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Virus-Based MicroRNA Silencing in Plants.  Aihua Sha, Jinping Zhao, Kangquan Yin, Yang Tang, Yan Wang, Xiang Wei, Yiguon Hong, and Yule Liu

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Molecular and metabolic analysis in tobacco plants after virus-induced gene silencing uncovers different pathways of amino acid biosynthesis within the plastids.

Leaf Oil Body Functions as a Subcellular Factory for the Production of a Phytoalexin in Arabidopsis. Takashi L. Shimada, Yoshitaka Takeo, Tomoo Shimada, Masayuki Fujiwara, Yoichiro Fukao, Masashi Mori, Yozo Okazaki, Kazuki Sai, Ryosuke Sasaki, Koh Aoki, and Ikuko Hara-Nishimura

Leaf oil bodies are the source of a novel phytoalexin produced in response to fungal infection and senescence.

Deletion Mutagenesis Identifies a Haploinsufficient Role for γ-Zein in opaque2 Endosperm Modification. Lingling Yuan, Yongchao Dou, Shahryar F. Kianian, Chi Zhang, and David R. Holding

A haploinsufficient role is identified for γ-zein in maize mutant endosperm modification.

Stable Carbon Isotope Discrimination Is under Genetic Control in the C₄ Species Maize with Several Genomic Regions Influencing Trait Expression. Sebastian Gresset, Peter Westermeier, Svenja Rademacher, Milena Ouzunova, Thomas Presterl, Peter Westhoff, and Chris-Carolin Schön

Multiplatform-based phenotyping and high-density genotyping uncovers multiple genomic regions controlling stable carbon isotope discrimination in a maize introgression library.


Genome-wide association analysis and spatial patterning of single-nucleotide polymorphism data guide reverse genetics to identify new genes linking stress-induced proline accumulation with cellular redox and energy status.

Feruloyl-CoA 6'-Hydroxylase1-Dependent Coumarins Mediate Iron Acquisition from Alkaline Substrates in Arabidopsis. Nicole B. Schmid, Ricardo F.H. Giehl, Stefanie Döll, Hans-Peter Mock, Nadine Strehmel, Dierk Scheel, Xiaole Kong, Robert C. Hider, and Nicolaus von Wirén

The release of F coumarins is a component of the reduction-based iron acquisition machinery that helps plants to mobilize iron under alkaline conditions.

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Characterization and Identification of cis-Regulatory Elements in Arabidopsis Based on Single-Nucleotide Polymorphism Information. Paula Korkut, Jos H.M. Schippers, and Dirk Walther

A plant homolog of a bacterial ribosome biogenesis factor functions in chloroplasts, associates with thylakoid membranes, and is involved in maturation of ribosomal RNA. Rikard Fristedt, Lars B. Scharff, Cornelia A. Clarke, Qin Wang, Chentao Lin, Subeeya S. Merchant, and Ralph Bock

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GCR1 shares the fold and key functional motifs of class A, class B, and class E G protein-coupled receptors.
Glucose Elevates NITRATE TRANSPORTER2.1 Protein Levels and Nitrate Transport Activity Independently of Its HEXOKINASE1-Mediated Stimulation of NITRATE TRANSPORTER2.1 Expression. Femke de Jong, Kate Thodney, Laurence V. Lejay, and Michael W. Bevan

Independent mechanisms link photosynthetic availability with nitrate uptake and assimilation into amino acids.

**SIGNALLING AND RESPONSE**

**[W]** Terpene Down-Regulation Triggers Defense Responses in Transgenic Orange Leading to Resistance against Fungal Pathogens. Ana Rodríguez, Takehiko Shimada, Magdalena Cervera, Berta Alquézar, José Gadea, Aurelio Gómez-Cadenas, Carlos José De Ollas, María Jesús Rodrigo, Lorenzo Zacarías, and Leandro Peña

Down-regulation of a β-limonene synthase gene in orange fruit triggers defense cascades linked to isoprenoid metabolism and resistance to necrotroph pathogens.

**[W]** Recognition of the Protein Kinase AVRPPHB SUSCEPTIBLE1 by the Disease Resistance Protein RESISTANCE TO PSEUDOMONAS SYRINGAE5 Is Dependent on S-Acylation and an Exposed Loop in AVRPPHB SUSCEPTIBLE1. Dong Qi, Ulrich Dubiella, Sang Hee Kim, D. Isaiah Sloss, Robert H. Dowen, Jack E. Dixon, and Roger W. Innes

A nucleotide-binding protein distinguishes among closely related protein kinases based on plasma membrane localization and an exposed loop in the C-terminal third of the kinase domain.

**[W]** Fungal Endopolygalacturonases Are Recognized as Microbe-Associated Molecular Patterns by the Arabidopsis Receptor-Like Protein RESPONSIVENESS TO BOTRYTIS POLYGALACTURONASES1. Lisha Zhang, Ilona Kars, Bert Essenstam, Thomas W.H. Liebrand, Lia Wagemakers, Joyce Elberse, Panagiota Tagkalaki, Devlin Tjoitang, Guido van den Ackerveken, and Jan A.L. van Kan

Fungal pectin-degrading enzymes act as microbe-associated molecular patterns that are recognized by a pattern recognition receptor from Arabidopsis.

**[W]** The Basic Leucine Zipper Transcription Factor ABSCISIC ACID RESPONSE ELEMENT-BINDING FACTOR2 Is an Important Transcriptional Regulator of Abscisic Acid-Dependent Grape Berry Ripening Processes. Philippe Nicolas, David Lecourieux, Christian Kappel, Stéphanie Cluzet, Grant Cramer, Serge Delrot, and Fatma Lecourieux

A basic leucine zipper family transcription factor is an important transcriptional regulator of abscisic acid-dependent grape berry ripening.


Analysis of genome-wide Arabidopsis responses to spider mite identifies the secondary metabolites that limit the mite’s ability to use Arabidopsis as a host.

**[W]** Regulation of Drought Tolerance by the F-Box Protein MAX2 in Arabidopsis. Qingyun Bu, Tianxiao Lv, Hui Shen, Phi Luong, Jimmy Wang, Zhenyu Wang, Zhigang Huang, Langhao Xiao, Cawas Engineer, Tae Houn Kim, Julian I. Schroeder, and Enamul Huq

An F-box protein regulates drought and osmotic stress responses in a strigolactone-independent manner in Arabidopsis.


Ligand-induced degradation of endogenous flagellin receptor desensitizes cells to its stimulus, likely to remove ligand-bound receptors from the site of perception, and subsequent de novo receptor synthesis resensitizes cells for a new round of stimulus perception.

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A nitrate-induced decline in nitrogenase activity in Medicago truncatula nodules is connected with a strong down-regulation of genes for nodule-specific cysteine-rich peptides and leghemoglobins, changes in inner cell iron allocation, and a decline in nodule respiration efficiency.

A genome-wide physical map of barley was constructed and anchored genetically by a novel method involving whole-genome resequencing of a mapping population.

Heterologous expression in plant seeds of two lipid-modifying enzymes enables a synthetic cycle that enriches for the accumulation of cyclopropane fatty acids at both sn-1 and sn-2 positions of phosphatidylcholine.

Meta-analysis of differentially expressed rice genes under different stress conditions accurately classified them using machine learning approaches and identified genes likely to confer broad resistance to multiple abiotic and biotic stresses.