

On the Cover: The architecture of wheat inflorescence and its complexity are among the most important agronomic traits that influence yield. Wheat spikes vary considerably in the number of spikelets, which are specialized reproductive branches. The large and repetitive nature of the three homologous and highly similar subgenomes of wheat has impeded attempts at using genetic approaches to uncover beneficial alleles that can be utilized for yield improvement. In this issue, Wang et al. (pp. 746–757) used a population associative transcriptomic approach. They analyzed the transcriptomes of developing spikes in 90 wheat lines and correlated expression with variations in spike complexity traits. In combination with coexpression network analysis, the identities of genes related to spike complexity were predicated. Further experimental studies identified regulatory genes, the expression of which is associated with and influences spike complexity. Thus, the approach utilized in this study allows rapid identification of the genetic basis of important agronomic traits in crops with complex genomes. The cover image is a false-colored scanning electron micrograph of a wheat cv KN199 spike at the double ridge stage, a key stage determining the number of spikelets per spike. The spike meristem forms a limited number of lateral spikelet meristems (yellow) per rachis node and a single terminal spike meristem (yellow) at the distal end. Each spikelet meristem is indeterminate and will typically produce two to four fertile florets that produce seeds. Image by Yuange Wang.

ON THE INSIDE

Peter V. Minorsky 584

LETTER TO THE EDITOR

^[CC-BY]Chloroplast Ubiquitin E3 Ligase SP1: Does It Really Function in Peroxisomes? Qihua Ling, Na Li, and Paul Jarvis 586

UPDATE

^[OPEN]Orthodox Seeds and Resurrection Plants: Two of a Kind? Maria-Cecília D. Costa, Keren Cooper, Henk W.M. Hilhorst, and Jill M. Farrant

Understanding shared strategies for desiccation tolerance in orthodox seeds and resurrection plants can yield insights for agricultural improvement. 589

BREAKTHROUGH TECHNOLOGIES

^[CC-BY]Structure Annotation and Quantification of Wheat Seed Oxidized Lipids by High-Resolution LC-MS/MS. David Riewe, Janine Wiebach, and Thomas Altmann

Acyl composition annotation and quantification of hundreds of oxidized and nonoxidized lipids in naturally aged wheat seeds by high-resolution LC-MS/MS reveals enhanced lipid oxidation at ambient versus cold conditions. 600

^[OPEN]Identification of Novel Growth Regulators in Plant Populations Expressing Random Peptides. Zhilong Bao, Maureen A. Clancy, Raquel F. Carvalho, Kiona Elliott, and Kevin M. Folta

New peptide-based plant growth regulators may be identified by screening populations of plants with random peptide sequences that cause reproducible effects on biology, including plant growth inhibition, aberrant light response, and hastened developmental transitions. 619

^[OPEN]The G-Box Transcriptional Regulatory Code in Arabidopsis. Daphne Ezer, Samuel J.K. Shepherd, Anna Brestovitsky, Patrick Dickinson, Sandra Cortijo, Varodom Charoensawan, Mathew S. Box, Surojit Biswas, Katja E. Jaeger, and Philip A. Wigge

DNA-binding and gene expression data predict which bHLH or bZIP transcription factors are likely regulators of genes near perfect G-box (CACGTG) motifs. 628

Continued on next page

RESEARCH ARTICLES

BIOCHEMISTRY AND METABOLISM

[^{OPEN}] A Conifer UDP-Sugar Dependent Glycosyltransferase Contributes to Acetophenone Metabolism and Defense against Insects. *Melissa H. Mageroy, Sharon Jancsik, Macaire Man Saint Yuen, Michael Fischer, Stephen G. Withers, Christian Paetz, Bernd Schneider, John Mackay, and Joerg Bohlmann*

A conifer glycosyltransferase is involved in the chemical resistance against spruce budworm, a major forest defoliator. 641

[^{OPEN}] Thioredoxin and NADPH-Dependent Thioredoxin Reductase C Regulation of Tetrapyrrole Biosynthesis. *Qingen Da, Peng Wang, Menglong Wang, Ting Sun, Honglei Jin, Bing Liu, Jinfa Wang, Bernhard Grimm, and Hong-Bin Wang*

TRX and NTRC coordinate the stability and activity of Mg-protoporphyrin IX methyltransferase. 652

[^{OPEN}] Diacylglycerol Acyltransferase 1 Is Regulated by Its N-Terminal Domain in Response to Allosteric Effectors. *Kristian Mark P. Caldo, Jeella Z. Acedo, Rashmi Panigrahi, John C. Vederas, Randall J. Weselake, and M. Joanne Lemieux*

The N-terminal domain of Brassica diacylglycerol acyltransferase1 binds CoA and acyl-CoA, contributing to feedback inhibition and activation, respectively, of triacylglycerol biosynthesis. 667

[^{OPEN}] Bioenergetics of Monoterpenoid Essential Oil Biosynthesis in Nonphotosynthetic Glandular Trichomes. *Sean R. Johnson, Iris Lange, Narayanan Srividya, and B. Markus Lange*

In nonphotosynthetic glandular trichomes, terpenoid metabolism is powered by oxidative phosphorylation, fermentation and a unique ferredoxin/ferredoxin-NADP⁺ reductase pair. 681

[^{OPEN}] Sugar Potentiation of Fatty Acid and Triacylglycerol Accumulation. *Zhiyang Zhai, Hui Liu, Changcheng Xu, and John Shanklin*

Repressing leaf sugar export and starch synthesis in Arabidopsis increases sugar levels potentiating fatty acid and triacylglycerol accumulation by stabilizing WRINKLED1 and increasing the fatty acid synthesis rate. 696

CELL BIOLOGY

[^{CC-BY}] Clathrin Heavy Chain Subunits Coordinate Endo- and Exocytic Traffic and Affect Stomatal Movement. *Emily R. Larson, Eva Van Zelm, Camille Roux, Annie Marion-Poll, and Michael R. Blatt*

The endocytic clathrin heavy chain (chc) mutants have diminished endo/exocytosis rates that affect stomatal movement and plant growth. 708

ECOPHYSIOLOGY AND SUSTAINABILITY

Light Sheet Microscopy Imaging of Light Absorption and Photosynthesis Distribution in Plant Tissue. *Mads Lichtenberg, Erik C.L. Trampe, Thomas C. Vogelmann, and Michael Kühl*

Fine-scale characterization of light absorption and photosynthesis across plant tissue sections shows that quantum yields of PSII are highly affected by tissue light gradients. 721

Continued on next page

Etiolated Stem Branching Is a Result of Systemic Signaling Associated with Sucrose Level. Bolaji Babajide Salam, Siva Kumar Malka, Xiaobiao Zhu, Huiling Gong, Carmit Ziv, Paula Teper-Bamnolker, Naomi Ori, Jiming Jiang, and Dani Eshel

Hot or cold storage of potato tuber, a swollen stem, induces sucrose accumulation in the parenchyma that enhances branching during sprouting under dark conditions.

734

GENES, DEVELOPMENT, AND EVOLUTION

[OPEN] Transcriptome Association Identifies Regulators of Wheat Spike Architecture. Yuange Wang, Haopeng Yu, Caihuan Tian, Muhammad Sajjad, Caixia Gao, Yiping Tong, Xiangfeng Wang, and Yuling Jiao

Network analysis identifies wheat genes causally related to spike complexity, a key determinate of crop yield potential.

746

[OPEN] Arabidopsis LORELEI, a Maternally Expressed Imprinted Gene, Promotes Early Seed Development. Yanbing Wang, Tatsuya Tsukamoto, Jennifer A. Noble, Xunliang Liu, Rebecca A. Mosher, and Ravishankar Palanivelu

LORELEI expression in the seed is paternally silenced, and the maternal expression is critical for early seed development.

758

[OPEN] The Conserved and Unique Genetic Architecture of Kernel Size and Weight in Maize and Rice. Jie Liu, Juan Huang, Huan Guo, Liu Lan, Hongze Wang, Yuancheng Xu, Xiaohong Yang, Wenqiang Li, Hao Tong, Yingjie Xiao, Qingchun Pan, Feng Qiao, Mohammad Sharif Raihan, Haijun Liu, Xuehai Zhang, Ning Yang, Xiaqing Wang, Min Deng, Minliang Jin, Lijun Zhao, Xin Luo, Yang Zhou, Xiang Li, Wei Zhan, Nannan Liu, Hong Wang, Gengshen Chen, Qing Li, and Jianbing Yan

Ten segregating populations yield both conserved and species-specific genetic architecture of kernel size and weight in maize and rice.

774

Catastrophic Unbalanced Genome Rearrangements Cause Somatic Loss of Berry Color in Grapevine. Pablo Carbonell-Bejerano, Carolina Royo, Rafael Torres-Pérez, Jérôme Grimplet, Lucie Fernandez, José Manuel Franco-Zorrilla, Diego Lijavetzky, Elisa Baroja, Juana Martínez, Enrique García-Escudero, Javier Ibáñez, and José Miguel Martínez-Zapater

Chromothripsis-like genome rearrangements cause somatic loss of fruit pigmentation and alter sexual reproductive development in grapevine.

786

[OPEN] The Chickpea Early Flowering 1 (Efl1) Locus Is an Ortholog of Arabidopsis ELF3. Stephen Ridge, Amit Deokar, Robyn Lee, Ketema Daba, Richard C. Macknight, James L. Weller, and Bunyamin Tar'an

A mutation in a gene implicated in circadian clock function is associated with early flowering in a commercially significant chickpea cultivar.

802

[OPEN] Cell-Fate Specification in Arabidopsis Roots Requires Coordinative Action of Lineage Instruction and Positional Reprogramming. Qiaozhi Yu, Pengxue Li, Nengsong Liang, Hong Wang, Meizhi Xu, and Shuang Wu

Cell-fate determination in Arabidopsis roots utilizes lineage-dependent mechanisms at early stages and positional-dependent signaling at later stages.

816

Continued on next page

[OPEN]Global Analysis of Gene Expression in Response to Whole-Chromosome Aneuploidy in Hexaploid Wheat. *Ai Zhang, Ning Li, Lei Gong, Xiaowan Gou, Bin Wang, Xin Deng, Changping Li, Qianli Dong, Huakun Zhang, and Bao Liu*

Aneuploidy in hexaploid wheat induces dysregulated gene expression due to the combined action of dosage effect, dosage compensation, and transcriptional response, which brings about diverse phenotypes. 828

[OPEN]The BABY BOOM Transcription Factor Activates the LEC1-ABI3-FUS3-LEC2 Network to Induce Somatic Embryogenesis. *Anneke Horstman, Mengfan Li, Iris Heidmann, Mieke Weemen, Baojian Chen, Jose M. Muino, Gerco C. Angenent, and Kim Boutilier*

BBM and other AIL transcription factors induce somatic embryogenesis in a dose- and context-dependent mechanism and through direct transcriptional regulation of major embryo identity genes. 848

[OPEN]The Genetic Basis of Plant Architecture in 10 Maize Recombinant Inbred Line Populations. *Qingchun Pan, Yuancheng Xu, Kun Li, Yong Peng, Wei Zhan, Wenqiang Li, Lin Li, and Jianbing Yan*

A large-scale QTL mapping on 10 plant architecture traits across 10 RIL populations reveals the complex genetic basis of plant architecture in maize. 858

[OPEN]Roles of miR319 and TCP Transcription Factors in Leaf Development. *Tomotsugu Koyama, Fumihiko Sato, and Masaru Ohme-Takagi*

Combinations of mutations in miR319 and TCP transcription factor genes in Arabidopsis thaliana generate cotyledon fusion and various leaf forms with a broad range of complexity. 874

[OPEN]Seasonal Regulation of Petal Number. *Sarah M. McKim, Anne-Lise Routier-Kierzkowska, Marie Monniaux, Daniel Kierzkowski, Bjorn Pieper, Richard S. Smith, Miltos Tsiantis, and Angela Hay*

The number of petals in hairy bittercress flowers varies according to seasonal changes in the environment such as spring versus summer temperatures. 886

MEMBRANES, TRANSPORT, AND BIOENERGETICS

[OPEN]Phloem Loading through Plasmodesmata: A Biophysical Analysis. *Jean Comtet, Robert Turgeon, and Abraham D. Stroock*

A mathematical model of symplastic loading addresses the mechanisms and roles of active and passive phloem loading. 904

TransDetect Identifies a New Regulatory Module Controlling Phosphate Accumulation. *Sikander Pal, Mushtak Kisko, Christian Dubos, Benoit Lacombe, Pierre Berthomieu, Gabriel Krouk, and Hatem Rouached*

TransDetect uses nondynamic transcriptomes to define regulatory pathways controlling phosphate accumulation in zinc-deficient plants. 916

SIGNALING AND RESPONSE

Argonaute 8 (AGO8) Mediates the Elicitation of Direct Defenses against Herbivory. *Maitree Pradhan, Priyanka Pandey, Klaus Gase, Murali Sharaff, Ravi K. Singh, Avinash Sethi, Ian T. Baldwin, and Shree P. Pandey*

AGO8 forms an important component of induced direct defense machinery as it modulates several regulatory nodes in signaling and response networks during herbivore attack in wild tobacco. 927

[CC-BY] Sucrose and Ethylene Signaling Interact to Modulate the Circadian Clock. *Michael J. Haydon, Olga Mielczarek, Alexander Frank, Ángela Román, and Alex A.R. Webb*

There are conditional effects of sucrose through ethylene signaling and the F-box protein ZTL that act on GI to provide input from metabolism to adjust the circadian clock in Arabidopsis. 947

[OPEN] LAZY Genes Mediate the Effects of Gravity on Auxin Gradients and Plant Architecture. *Takeshi Yoshihara and Edgar P. Spalding*

The AtLAZY genes act early in a pathway to transduce gravity signals into auxin gradients that orient the growth of roots and shoots and their branches. 959

Phospholipase C2 Affects MAMP-Triggered Immunity by Modulating ROS Production. *Juan Martín D'Ambrosio, Daniel Couto, Georgina Fabro, Denise Scuffi, Lorenzo Lamattina, Teun Munnik, Mats X. Andersson, María E. Álvarez, Cyril Zipfel, and Ana M. Laxalt*

Arabidopsis Phospholipase C2 (PLC2) participates in a branch of microbe-associated molecular pattern-triggered immunity that involves reactive oxygen species-regulated processes. 970

Protoplast Swelling and Hypocotyl Growth Depend on Different Auxin Signaling Pathways. *Renate I. Dahlke, Simon Fraas, Kristian K. Ullrich, Kirka Heinemann, Maren Romeiks, Thomas Rickmeyer, Gerhard Klebe, Klaus Palme, Hartwig Lüthen, and Bianka Steffens*

AUXIN BINDING PROTEIN1 is required for auxin-dependent protoplast swelling in Arabidopsis. 982

CORRECTION

Identification and Metabolite Profiling of Chemical Activators of Lipid Accumulation in Green Algae. *Wase N., Tu B., Allen J.W., Black P.N., and DiRusso C.C.*

995

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