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

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

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

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.

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.

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.

Trans-Homolog Interactions Facilitating Paramutation in Maize. Brian John Giacopelli 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.
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.

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.

Qing Li, J axiom 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.

[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, Yunchao 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.

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-toadult phase transition in Arabidopsis through the regulation of specific miRNA levels.

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.

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, Yingxin Yao, Zhaorong Hu, Huiru Peng, Mingming Xin, Futong Yu, Daoxiu Zhou, and Zhongfu Ni

A histone acetyltransferase contributes to the regulation of iron homeostasis.

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.
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.

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

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

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

Histone H2B monoubiquitination is essential for anther development.

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

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

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

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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.

Metal Binding in Photosystem II Super- and Subcomplexes from Barley Thylakoids. Sidsel Birkeland Schmidt, Daniel Pergament Persson, Marta Powikrowska, Jens Frødensvang, 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.

RESEARCH ARTICLES

BIOCHEMISTRY AND METABOLISM

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.

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.

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 tricin requires specific hydroxylation catalyzed by a phylogenetically distinct hydroxylase.
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.


Apocarotenoid glycosides contribute to carotenoid biosynthetic pathway flux compensation.

CELL BIOLOGY

Putting the Squeeze on Plasmodesmata: A Role for Reticulons in Primary Plasmodesmata Formation. Kirsten Knox, Pengwei Wang, Verena Krieckbaumer, 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.

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.

ECOPHYSIOLOGY AND SUSTAINABILITY


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.

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.

How Does Leaf Anatomy Influence Water Transport outside the Xylem? Thomas N. Buckley, Grace P. John, Christine Scoffoni, and Lawren 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.

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.

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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, Jabin 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.

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, Yang-I Lee, and Chang-Hsien Yang

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

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.

MicroRNA396-Targeted SHORT VEGETATIVE PHASE Is Required to Repress Flowering and Is Related to the Development of Abnormal Flower Symptoms by the Phyllody Symptoms\(^1\) Effector. Chiao-Yin Yang, Yu-Hsin Huang, Chun-Pin Lin, Yu-Lin, Hao-Chun Hsu, Chun-Neng Wang, Li-Yu Daisy Liu, Bing-Nan Shen, and Shih-Shun Lin

A PHYL1 effector protein interferes with miR396-mediated transcriptional regulator mRNA decay, enhancing the transcription factor for abnormal flower development.

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.

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, Boaoui Liu, Tetsuya Yamada, and Jun Abe

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

MEMBRANES, TRANSPORT, AND BIOENERGETICS

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

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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

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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, Huiing Zhang, Meng Li, Uwe Sonnewald, Botao Song, and Conghua Xie

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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
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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