On the Cover: The epigenetic control (epi1) 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 epi1 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 epi1 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

Epigenetic changes in hybrids 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

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.

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.

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 Aiwa 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-to-adult phase transition in Arabidopsis through the regulation of specific miRNA levels.

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

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GENERAL CONTROL NONREPRESSSED PROTEIN5-Mediated Histone Acetylation of FERRIC REDUCTASE DEFECTIVE3 Contributes to Iron Homeostasis in Arabidopsis.  
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A histone acetyltransferase contributes to the regulation of iron homeostasis.

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

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

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RESEARCH ARTICLES

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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

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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

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

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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

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

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