

On the Cover: The *epigenetic control1* (*epic1*) mutant was isolated in a screen for epigenetic regulators in *Arabidopsis* (*Arabidopsis thaliana*). The GFP protein that is expressed in the young leaves is green, and the chlorophyll autofluorescence is red. The *epic1* mutant is defective in the histone deacetylase HDA6, which causes release of transcriptionally silenced GFP expression in the young leaves. This allele differs from previously reported alleles because it does not affect DNA methylation and has only a modest effect on the release of transposable elements and other heterochromatic transcripts. The outer ring represents the five *Arabidopsis* chromosomes, the green lines represent the distribution of transposable element genes, and the blue and red lines mark the up-regulated transcripts in an *hda6* null mutant and the *epic1* allele, respectively. The chromosomes and the transcriptome data were plotted using the CIRCOS software package (www.circos.ca). Cover image credits: Etienne Bucher, Institut de Recherche en Horticulture et Semences Université d'Angers, France).

FOCUS ON CHROMATIN/EPIGENETICS

EDITORIAL

Chromatin and Epigenetics. *Anna Amtmann, Hong Ma, and Doris Wagner* 1185

UPDATES

Epigenetic Mechanisms Are Critical for the Regulation of *WUSCHEL* Expression in Floral Meristems.
Xiurwei Cao, Zishan He, Lin Guo, and Xigang Liu

Epigenetic mechanisms play a critical role in floral meristem maintenance and determinacy. 1189

Epigenetic Changes in Hybrids. *Ian K. Greaves, Rebeca Gonzalez-Bayon, Li Wang, Anyu Zhu, Pei-Chuan Liu, Michael Groszmann, W. James Peacock, and Elizabeth S. Dennis*

Hybrid systems show altered DNA methylation and siRNA patterns that potentially contribute to the hybrid vigor phenotype. 1197

DNA Damage Repair in the Context of Plant Chromatin. *Mattia Donà and Ortrun Mittelsten Scheid*

Efficient repair of DNA damage in plants depends on chromatin remodeling factors, histone chaperones, and histone modifiers. 1206

DNA Methylation within Transcribed Regions. *Taiko K. To, Hidetoshi Saze, and Tetsuji Kakutani*

Although DNA methylation within transcribed genes is commonly found in diverse animals and plants, recent advances highlight the remaining mystery regarding intragenic DNA methylation. 1219

Trans-Homolog Interactions Facilitating Paramutation in Maize. *Brian John Giacomelli and Jay Brian Hollick*

Recent work highlights the functional roles of alternative DNA-dependent RNA polymerases and unique non-coding sequences in mediating paramutation behaviors in maize. 1226

Continued on next page

Flowering Locus C's Lessons: Conserved Chromatin Switches Underpinning Developmental Timing and Adaptation. *Jo Hepworth and Caroline Dean*

Vernalization has proven to pivot around chromatin changes, so that the balance of antagonistic chromatin-modifying complexes provides a fine level of control that is a target for adaptation. 1237

RESEARCH ARTICLES

[OPEN] A Genome-Wide Chronological Study of Gene Expression and Two Histone Modifications, H3K4me3 and H3K9ac, during Developmental Leaf Senescence. *Judy A. Brusslan, Giancarlo Bonora, Ana M. Rus-Canterbury, Fayha Tariq, Artur Jaroszewicz, and Matteo Pellegrini*

The presence and breadth of two histone modifications associated with active genes correlate to changes in gene expression during leaf aging, supporting senescence-related chromatin structural changes. 1246

[OPEN] Examining the Causes and Consequences of Context-Specific Differential DNA Methylation in Maize. *Qing Li, Jawon Song, Patrick T. West, Greg Zynda, Steven R. Eichten, Matthew W. Vaughn, and Nathan M. Springer*

Natural variation of DNA methylation in maize is evident among five diverse maize inbred lines. 1262

[OPEN] MORF-RELATED GENE702, a Reader Protein of Trimethylated Histone H3 Lysine 4 and Histone H3 Lysine 36, Is Involved in Brassinosteroid-Regulated Growth and Flowering Time Control in Rice. *Jing Jin, Jinlei Shi, Bing Liu, Yanchao Liu, Ying Huang, Yu Yu, and Aiwu Dong*

A histone reader protein of trimethylation deciphers the epigenetic information to affect the brassinosteroid signaling and flowering. 1275

Deciphering the Role of POLYCOMB REPRESSIVE COMPLEX1 Variants in Regulating the Acquisition of Flowering Competence in Arabidopsis. *Sara Picó, M. Isabel Ortiz-Marchena, Wiam Merini, and Myriam Calonje*

Two different variants of polycomb group proteins, epigenetic regulators, coordinate the acquisition of flowering competence during the juvenile-to-adult phase transition in Arabidopsis through the regulation of specific miRNA levels. 1286

[OPEN] HISTONE DEACETYLASE6 Controls Gene Expression Patterning and DNA Methylation-Independent Euchromatic Silencing. *Emilija Hristova, Kateryna Fal, Laurin Klemme, David Windels, and Etienne Bucher*

Mutation in a highly conserved domain of a histone deacetylase releases euchromatic silencing without affecting DNA methylation. 1298

GENERAL CONTROL NONREPPRESSED PROTEIN5-Mediated Histone Acetylation of FERRIC REDUCTASE DEFECTIVE3 Contributes to Iron Homeostasis in Arabidopsis. *Jiewen Xing, Tianya Wang, Zhenshan Liu, Jianqin Xu, Yingyin Yao, Zhaorong Hu, Huiru Peng, Mingming Xin, Futong Yu, Daoxiu Zhou, and Zhongfu Ni*

A histone acetyltransferase contributes to the regulation of iron homeostasis. 1309

[OPEN] Expansion and Functional Divergence of Jumonji C-Containing Histone Demethylases: Significance of Duplications in Ancestral Angiosperms and Vertebrates. *Shengzhan Qian, Yingxiang Wang, Hong Ma, and Liangsheng Zhang*

Duplication and sequence divergence of a gene family for histone demethylases likely contributed to enhanced, chromatin-based regulation in angiosperms and vertebrates. 1321

Continued on next page

[OPEN] Selection for Improved Energy Use Efficiency and Drought Tolerance in Canola Results in Distinct Transcriptome and Epigenome Changes. *Aurine Verkest, Marina Byzova, Cindy Martens, Patrick Willems, Tom Verwulgen, Bram Slabbinck, Debbie Rombaut, Jan Van de Velde, Klaas Vandepoele, Evi Standaert, Marrit Peeters, Mieke Van Lijsebettens, Frank Van Breusegem, and Marc De Block*

Selection for both energy use efficiency and drought tolerance in canola leads to stable epilines with distinct transcriptome and chromatin modification profiles, supporting their superior performance.

1338

[OPEN] Florigen-Encoding Genes of Day-Neutral and Photoperiod-Sensitive Maize Are Regulated by Different Chromatin Modifications at the Floral Transition. *Iride Mascheretti, Katie Turner, Roberta S. Brivio, Andrew Hand, Joseph Colasanti, and Vincenzo Rossi*

Florigen-encoding genes have different chromatin signatures associated with the floral transition in ancestral and modern maize.

1351

[OPEN] The Methylome of Soybean Roots during the Compatible Interaction with the Soybean Cyst Nematode. *Aditi Rambani, J. Hollis Rice, Jinyi Liu, Thomas Lane, Priya Ranjan, Mitra Mazarei, Vince Pantalone, C. Neal Stewart Jr., Meg Staton, and Tarek Hewezi*

The soybean cyst nematode induces genomewide differential DNA methylation that impacts a large number of structural genes and biological functions.

1364

[OPEN] Photosynthetic Genes and Genes Associated with the C4 Trait in Maize Are Characterized by a Unique Class of Highly Regulated Histone Acetylation Peaks on Upstream Promoters. *Renke Perduns, Ina Horst-Niessen, and Christoph Peterhansel*

Developmentally regulated epigenetic modifications of upstream promoters are involved in photosynthesis and C4 metabolism.

1378

[OPEN] Histone H2B Monoubiquitination Mediated by HISTONE MONOUBIQUITINATION1 and HISTONE MONOUBIQUITINATION2 Is Involved in Anther Development by Regulating Tapetum Degradation-Related Genes in Rice. *Hong Cao, Xiaoying Li, Zhi Wang, Meng Ding, Yongzhen Sun, Fengqin Dong, Fengying Chen, Li'an Liu, James Doughty, Yong Li, and Yong-Xiu Liu*

Histone H2B monoubiquitination is essential for anther development.

1389

[OPEN] Genome-Wide Nucleosome Occupancy and Positioning and Their Impact on Gene Expression and Evolution in Plants. *Tao Zhang, Wenli Zhang, and Jiming Jiang*

Nucleosome dynamics impacts on gene expression and evolution in rice and Arabidopsis.

1406

[OPEN] Global Analysis Reveals the Crucial Roles of DNA Methylation during Rice Seed Development. *Mei-Qing Xing, Yi-Jing Zhang, Shi-Rong Zhou, Wen-Yan Hu, Xue-Ting Wu, Ya-Jin Ye, Xiao-Xia Wu, Yun-Ping Xiao, Xuan Li, and Hong-Wei Xue*

DNA methylome dynamics show crucial roles for DNA methylation in seed development.

1417

[OPEN] A Comparative Epigenomic Analysis of Polyploidy-Derived Genes in Soybean and Common Bean. *Kyung Do Kim, Moaine El Baidouri, Brian Abernathy, Aiko Iwata-Otsubo, Carolina Chavarro, Michael Gonzales, Marc Libault, Jane Grimwood, and Scott A. Jackson*

Reference methylomes provide insights into the evolutionary role of DNA methylation in paleopolyploid genomes.

1433

HISTONE DEACETYLASE6-Defective Mutants Show Increased Expression and Acetylation of ENHANCER OF TRIPTYCHON AND CAPRICE1 and GLABRA2 with Small But Significant Effects on Root Epidermis Cellular Pattern. Dong-Xu Li, Wen-Qian Chen, Zhi-Hong Xu, and Shu-Nong Bai

HDA6 affects the cellular patterning of Arabidopsis root epidermis by altering the histone acetylation status of two promoters. 1448

REGULAR ISSUE

ON THE INSIDE

Peter V. Minorsky 1459

COMMENTARY

Bringing Anatomy Back into the Equation. Timothy J. Brodribb 1461

BREAKTHROUGH TECHNOLOGIES

Subfamily-Specific Fluorescent Probes for Cysteine Proteases Display Dynamic Protease Activities during Seed Germination. Haibin Lu, Balakumaran Chandrasekar, Julian Oeljeklaus, Johana C. Misas-Villamil, Zheming Wang, Takayuki Shindo, Matthew Bogyo, Markus Kaiser, and Renier A.L. van der Hoorn

Probes for aleurains, cathepsins and vacuolar processing enzymes display protease activities that coincide with seed storage protein remobilization. 1462

^[OPEN]**Integrating Image-Based Phenomics and Association Analysis to Dissect the Genetic Architecture of Temporal Salinity Responses in Rice.** Malachy T. Campbell, Avi C. Knecht, Bettina Berger, Chris J. Brien, Dong Wang, and Harkamal Walia

The genetic basis of dynamic salinity stress responses is elucidated using image-based phenomics and functional association analysis. 1476

Metal Binding in Photosystem II Super- and Subcomplexes from Barley Thylakoids. Sidsel Birkelund Schmidt, Daniel Pergament Persson, Marta Powikrowska, Jens Frydenvang, Jan K. Schjoerring, Poul Erik Jensen, and Søren Husted

A new ICP-MS-based method quantifies the metal binding in PSII super- and subcomplexes from barley thylakoids. 1490

RESEARCH ARTICLES

BIOCHEMISTRY AND METABOLISM

^[OPEN]**Chlorophyll Synthase under Epigenetic Surveillance Is Critical for Vitamin E Synthesis, and Altered Expression Affects Tocopherol Levels in Arabidopsis.** Chunyu Zhang, Wei Zhang, Guodong Ren, Delin Li, Rebecca E. Cahoon, Ming Chen, Yongming Zhou, Bin Yu, and Edgar B. Cahoon

Epigenetic analysis of chlorophyll synthase expression demonstrates its effects on chlorophyll and tocopherol synthesis. 1503

^[OPEN]**Analysis of Loss-of-Function Mutants in Aspartate Kinase and Homoserine Dehydrogenase Genes Points to Complexity in the Regulation of Aspartate-Derived Amino Acid Contents.** Teresa J. Clark and Yan Lu

Aspartate family amino acid contents increase in loss-of-function mutants for specific isoforms of the early steps of the biosynthesis pathways. 1512

Completion of Tricin Biosynthesis Pathway in Rice: Cytochrome P450 75B4 Is a Unique Chrysoeriol 5'-Hydroxylase. Pui Ying Lam, Hongjia Liu, and Clive Lo

Biosynthesis of triclin requires specific hydroxylation catalyzed by a phylogenetically distinct hydroxylase. 1527

Continued on next page

[OPEN] Complete Mitochondrial Complex I Deficiency Induces an Up-Regulation of Respiratory Fluxes That Is Abolished by Traces of Functional Complex I. *Kristina Kühn, Toshihiro Obata, Kristen Feher, Ralph Bock, Alisdair R. Fernie, and Etienne H. Meyer*

Respiratory chain complex I acts as a negative regulator of fluxes through glycolysis and the TCA cycle. 1537

Tissue-Specific Apocarotenoid Glycosylation Contributes to Carotenoid Homeostasis in Arabidopsis Leaves. *Kira Lätari, Florian Wüst, Michaela Hübner, Patrick Schaub, Kim Gabriele Beisel, Shizue Matsubara, Peter Beyer, and Ralf Welsch*

Apocarotenoid glycosides contribute to carotenoid biosynthetic pathway flux compensation. 1550

CELL BIOLOGY

Putting the Squeeze on Plasmodesmata: A Role for Reticulons in Primary Plasmodesmata Formation. *Kirsten Knox, Pengwei Wang, Verena Kriechbaumer, Jens Tilsner, Lorenzo Frigerio, Imogen Sparkes, Chris Hawes, and Karl Oparka*

Reticulon proteins involved in membrane curvature are targeted to the developing cell plate and label desmotubules in primary plasmodesmata. 1563

[OPEN] Large Cellular Inclusions Accumulate in Arabidopsis Roots Exposed to Low-Sulfur Conditions. *Terry L. Jackson, Ginger W. Baker, Floyd R. Wilks Jr., Vladimir A. Popov, Jaideep Mathur, and Philip N. Benfey*

Sizable inclusions aggregate within the cytoplasm of sulfur-deprived Arabidopsis roots exposed to light. 1573

ECOPHYSIOLOGY AND SUSTAINABILITY

[OPEN] Water Transport Properties of the Grape Pedicel during Fruit Development: Insights into Xylem Anatomy and Function Using Microtomography. *Thorsten Knipfer, Jiong Fei, Gregory A. Gambetta, Andrew J. McElrone, Kenneth A. Shackel, and Mark A. Matthews*

Xylem flow into the grape fruit declines before the onset of ripening, and losses in pedicel hydraulic conductivity could be attributed to xylem vessel blockages. 1590

[OPEN] Reduced Lateral Root Branching Density Improves Drought Tolerance in Maize. *Ai Zhan, Hannah Schneider, and Jonathan P. Lynch*

Maize genotypes with reduced lateral root branching density have superior water capture, growth, and yield under drought. 1603

[OPEN] How Does Leaf Anatomy Influence Water Transport outside the Xylem? *Thomas N. Buckley, Grace P. John, Christine Scoffoni, and Lauren Sack*

Anatomical data from diverse species, applied to a novel integrative model, elucidate the mechanistic basis of differences in water transport outside the xylem in leaves. 1616

[OPEN] Easy Come, Easy Go: Capillary Forces Enable Rapid Refilling of Embolized Primary Xylem Vessels. *Vivien Rolland, Dana M. Bergstrom, Thomas Lenné, Gary Bryant, Hua Chen, Joe Wolfe, N. Michele Holbrook, Daniel E. Stanton, and Marilyn C. Ball*

Physical properties of protoxylem promote rapid refilling of embolized vessels in two herbaceous species, with implications for vascular function of leaves and elongating stems and roots. 1636

GENES, DEVELOPMENT, AND EVOLUTION

[OPEN]A Comprehensive Analysis of Chromoplast Differentiation Reveals Complex Protein Changes Associated with Plastoglobule Biogenesis and Remodeling of Protein Systems in Sweet Orange Flesh. Yunliu Zeng, Jiabin Du, Lun Wang, Zhiyong Pan, Qiang Xu, Shunyuan Xiao, and Xiuxin Deng

Two major chromoplasts are region-specifically formed in citrus and converted from amyloplast precursors. 1648

FOREVER YOUNG FLOWER Negatively Regulates Ethylene Response DNA-Binding Factors by Activating an Ethylene-Responsive Factor to Control Arabidopsis Floral Organ Senescence and Abscission. Wei-Han Chen, Pei-Fang Li, Ming-Kun Chen, Yung-I Lee, and Chang-Hsien Yang

A MADS box gene that affects ethylene signaling also regulates floral organ senescence and abscission. 1666

[OPEN]Comprehensive Tissue-Specific Transcriptome Analysis Reveals Distinct Regulatory Programs during Early Tomato Fruit Development. Richard J. Pattison, Fabiana Csukasi, Yi Zheng, Zhangjun Fei, Esther van der Knaap, and Carmen Catalá

Distinct transcriptional programs and hormonal pathways underlie the ovary-to-fruit transition. 1684

MicroRNA396-Targeted *SHORT VEGETATIVE PHASE* Is Required to Repress Flowering and Is Related to the Development of Abnormal Flower Symptoms by the Phyllody Symptoms1 Effector. Chiao-Yin Yang, Yu-Hsin Huang, Chan-Pin Lin, Yen-Yu Lin, Hao-Chun Hsu, Chun-Neng Wang, Li-Yu Daisy Liu, Bing-Nan Shen, and Shih-Shun Lin

A PHYLL1 effector protein interferes with miR396-mediated transcriptional regulator mRNA decay, enhancing the transcription factor for abnormal flower development. 1702

[OPEN]Molecular Evidence for Functional Divergence and Decay of a Transcription Factor Derived from Whole-Genome Duplication in *Arabidopsis thaliana*. Melissa D. Lehti-Shiu, Sahra Uygun, Gaurav D. Moghe, Nicholas Panchy, Liang Fang, David E. Hufnagel, Hannah L. Jasicki, Michael Feig, and Shin-Han Shiu

Functional decay of a transcription factor retained after whole-genome duplication suggests that duplicate gene loss is a prolonged process occurring over tens of millions of years. 1717

[OPEN]The Soybean-Specific Maturity Gene *E1* Family of Floral Repressors Controls Night-Break Responses through Down-Regulation of *FLOWERING LOCUS T* Orthologs. Meilan Xu, Noriko Yamagishi, Chen Zhao, Ryoma Takeshima, Megumi Kasai, Satoshi Watanabe, Akira Kanazawa, Nobuyuki Yoshikawa, Baohui Liu, Tetsuya Yamada, and Jun Abe

Light-dependent phytochrome A-regulated transcription of floral repressors affects photoperiodic induction of flowering. 1735

MEMBRANES, TRANSPORT, AND BIOENERGETICS

[OPEN]In Vivo Identification of Photosystem II Light Harvesting Complexes Interacting with PHOTOSYSTEM II SUBUNIT S. Caterina Gerotto, Cinzia Franchin, Giorgio Arrigoni, and Tomas Morosinotto

Specific protein-protein interactions are likely involved in the modulation of photosynthetic apparatus activity. 1747

Continued on next page

Integrative Comparison of the Role of the PHOSPHATE RESPONSE1 Subfamily in Phosphate Signaling and Homeostasis in Rice. *Meina Guo, Wenyuan Ruan, Changying Li, Fangliang Huang, Ming Zeng, Yingyao Liu, Yanan Yu, Xiaomeng Ding, Yunrong Wu, Zhongchang Wu, Chuanzao Mao, Keke Yi, Ping Wu, and Xiaorong Mo*

A subfamily of phosphate-responsive genes is functionally diverse in the regulation of phosphate signaling and homeostasis.

1762

Ethylene Inhibits Root Elongation during Alkaline Stress through AUXIN1 and Associated Changes in Auxin Accumulation. *Juan Li, Heng-Hao Xu, Wen-Cheng Liu, Xiao-Wei Zhang, and Ying-Tang Lu*

Ethylene promotes auxin transporter expression and auxin biosynthesis to modulate root elongation during alkaline stress.

1777

SIGNALING AND RESPONSE

Lateral Organ Boundaries Domain16 and 18 Act Downstream of the AUXIN1 and LIKE-AUXIN3 Auxin Influx Carriers to Control Lateral Root Development in Arabidopsis. *Han Woo Lee, Chuloh Cho, and Jungmook Kim*

Two auxin influx carriers are required for auxin signaling that activates transcriptional control in lateral root development.

1792

Subtle Regulation of Potato Acid Invertase Activity by a Protein Complex of Invertase, Invertase Inhibitor, and SUCROSE NONFERMENTING1-RELATED PROTEIN KINASE. *Yuan Lin, Tengfei Liu, Jun Liu, Xun Liu, Yongbin Ou, Huiling Zhang, Meng Li, Uwe Sonnewald, Botao Song, and Conghua Xie*

Invertase activity is affected by a protein complex to modulate accumulation of reducing sugars in cold-stored potato tubers.

1807

^[OPEN]Strigolactone Inhibition of Branching Independent of Polar Auxin Transport. *Philip B. Brewer, Elizabeth A. Dun, Renyi Gui, Michael G. Mason, and Christine A. Beveridge*

Strigolactones act independently of auxin transport/canalization to inhibit bud outgrowth.

1820

SYSTEMS AND SYNTHETIC BIOLOGY

^[OPEN]Cross-Species Network Analysis Uncovers Conserved Nitrogen-Regulated Network Modules in Rice. *Mariana Obertello, Stuti Shrivastava, Manpreet S. Katari, and Gloria M. Coruzzi*

Integration of gene interaction data across a model dicot and a monocot identifies conserved and distinct regulatory network modules involved in nitrogen use, enabling translational discoveries from models to crops.

1830

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