.


Impaired stomatal closure in an anion channel mutant is accompanied by increased mesophyll conductance, photosynthesis, and leaf area, ultimately enhancing biomass accumulation under controlled conditions.


Rapid, reversible induction of Crassulacean acid metabolism (CAM) in conjunction with pronounced reconfiguration of carbon metabolism enables Talinum to survive cycles of severe drought.


Assembly into stable trimers provides strong evidence for 18 protein subunits to assemble in a cellulose synthesis complex that synthesizes an 18-chain cellulose microfibril.

[OPEN] Combining Quantitative Genetics Approaches with Regulatory Network Analysis to Dissect the Complex Metabolism of the Maize Kernel. Weiwei Wen, Haijun Liu, Yang Zhou, Min Jin, Ning Yang, Dong Li, Jie Luo, Yingjie Xiao, Qingchun Pan, Takayuki Tohge, Alisdair R. Fernie, and Jianbing Yan

A metabolic quantitative trait loci study combined with a regulatory network unraveled the genetic architecture of the natural variation of 155 metabolites in mature maize kernels.
Chloroplast chaperone Hsp93 associates with the inner envelope membrane via interaction with the Tic110 translocon and likely functions in quality control but not in import propulsion of translocating preproteins.

Arabidopsis GPAT9 is a highly conserved, single-copy, and essential glycerol-3-phosphate acyltransferase involved in seed oil biosynthesis.

Disruption of the ABHD11 hydrolase causes polar lipids accumulation, thereby enhancing plant growth.

Basic helix-loop-helix family transcription factors from subclade IVa specifically regulate the biosynthesis of the triterpene saponins in a model legume.

The Arabidopsis AP-4 adaptor complex functions in vacuolar sorting at a subdomain of the TGN by directly recognizing a Tyr-based motif of the receptor.

Analysis of single actin filament dynamics reveals a novel role for profilin and formins in the generation of branched filament networks in living epidermal cells.

A mutant lacking xyloglucan in its cell walls has bundled, aligned cellulose and unstable microtubules that uncover new links between cell wall and cytoskeletal integrity.

A plant-specific chloroplast division protein has multiple functions in coordinating and influencing the assembly of internal and external contractile rings across the two envelope membranes.

Optical tweezers show that peroxisomes are strongly tethered to chloroplasts and more weakly to other structures.

ECOPHYSIOLOGY AND SUSTAINABILITY

Noninvasive Measurement of Vulnerability to Drought-Induced Embolism by X-Ray Microtomography. Brendan Choat, Eric Badel, Regis Burlett, Sylvain Delzon, Herve Cochard, and Steven Jansen

X-ray computed microtomography provides a high-resolution, noninvasive method to evaluate vulnerability to drought-induced embolism in living, intact plants.

GENES, DEVELOPMENT AND EVOLUTION

AINTEGUMENTA and AINTEGUMENTA-LIKE6/PLETHORA3 Induce LEAFY Expression in Response to Auxin to Promote the Onset of Flower Formation in Arabidopsis. Nobutoshi Yamaguchi, Cheol Woong Jeong, Staci Nole-Wilson, Beth A. Krizek, and Doris Wagner

Two parallel pathways confer floral identity on developing lateral primordia downstream of auxin.

RNA Recognition Motif-Containing Protein ORRM4 Broadly Affects Mitochondrial RNA Editing and Impacts Plant Development and Flowering. Xiaowen Shi, Arnaud Germain, Maureen R. Hanson, and Stéphane Bentolila

Growth and development of Arabidopsis is affected by mutation of a member of the RNA recognition motif gene family that is required for RNA editing of more than 40% of the mitochondrial C targets in Arabidopsis.

Targets of the StBEL5 Transcription Factor Include the FT Ortholog StSP6A. Pooja Sharma, Tian Lin, and David J. Hannapel

Among the targets of a BEL1-like homeodomain transcription factor are genes involved in growth and hormone metabolism as well as two key tuberization signals.

CONSTANS Controls Floral Repression by Up-Regulating VERNALIZATION2 (VRN-H2) in Barley. Muhammad Aman Mulki and Maria von Korff

The functional characterization of homologs of a flowering-time transcription factor provides new insights into the control of floral repression before vernalization in barley.

Novel Vein Patterns in Arabidopsis Induced by Small Molecules. Francine Carland, Andrew Defries, Sean Cutler, and Timothy Nelson

Numerous compounds inducing leaf vein pattern defects target auxin biology.

The MTL1 Pentatricopeptide Repeat Protein Is Required for Both Translation and Splicing of the Mitochondrial NADH DEHYDROGENASE SUBUNIT7 mRNA in Arabidopsis. Nawel Haïli, Noelya Planchard, Nadège Arnal, Martine Quadrado, Nathalie Vrielynck, Jennifer Dahan, Catherine Colas des Francs-Small, and Hakim Mireau

A mitochondria-targeted pentatricopeptide repeat protein specifically facilitates the translation of a respiratory chain transcript without inducing any cleavage in its upstream noncoding region.
MEMBRANES, TRANSPORT AND BIOENERGETICS


Glycosyl-Inositol-Phosphoryl-Ceramides are major lipids of the plasma membrane and form rafts in the outer leaflet, yet extend into the inner leaflet of the membrane through very long-chain fatty acids to interdigitate across the membrane. 367

The EXS Domain of PHO1 Participates in the Response of Shoots to Phosphate Deficiency via a Root-to-Shoot Signal. Stefanie Wege, Ghazanfar Abbas Khan, Ji-Yul Jung, Evangelia Vogiatzaki, Sylvain Pradervand, Isabel Aller, Andreas J. Meyer, and Yves Poirier 385

A key hydrophobic domain of the PHO1 phosphate exporter plays an important role in the response of shoots to phosphate deficiency.


H+—pumping pyrophosphatases appear to function in companion cells to increase phloem loading and long-distance transport, leading to more robust plants with enhanced growth.

SIGNALING AND RESPONSE

Protein S-Acyltransferase 14: A Specific Role for Palmitoylation in Leaf Senescence in Arabidopsis. Yaxiao Li, Rod Scott, James Doughty, Murray Grant, and Baoxiu Qi 415

A protein S-acyltransferase is involved in leaf senescence via modulating salicylic acid metabolism and perception.

The RING Finger Ubiquitin E3 Ligase OsHTAS Enhances Heat Tolerance by Promoting H2O2-Induced Stomatal Closure in Rice. Jianping Liu, Cuicui Zhang, Chuchu Wei, Xin Liu, Muqiu Wang, Feifei Yu, Qi Xie, and Jumin Tu 429

A RING finger ubiquitin ligase functions enhances heat tolerance through the modulation of H2O2—induced stomatal closure.

The Synthetic Elicitor 2-(5-Bromo-2-Hydroxy-Phenyl)-Thiazolidine-4-Carboxylic Acid Links Plant Immunity to Hormesis. Melinda Rodriguez-Salus, Yasemin Bektas, Mercedes Schroeder, Colleen Knoth, Trang Vu, Philip Roberts, Isgouhi Kaloshian, and Thomas Eulgem 444

Immunity triggered by high doses a and hormetic growth enhancement triggered by low doses of a synthetic elicitor doses are associated with distinct transcriptional profiles.

Phytochrome A and B Function Antagonistically to Regulate Cold Tolerance via Abscisic Acid-Dependent Jasmonate Signaling. Feng Wang, Zhixin Guo, Huizi Li, Mengmeng Wang, Eugen Onac, Jie Zhou, Xiaojian Xia, Kai Shi, Jingquan Yu, and Yanhong Zhou 459

Low red/far-red light ratios increase cold tolerance in tomato via the activation of phytochrome A and ABA-dependent JA signaling.

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Genetic Variation for Thermotolerance in Lettuce Seed Germination Is Associated with Temperature-Sensitive Regulation of ETHYLENE RESPONSE FACTOR1 (ERF1). Fei-Yian Yoong, Laurel K. O’Brien, Maria Jose Truco, Heqiang Hao, Rebecca Sideman, Ryan Hayes, Richard W. Michelmore, and Kent J. Bradford

An allele of a gene encoding a transcription factor involved in the ethylene response pathway is associated with the ability of lettuce seeds to germinate at warm temperatures.

Profiling of the Early Nitrogen Stress Response in the Diatom Phaeodactylum tricornutum Reveals a Novel Family of RING-Domain Transcription Factors. Michiel Matthijs, Michele Fabris, Stefan Broos, Wim Vyverman, and Alain Goossens

A new family of RING-domain transcription factors associated with nitrogen stress is conserved in diatoms.

Arabidopsis PHL2 and PHR1 Act Redundantly as the Key Components of the Central Regulatory System Controlling Transcriptional Responses to Phosphate Starvation. Lichao Sun, Li Song, Ye Zhang, Zai Zheng, and Dong Liu

Two transcription factors act redundantly to regulate the transcriptional responses to phosphate starvation at genomic level.

Differential Roles of Two Homologous Cyclin-Dependent Kinase Inhibitor Genes in Regulating Cell Cycle and Innate Immunity in Arabidopsis. Safae Hamdoun, Chong Zhang, Manroop Gill, Narender Kumar, Michelle Churchman, John C. Larkin, Ashley Kwon, and Hua Lu

Two homologous kinase inhibitor proteins play differential roles in regulating plant cell cycle and defense.


ZINC FINGER OF ARABIDOPSIS THALIANA12 (ZAT12) Interacts with FER-LIKE IRON DEFICIENCY-INDUCED TRANSCRIPTION FACTOR (FIT) Linking Iron Deficiency and Oxidative Stress Responses. Cham Thi Tuyet Le, Tzvetina Brumbarova, Rumen Ivanov, Claudia Stoof, Eva Weber, Julia Mohrbacher, Claudia Fink-Straube, and Petra Bauer

Two transcription factors interact and negatively regulate the plant response to prolonged iron deficiency.


Putrescine enhances Fe deficiency-induced accumulation of nitric oxide which ultimately leads to the reutilization of cell wall Fe under Fe-deficient conditions.

SYSTEMS AND SYNTHETIC BIOLOGY

A Systems Genetics Approach Identifies Gene Regulatory Networks Associated with Fatty Acid Composition in Brassica rapa Seed. Ram Kumar Basnet, Dunia Pino Del Carpio, Dong Xiao, Johan Bucher, Mina Jin, Kerry Boyle, Pierre Fobert, Richard G.F. Visser, Chris Maliepaard, and Guusje Bonnema

A systems genetics approach identifies gene regulatory networks associated with fatty acid composition in Brassica rapa seed.
Alternative splicing is common during development and drought, with a high degree of tissue specificity even among related tissue types.