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On the Cover: *Brachypodium* (*Brachypodium distachyon*), or purple false brome, is a member of the grass subfamily Pooideae, which also includes two of the world's economically important crop species, wheat (*Triticum aestivum*) and barley (*Hordeum vulgare*). This small and rapid cycling temperate grass species has a relatively small genome, making it ideal as a genetic model system for fundamental and comparative studies of grasses, and as a valuable tool for understanding the biology of wheat. A mainstay of model species has been the ability to generate phenotypic mutants and to subsequently identify the genes that are involved in discrete developmental or physiological processes. In this issue, Derbyshire and Byrne (pp. 1291–1302) report the generation of *Brachypodium* fast neutron-induced inflorescence mutants to understand the genetic regulation of inflorescence development. The inflorescence is a key feature distinguishing different grass species. For instance, the crops maize (*Zea mays*) and rice (*Oryza sativa*) have a branched inflorescence, whereas the inflorescence of *Brachypodium* is similar to that of wheat and is an unbranched spike. The *Brachypodium* spike comprises a terminal spikelet and three to four lateral spikelets. The spikelets produce a number of florets. The cover image is a false colored scanning electron micrograph of a wild-type *Brachypodium* terminal spikelet. The spikelet meristem (yellow), at the tip of the spikelet, produces a succession of floral meristems (yellow). These floral meristems progressively mature from the tip to the base of the spikelet. Each floral meristem produces floral organs and ultimately gives rise to a single floret. The first and most obvious floral organ to be produced is the outer lemma (green), which initiates from the flanks of the floral meristem and subsequently elongates to surround the meristem. In this image, five floral meristems are visible. Photo credit: Paul Derbyshire and Mary Byrne.

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^[W]Nomenclature for Members of the Two-Component Signaling Pathway of Plants. Alexander Heyl, Mathias Brault, Florian Frugier, Alena Kuderova, Ann-Cathrin Lindner, Václav Motyka, Aaron M. Rashotte, Klaus v. Schwartzberg, Radomira Vankova, and G. Eric Schaller 1063

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^{[C][W][OA]}Antagonistic Peptide Technology for Functional Dissection of *CLV3/ESR* Genes in Arabidopsis. Xiu-Fen Song, Peng Guo, Shi-Chao Ren, Ting-Ting Xu, and Chun-Ming Liu
A novel dominant-negative technology aids analysis of peptide hormones in plants. 1076

^{[W][OA]}RootScape: A Landmark-Based System for Rapid Screening of Root Architecture in Arabidopsis. Daniela Ristova, Ulises Rosas, Gabriel Krouk, Sandrine Ruffel, Kenneth D. Birnbaum, and Gloria M. Coruzzi
A landmark-based system quantifies root architecture using holistic trait capture methods. 1086

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^{[C][W]}“Round Up the Usual Suspects”: A Comment on Nonexistent Plant G Protein-Coupled Receptors. Daisuke Urano and Alan M. Jones
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[W][OA] Functional Characterization of Proanthocyanidin Pathway Enzymes from Tea and Their Application for Metabolic Engineering. Yongzhen Pang, I. Sarath B. Abeysinghe, Ji He, Xianzhi He, David Huhman, K. Mudith Mewan, Lloyd W. Sumner, Jianfei Yun, and Richard A. Dixon

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[W][OA] β -Galactosyl Yariv Reagent Binds to the β -1,3-Galactan of Arabinogalactan Proteins. Kiminari Kitazawa, Theodora Tryfona, Yoshihisa Yoshimi, Yoshihiro Hayashi, Susumu Kawauchi, Liudmil Antonov, Hiroshi Tanaka, Takashi Takahashi, Satoshi Kaneko, Paul Dupree, Yoichi Tsumuraya, and Toshihisa Kotake

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[C][W][OA] The Arabidopsis TUMOR PRONE5 Gene Encodes an Acetylornithine Aminotransferase Required for Arginine Biosynthesis and Root Meristem Maintenance in Blue Light. Nathalie Frémont, Michael Riefler, Andrea Stolz, and Thomas Schmülling

A mutant of arginine biosynthesis uncovers a novel role for the amino acid and blue light in regulating root meristem function. 1127

[W] PROTEIN L-ISOASPARTYL METHYLTRANSFERASE2 Is Differentially Expressed in Chickpea and Enhances Seed Vigor and Longevity by Reducing Abnormal Isoaspartyl Accumulation Predominantly in Seed Nuclear Proteins. Pooja Verma, Harmeet Kaur, Bhanu Prakash Petla, Venkateswara Rao, Saurabh C. Saxena, and Manoj Majee

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[W][OA] Overexpression of the Trehalase Gene AtTRE1 Leads to Increased Drought Stress Tolerance in Arabidopsis and Is Involved in Abscisic Acid-Induced Stomatal Closure. Hilde Van Houtte, Lies Vandesteene, Lorena López-Galvis, Liesbeth Lemmens, Ewaut Kissel, Sebastien Carpentier, Regina Feil, Nelson Avonce, Tom Beeckman, John E. Lunn, and Patrick Van Dijk

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[C][W][OA] ASR1 Mediates Glucose-Hormone Cross Talk by Affecting Sugar Trafficking in Tobacco Plants. Pia Guadalupe Dominguez, Nicolas Frankel, Jeannine Mazuch, Ilse Balbo, Norberto Iusem, Alisdair R. Fernie, and Fernando Carrari

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[W] Monolignol Pathway 4-Coumaric Acid:Coenzyme A Ligases in *Populus trichocarpa*: Novel Specificity, Metabolic Regulation, and Simulation of Coenzyme A Ligation Fluxes. Hsi-Chuan Chen, Jina Song, Cranos M. Williams, Christopher M. Shuford, Jie Liu, Jack P. Wang, Quanzi Li, Rui Shi, Emine Gokce, Joel Ducoste, David C. Muddiman, Ronald R. Sederoff, and Vincent L. Chiang

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[C][W][OA] The Arabidopsis Rho of Plants GTPase AtROP6 Functions in Developmental and Pathogen Response Pathways. Limor Poraty-Gavra, Philip Zimmermann, Sabine Haigis, Pawet Bednarek, Ora Hazak, Oksana Rogovoy Stelmakh, Einat Sadot, Paul Schulze-Lefert, Wilhelm Grissemer, and Shaul Yalovsky

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^{[W][OA]}Cortical Microtubule Arrays Are Initiated from a Nonrandom Prepattern Driven by Atypical Microtubule Initiation. *Jelmer J. Lindeboom, Antonios Lioutas, Eva E. Deinum, Simon H. Tindemans, David W. Ehrhardt, Anne Mie C. Emons, Jan W. Vos, and Bela M. Mulder*

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^{[W][OA]}OsTZF1, a CCCH-Tandem Zinc Finger Protein, Confers Delayed Senescence and Stress Tolerance in Rice by Regulating Stress-Related Genes. *Asad Jan, Kyonoshin Maruyama, Daisuke Todaka, Satoshi Kidokoro, Mitsuru Abo, Etsuro Yoshimura, Kazuo Shinozaki, Kazuo Nakashima, and Kazuko Yamaguchi-Shinozaki*

OsTZF1, a CCCH-type zinc finger protein, acts as a negative regulator of leaf senescence in rice under stress conditions and confers abiotic stress tolerance by delaying stress-response phenotypes, possibly through the control of RNA metabolism of stress-responsive genes. 1202

^{[C][W]}Wheat Oxophytodienoate Reductase Gene *TaOPR1* Confers Salinity Tolerance via Enhancement of Abscisic Acid Signaling and Reactive Oxygen Species Scavenging. *Wei Dong, Mengcheng Wang, Fei Xu, Taiyong Quan, Keqin Peng, Langtao Xiao, and Guangmin Xia*

Wheat oxophytodienoate reductase gene TaOPR1 enhances salinity tolerance by promoting an abscisic acid-dependent stress response pathway. 1217

^{[C][W][OA]}Enhanced Reactive Oxygen Species Scavenging by Overproduction of Superoxide Dismutase and Catalase Delays Postharvest Physiological Deterioration of Cassava Storage Roots. *Jia Xu, Xiaoguang Duan, Jun Yang, John R. Beeching, and Peng Zhang*

Overproduction of the copper/zinc superoxide dismutase and catalase in transgenic cassava dramatically improves ROS scavenging ability, abiotic stress resistance, and delayed postharvest deterioration. 1517

^[OA]Vascular Occlusions in Grapevines with Pierce's Disease Make Disease Symptom Development Worse. *Qiang Sun, Yuliang Sun, M. Andrew Walker, and John M. Labavitch*

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^{[W][OA]}Phenyl-Adenine, Identified in a *LIGHT-DEPENDENT SHORT HYPOCOTYLS4*-Assisted Chemical Screen, Is a Potent Compound for Shoot Regeneration through the Inhibition of CYTOKININ OXIDASE/DEHYDROGENASE Activity. *Hans Motte, Petr Galuszka, Lukáš Spíchal, Petr Tarkowski, Ondřej Plíhal, Mária Šmehilová, Pavel Jaworek, Danny Vereecke, Stefaan Werbrouck, and Danny Geelen*

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^{[W][OA]}Physical Interaction of Floral Organs Controls Petal Morphogenesis in Arabidopsis. *Seiji Takeda, Akira Iwasaki, Noritaka Matsumoto, Tomohiro Uemura, Kiyoshi Tatematsu, and Kiyotaka Okada*

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^{[C][W][OA]}Identification of Direct Targets of FUSCA3, a Key Regulator of Arabidopsis Seed Development. *Fangfang Wang and Sharyn E. Perry*

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- [C][W][OA] A Fasciclin-Like Arabinogalactan Protein, GhFLA1, Is Involved in Fiber Initiation and Elongation of Cotton. Geng-Qing Huang, Si-Ying Gong, Wen-Liang Xu, Wen Li, Peng Li, Chao-Jun Zhang, Deng-Di Li, Yong Zheng, Fu-Guang Li, and Xue-Bao Li
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- [C][W][OA] MORE SPIKELETS1 Is Required for Spikelet Fate in the Inflorescence of Brachypodium. Paul Derbyshire and Mary E. Byrne
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- [W][OA] *incurvata13*, a Novel Allele of AUXIN RESISTANT6, Reveals a Specific Role for Auxin and the SCF Complex in Arabidopsis Embryogenesis, Vascular Specification, and Leaf Flatness. David Esteve-Bruna, José Manuel Pérez-Pérez, María Rosa Ponce, and José Luis Micol
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- [C][W] Control of Root Meristem Size by DA1-RELATED PROTEIN2 in Arabidopsis. Yuancheng Peng, Wenying Ma, Liangliang Chen, Lei Yang, Shengjun Li, Hongtao Zhao, Yankun Zhao, Weihuan Jin, Na Li, Michael W. Bevan, Xia Li, Yiping Tong, and Yunhai Li
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- [W][OA] Variations in the Rhythms of Respiration and Nitrogen Fixation in Members of the Unicellular Diazotrophic Cyanobacterial Genus *Cyanothece*. Anindita Bandyopadhyay, Thanura Elvitigala, Michelle Liberton, and Himadri B. Pakrasi
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- [W][OA] Low pH, Aluminum, and Phosphorus Coordinately Regulate Malate Exudation through GmALMT1 to Improve Soybean Adaptation to Acid Soils. Cuiyue Liang, Miguel A. Piñeros, Jiang Tian, Zhufang Yao, Lili Sun, Jiping Liu, Jon Shaff, Alison Coluccio, Leon V. Kochian, and Hong Liao
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[W][O]A]Constitutive Expression of a miR319 Gene Alters Plant Development and Enhances Salt and Drought Tolerance in Transgenic Creeping Bentgrass. *Man Zhou, Dayong Li, Zhigang Li, Qian Hu, Chunhua Yang, Lihuang Zhu, and Hong Luo*

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[W][O]A]The MPK6-ERF6-ROS-Responsive cis-Acting Element7/GCC Box Complex Modulates Oxidative Gene Transcription and the Oxidative Response in Arabidopsis. *Pengcheng Wang, Yanyan Du, Xiaoliang Zhao, Yuchen Miao, and Chun-Peng Song*

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[W][O]A]Structure-Guided Engineering of Plant Phytochrome B with Altered Photochemistry and Light Signaling. *Junrui Zhang, Robert J. Stankey, and Richard D. Vierstra*

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^[W]^[OA]Carbon and Nitrogen Provisions Alter the Metabolic Flux in Developing Soybean Embryos.
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Altered substrate provision to developing soybeans leads to changes in metabolic pathway fluxes and carbon and nitrogen partitioning.

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^[W]^[OA]Network Inference Analysis Identifies an *APRR2-Like* Gene Linked to Pigment Accumulation in Tomato and Pepper Fruits. Yu Pan, Glyn Bradley, Kevin Pyke, Graham Ball, Chungui Lu, Rupert Fray, Alexandra Marshall, Subhalai Jayasuta, Charles Baxter, Rik van Wijk, Laurie Boyden, Rebecca Cade, Natalie H. Chapman, Paul D. Fraser, Charlie Hodgman, and Graham B. Seymour

A likely regulator of tomato ripening is identified from a gene network, its function is validated in transgenic plants, and an orthologous gene is shown to play a similar role in pepper.

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^[C] Some figures in this article are displayed in color online but in black and white in the print edition.

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