On the Cover: RNA-binding proteins control pre-mRNA processing and the transport, localization, translation, and stability of mRNAs. Many of these proteins contain one or more of a small number of RNA-binding motifs, and the most common of these motifs is the RNA recognition motif (RRM). Among RRM-containing proteins, the serine/arginine-rich (SR) factors are key regulators of constitutive and alternative splicing of mRNA precursors. Prototypical SR proteins have a modular structure, with one or two RRM domains and a variable-length carboxy-terminal region enriched in serine/arginine dipeptides. In this issue, Califice et al. (pp. 546–560) carried out a wide range of large-scale and refined phylogenetic analyses of the RRM domain to investigate the origin and evolution of SR proteins. Their main finding is that all prototypical SR splicing factors belong to an ancestral SR protein family that was already diversified in the last eukaryotic common ancestor. The analysis further supports a parsimonious scenario for their subsequent evolution and endorses the general view that the last eukaryotic common ancestor was a complex organism, especially concerning RNA processing. Pictured is a phylogenetic tree showing evolutionary relationships between RRM-containing proteins (depicted as tertiary structures of SRSF3/SRp20 and SRSF7/9G8; Protein Data Bank accession nos. 2I38 and 2HVZ, respectively). This comprehensive work provides a strong evolutionary foundation for a natural classification of SR splicing factors. Cover design and photography by Patrick Motte.

MES16, a Member of the Methylesterase Protein Family, Specifically Demethylates Fluorescent Chlorophyll Catabolites during Chlorophyll Breakdown in Arabidopsis. Bastien Christ, Silvia Schellert, Sylvia Aurbry, Iris Süssenbacher, Thomas Müller, Bernhard Kräutler, and Stefan Hörtensteiner


Arabidopsis Deficient in Cutin Ferulate Encodes a Transferase Required for Feruloylation of ω-Hydroxy Fatty Acids in Cutin Polyester. Carsten Rautengarten, Berit Ebert, Mario Ouellet, Majse Naafs, Edward E.K. Baidoo, Peter Benke, Maria Stranne, Aindrina Mukhopadhyay, Jay D. Keasling, Yumiko Sakuragi, and Henrik Vibe Scheller

Biosynthesis of Proanthocyanidins in White Clover Flowers: Cross Talk within the Flavonoid Pathway. Shamila Weerakoon Abeynayake, Stephen Panter, Ross Chapman, Tracie Webster, Simone Rochfort, Aidyn Mouradov, and German Spangenberg

Functional Interactions between Starch Synthase III and Isoamylase-Type Starch-Debranching Enzyme in Maize Endosperm. Qiuhui Lin, Binqing Huang, Xingyu Zhang, Xiaoli Zhang, Joshua Rivenbark, Ryan L. Lappe, Martha G. James, Alan M. Myers, and Tracie A. Hennen-Bierwagen

The Function of RH22, a DEAD RNA Helicase, in the Biogenesis of the 50S Ribosomal Subunits of Arabidopsis Chloroplasts. Wei Chi, Baoye He, Juan Mao, Qiannan Li, Jinfang Ma, Daili Ji, Meijuan Zou, and Lixin Zhang

Assembly of the Light-Harvesting Chlorophyll Antenna in the Green Alga Chlamydomonas reinhardtii Requires Expression of the TLA2-CpFTSY Gene. Henning Kirst, Jose Gines Garcia-Cerdan, Andreas Zurbriggen, and Anastasios Melis

Cellulose Synthase-Like D1 Is Integral to Normal Cell Division, Expansion, and Leaf Development in Maize. Charles T. Hunter, Daniel Hill Kirienko, Anne W. Sylvester, Gary F. Peter, Donald R. McCarty, and Karen E. Koch

N-3-Oxo-Decanoyl-l-Homoserine-Lactone Activates Auxin-Induced Adventitious Root Formation via Hydrogen Peroxide- and Nitric Oxide-Dependent Cyclic GMP Signaling in Mung Bean. Xuegui Bai, Christopher D. Todd, Radhika Desikan, Yongping Yang, and Xiangyang Hu

Copper Chaperone-Dependent and -Independent Activation of Three Copper-Zinc Superoxide Dismutase Homologs Localized in Different Cellular Compartments in Arabidopsis. Chien-Hsun Huang, Wen-Yu Kuo, Celeste Weiss, and Tsung-Luo Jinn

Antagonistic Interaction of BLADE-ON-PETIOLE1 and 2 with BREVIPEDICELLUS and PENNYWISE Regulates Arabidopsis Inflorescence Architecture. Madhav Khan, Mingli Xu, Jhadeswar Murmu, Paul Tabb, Yuanyuan Liu, Kathryn Storey, Sarah M. McKim, Carl J. Douglas, and Shelley R. Hepworth

An Abscisic Acid-AtNAP Transcription Factor-SAG113 Protein Phosphatase 2C Regulatory Chain for Controlling Dehydration in Senescing Arabidopsis Leaves. Kekei Zhang and Su-Sheng Gan

BIOENERGETICS AND PHOTOSYNTHESIS

CELL BIOLOGY AND SIGNAL TRANSDUCTION

DEVELOPMENT AND HORMONE ACTION
Selective Inhibition of Clade A Phosphatases Type 2C by PYR/PYL/RCAR Abscisic Acid Receptors.

ENVIRONMENTAL STRESS AND ADAPTATION TO STRESS
Recent Gene Duplication and Subfunctionalization Produced a Mitochondrial GrpE, the Nucleotide Exchange Factor of the Hsp70 Complex, Specialized in Thermotolerance to Chronic Heat Stress in Arabidopsis. Catherine Hu, Siou-ying Lin, Wen-tzu Chi, and Yee-yung Charng

Silencing MPK4 in Nicotiana attenuata Enhances Photosynthesis and Seed Production But Compromises Abscisic Acid-Induced Stomatal Closure and Guard Cell-Mediated Resistance to Pseudomonas syringae pv tomato DC3000. Christian Hettenhausen, Ian T. Baldwin, and Jianqiang Wu

Identification of a Protein Network Interacting with TdRF1, a Wheat RING Ubiquitin Ligase with a Protective Role against Cellular Dehydration. Davide Guerra, Anna Maria Mastrangelo, Gema Lopez-Torrejon, Stephan Marzin, Patrick Schweizer, Antonio Michele Stanca, Juan Carlos del Pozo, Luigi Cattivelli, and Elisabetta Mazzucotelli

Co-Overexpression FIT with AtbHLH38 or AtbHLH39 in Arabidopsis-Enhanced Cadmium Tolerance via Increased Cadmium Sequestration in Roots and Improved Iron Homeostasis of Shoots. Huilan Wu, Chunlin Chen, Juan Du, Honglei Liu, Cui Yan, Yue Zhang, Yueping He, Yaqing Wang, Chengcai Chu, Zongyun Feng, Junming Li, and Hong-Qing Ling

GENETICS, GENOMICS, AND MOLECULAR EVOLUTION
Hybrid Incompatibility in Arabidopsis Is Determined by a Multiple-Locus Genetic Network. Diana Burkart-Waco, Caroline Josefsson, Brian Diklos, Nora Kozloff, Otto Torjek, Rhonda Meyer, Thomas Altmann, and Luca Comai

Small RNA Profiling in Two Brassica napus Cultivars Identifies MicroRNAs with Oil Production- and Development-Correlated Expression and New Small RNA Classes. Ying-Tao Zhao, Meng Wang, San-Xiong Fu, Wei-Cai Yang, Cun-Kou Qi, and Xue-Jie Fang


A Reevaluation of Rice Mitochondrial Evolution Based on the Complete Sequence of Male-Fertile and Male-Sterile Mitochondrial Genomes. Stéphane Bentolila and Stefan Stefanov

Characterization of a PDK1 Homologue from the Moss Physcomitrella patens. Anna C. Nelson Dittrich and Timothy P. Devarenne

PLANTS INTERACTING WITH OTHER ORGANISMS
Descendants of Primed Arabidopsis Plants Exhibit Resistance to Biotic Stress. Ana Slaughter, Xavier Daniel, Victor Flores, Estrella Luna, Barbara Holm, and Brigitte Mauch-Mani

Next-Generation Systemic Acquired Resistance. Estrella Luna, Toby J.A. Bruce, Michael R. Roberts, Victor Flores, and Jurijan Ton

Herbivory in the Previous Generation Primes Plants for Enhanced Insect Resistance. Sergio Rasmann, Martin De Vos, Clare L. Casteel, Donglan Tian, Rayko Halitschke, Joel Y. Sun, Anurag A. Agrawal, Gary W. Felton, and Georg Jander

Differential Expression of Biphenyl Synthase Gene Family Members in Fire-Blight-Infected Apple ‘Holsteiner Cox’. Cornelia Chizzali, Marianne M. Gaid, Asma K. Belheir, Robert Hansch, Klaus Richter, Henryk Flachowsky, Andreas Peil, Magda-Viola Hanke, Benge Liu, and Ludger Beerthues

Continued on next page
A CCCH-Type Zinc Finger Nucleic Acid-Binding Protein Quantitatively Confers Resistance against Rice Bacterial Blight Disease. Hanqing Deng (邓汉卿), Hongbo Liu (刘红波), Xianghua Li (李香花), Jinghua Xiao (肖景华), and Shiping Wang (王石平) 876


A Deletion in NRT2.1 Attenuates Pseudomonas syringae-Induced Hormonal Perturbation, Resulting in Primed Plant Defenses. Gemma Camañas, Victoria Pastor, Miguel Cerezo, Javier García-Andrade, Begonya Vicedo, Pilar García-Agustín, and Victor Flors 1054

SYSTEMS BIOLOGY, MOLECULAR BIOLOGY, AND GENE REGULATION

GbPDF1 Is Involved in Cotton Fiber Initiation via the Core cis-Element HDZIP2ATATHB2. Fenglin Deng, Lili Tu, Jiafu Tan, Yang Li, Yichun Nie, and Xianlong Zhang 890

Regulation of High-Affinity Nitrate Uptake in Roots of Arabidopsis Depends Predominantly on Posttranscriptional Control of the NRT2.1/NAR2.1 Transport System. Edith Laugier, Éléonore Bouguyon, Adeline Mauries, Pascal Tillard, Alain Gojon, and Laurence Lejay 1067

CCA1 and ELF3 Interact in the Control of Hypocotyl Length and Flowering Time in Arabidopsis. Sheen X. Lu, Candace J. Webb, Stephen M. Knowles, Sally H.J. Kim, Zhiyong Wang, and Elaine M. Tobin 1079

Seasonal Abscisic Acid Signal and a Basic Leucine Zipper Transcription Factor, DkbZIP5, Regulate Proanthocyanidin Biosynthesis in Persimmon Fruit. Takashi Akagi, Ayako Katayama-Ikegami, Shozo Kobayashi, Akihiko Sato, Atsushi Kono, and Keizo Yonemori 1089

CORRECTIONS

Focus Issue on Nuclear Architecture and Dynamics. Meng Chen, Yuda Fang, Jaideep Mathur, and Wojtek Pawlowski 1103

Some figures in this article are displayed in color online but in black and white in the print edition. Indicates Web-only data. Open Access articles can be viewed online without a subscription.