Recognizing Our Authors
2009–2013

“The only source of knowledge is experience.”

Albert Einstein

At ASPB, we are privileged to publish the work of a range of authors whose scientific experience and academic leadership have helped establish our journals, *Plant Physiology* and *The Plant Cell,* as highly respected sources of knowledge for the advancement of plant science.

In 2009, we analyzed citations to our journals for papers published between 2004 and 2008 to identify our authors from around the world publishing the most influential science. Now, in 2015, we are pleased to once again thank our authors for their role in the ongoing success of *Plant Physiology* and *The Plant Cell* and invite you to celebrate them with us. This new edition of Recognizing Our Authors acknowledges authors of our most highly cited papers published between 2009 and 2013. We've begun with researchers working in North America and Europe. Soon we will add plant biologists from Asia, Australasia, Central and South America, the Middle East, and Africa. We are grateful to them, just as we are grateful to all our authors, for making *Plant Physiology* and *The Plant Cell* what they are today.

Interested in submitting your best work to *Plant Physiology* and *The Plant Cell*? Please see our Instructions for Authors for both *The Plant Cell* (http://www.plantcell.org/misc/ifora.shtml) and *Plant Physiology* (http://www.plantphysiol.org/misc/ifora.shtml).

RECOGNIZING OUR AUTHORS

Contents

Asia

Australasia

Central & South America

continued on next page

RECOGNIZING OUR AUTHORS

Contents

Central & South America *(continued)*

Europe

Middle East & Africa

continued on next page

Middle East & Africa *(continued)*

North America

BACK TO CONTENTS

Xing Wang Deng

The Plant Cell, Plant Physiology

Xing Wang Deng is a university endowed professor of plant biology at Peking University. He graduated from Peking University in 1985 with an MS degree and then from the University of California, Berkeley, in 1989 with a PhD in plant biology. He joined the faculty of Yale University's Department of Molecular, Cell and Developmental Biology in 1992.

Before moving back to China, Xing Wang was Daniel C. Eaton Professor of Yale University until 2014. He worked on plant photomorphogenesis, noncoding RNAs, heterosis, and molecular design breeding in plants. He was rewarded with the Kumho Science International Award by the International Society for Plant Molecular Biology (ISPMB) in 2003 and elected to the U.S. National Academy of Sciences in 2013.

The Plant Cell Papers

- HFR1 sequesters PIF1 to govern the transcriptional network underlying light-initiated seed germination in Arabidopsis
- Photomorphogenesis, B-Box transcription factors, and the legacy of Magnus Holm
- The PP6 phosphatase regulates ABI5 phosphorylation and abscisic acid signaling in Arabidopsis
- Arabidopsis CSN5B interacts with VTC1 and modulates ascorbic acid synthesis
- UBIQUITIN-SPECIFIC PROTEASE16 modulates salt tolerance in Arabidopsis by regulating Na^+/H^+ antiport activity and serine hydroxymethyltransferase stability
- Arabidopsis FHY3 and HY5 positively mediate induction of COP1 transcription in response to photomorphogenic UV-B Light
- A PP6-type phosphatase holoenzyme directly regulates PIN phosphorylation and auxin efflux in Arabidopsis
- Phosphorylation of FAR-RED ELONGATED HYPOCOTYL1 is a key mechanism defining signaling dynamics of Phytochrome A under red and far-red light in Arabidopsis
- Genome-wide analysis of DNA methylation and gene expression changes in two Arabidopsis ecotypes and their reciprocal hybrids
- Genome-wide binding site analysis of FAR-RED ELONGATED HYPOCOTYL3 reveals its novel function in Arabidopsis development
- Geminiviruses subvert ubiquitination by altering CSN-mediated derubylation of SCF E3 ligase complexes and inhibit jasmonate signaling in Arabidopsis thaliana
- Arabidopsis transcription factor ELONGATED HYPOCOTYL5 plays a role in the feedback regulation of Phytochrome A signaling

continued on next page

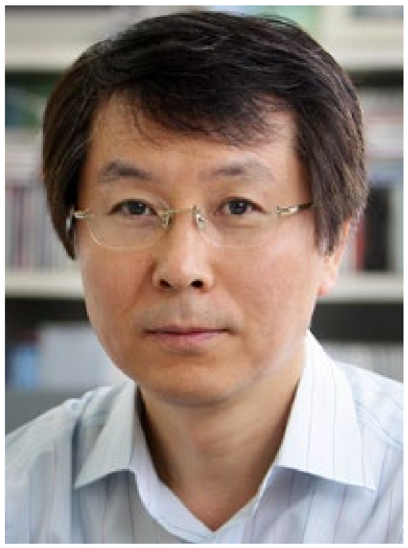
BACK TO CONTENTS

Xing Wang Deng *continued from page 1*

- DWA1 and DWA2, two Arabidopsis DWD protein components of CUL4-Based E3 ligases, act together as negative regulators in ABA signal transduction
- The Arabidopsis chaperone J3 regulates the plasma membrane H^+-ATPase through interaction with the PKS5 Kinase
- Global epigenetic and transcriptional trends among two rice subspecies and their reciprocal hybrids
- Arabidopsis CULLIN4-damaged DNA binding protein 1 interacts with CONSTITUTIVELY PHOTOMORPHOGENIC1-SUPPRESSOR OF PHYA complexes to regulate photomorphogenesis and flowering time
- Dynamic landscapes of four histone modifications during deetiolation in Arabidopsis
- Biochemical insights on degradation of Arabidopsis DELLA proteins gained from a cell-free assay system
- Genome-wide and organ-specific landscapes of epigenetic modifications and their relationships to mRNA and small RNA transcriptomes in maize
- Phytochrome A mediates rapid red light–induced phosphorylation of Arabidopsis FAR-RED ELONGATED HYPOCOTYL1 in a low fluence response

Plant Physiology **Papers**

- The COP9 signalosome: its regulation of cullin-based E3 ubiquitin ligases and role in photomorphogenesis
- Genome-wide direct target analysis reveals a role for SHORT-ROOT in root vascular patterning through cytokinin homeostasis



BACK TO CONTENTS

Inhwan Hwang

The Plant Cell, Plant Physiology

Inhwan Hwang received his BS and MS degrees from the Department of Chemistry, Seoul National University, in 1977–1981 and 1981–1983, respectively, and his PhD degree (molecular biology, adviser: Chi-Bom Chae) from the Department of Biochemistry University of North Carolina at Chapel Hill, in 1984–1988. He was a postdoc (adviser: Howard M. Goodman) at the Department of Genetics, Harvard Medical School, in 1988–1993, assistant professor in the Department of Molecular Biology, Gyeongsang National University, in 1993–1998, and associate professor in the same department in 1998–1999. Since 1999, Inhwan works as a Professor at the Department of Life Science, Pohang University of Science and Technology.

His research areas of interest are intracellular trafficking and targeting in plant cells, organelle biogenesis and communication between organelles, cellular reprogramming, development of plant cells as a bioreactor system, and ABA metabolism and signaling.

The Plant Cell Papers

- The Arabidopsis NAC transcription factor ANAC096 cooperates with bZIP-Type transcription factors in dehydration and osmotic stress responses
- Adaptor protein complex 2–Mediated endocytosis is crucial for male reproductive organ development in Arabidopsis
- The clathrin adaptor complex AP-2 mediates endocytosis of BRASSINOSTEROID INSENSITIVE1 in Arabidopsis
- Mitochondrial targeting of the Arabidopsis F1-ATPase γ-Subunit via multiple compensatory and synergistic presequence motifs
- Trafficking of vacuolar proteins: the crucial role of Arabidopsis vacuolar protein sorting 29 in recycling vacuolar sorting receptor
- A vacuolar β-Glucosidase homolog that possesses glucose-conjugated abscisic acid hydrolyzing activity plays an important role in osmotic stress responses in Arabidopsis secretory pathway
- Both the hydrophobicity and a positively charged region flanking the C-Terminal region of the transmembrane domain of signal-anchored proteins play critical roles in determining their targeting specificity to the endoplasmic reticulum or endosymbiotic organelles in Arabidopsis cells
- Phosphoinositides regulate clathrin-dependent endocytosis at the tip of pollen tubes in Arabidopsis and tobacco
- Heat Shock Protein Cognate 70-4 and an E3 Ubiquitin Ligase, CHIP, Mediate Plastid-Destined Precursor Degradation through the Ubiquitin-26S Proteasome System in Arabidopsis
- A 1-Megadalton Translocation Complex Containing Tic20 and Tic21 Mediates

continued on next page

BACK TO CONTENTS

Inhwan Hwang *continued from page 3*

Chloroplast Protein Import at the Inner Envelope Membrane

- Drought Stress-Induced Rma1H1, a RING Membrane-Anchor E3 Ubiquitin Ligase Homolog, Regulates Aquaporin Levels via Ubiquitination in Transgenic Arabidopsis Plants

Plant Physiology Papers

- Recruitment of Arf1-GDP to Golgi by Glo3p-Type ArfGAPs is crucial for Golgi maintenance and plant growth
- Functional identification of sorting receptors involved in trafficking of soluble lytic vacuolar proteins in vegetative cells of Arabidopsis
- An A/ENTH domain-containing protein functions as an adaptor for clathrin-coated vesicles on the growing cell plate in Arabidopsis root cells
- An Arabidopsis Prenylated Rab Acceptor 1 Isoform, AtPRA1.B6, displays differential inhibitory effects on anterograde trafficking of proteins at the endoplasmic reticulum
- Small heat shock protein Hsp17.8 functions as an AKR2A cofactor in the targeting of chloroplast outer membrane proteins in Arabidopsis
- Homomeric interaction of AtVSR1 is essential for its function as a vacuolar sorting receptor
- Multiple sequence motifs in the rubisco small subunit transit peptide independently contribute to Toc159-dependent import of proteins into chloroplasts
- Disruption of glycosylphosphatidylinositol-anchored lipid transfer protein gene altered cuticular lipid composition, increased plastoglobules, and enhanced susceptibility to infection by the fungal pathogen Alternaria brassicicola

BACK TO CONTENTS

Yuji Kamiya

The Plant Cell, Plant Physiology

Yuji Kamiya obtained his PhD from the University of Tokyo's Department of Agriculture in 1975 and immediately joined RIKEN. From 1980 to 1982, he studied biosynthesis of gibberellins at the University of Göttingen as an Alexander von Humboldt fellow. After returning to RIKEN, he continued to study biosynthesis of GAs together with other hormones. He was appointed head of the Plant Hormone Function Team of RIKEN from 1991 to 1998. He contributed to molecular cloning of major genes related to gibberellin biosynthesis.Yuji joined the Plant Science Center as director of the plant growth regulation research group from 2000 to March 2013. He is currently a coordinator at the RIKEN Center for Sustainable Resource Science (CSRS) and staff at the Global Relations & Research Coordination Office (April 2013).

The Plant Cell Papers

- IAA-Ala Resistant3, an evolutionarily conserved target of miR167, mediates Arabidopsis root architecture changes during high osmotic stress
- Novel plant immune-priming compounds identified via high-throughput chemical screening target salicylic acid glucosyltransferases in Arabidopsis
- The small subunit of snapdragon geranyl diphosphate synthase modifies the chain length specificity of tobacco geranylgeranyl diphosphate synthase in planta
- Autophagy negatively regulates cell death by controlling NPR1-dependent salicylic acid signaling during senescence and the innate immune response in Arabidopsis
- Genome-wide analysis of genes targeted by PHYTOCHROME INTERACTING FACTOR 3-LIKE5 during seed germination in Arabidopsis

Plant Physiology Papers

- Lignin modification leads to increased nodule numbers in alfalfa
- Basic Helix-Loop-Helix transcription factors JASMONATE-ASSOCIATED MYC2-LIKE1 (JAM1), JAM2, and JAM3 are negative regulators of jasmonate responses in Arabidopsis
- DELLA-interacting SWI3C core subunit of switch/sucrose nonfermenting chromatin remodeling complex modulates gibberellin responses and hormonal cross talk in Arabidopsis
- Increased leaf size: different means to an end
- CHOTTO1, a putative double APETALA2 repeat transcription factor, is involved in abscisic acid-mediated repression of gibberellin biosynthesis during seed germination in Arabidopsis
- High humidity induces abscisic acid 8′-hydroxylase in stomata and vasculature to regulate local and systemic abscisic acid responses in Arabidopsis
- The Arabidopsis abscisic acid catabolic gene CYP707A2 plays a key role in nitrate control of seed dormancy

BACK TO CONTENTS

Jian Feng Ma

The Plant Cell, Plant Physiology

From 2010 to present, Jian Feng Ma has been professor, unit leader, and group leader at the Institute of Plant Science and Resources, Okayama University, Japan. He holds a PhD in plant nutrition from Kyoto University and is the recipient of a number of awards, including the Japan Academy Medal (2006), the JSPS Prize (2006), the Award of the Japanese Society of Soil Science and Plant Nutrition (2007), and the Kihara Award (2012).

The goal of his lab is to improve productivity and safety of crops with a focus on plant mineral stress tolerance and mineral transport systems in plants. His group has identified a number of Al tolerance genes in rice and barley and recently elucidated the mechanisms regulating the expression of Al-tolerance genes. Many genes involved in uptake, translocation, distribution, and redistribution of mineral nutrients including Fe, Zn, Cu, Mn, and Si have been identified in rice and other plants. Furthermore, transporters for toxic elements such as As and Cd have also been identified.

The Plant Cell Papers

- YSL16 is a phloem-localized transporter of the copper-nicotianamine complex that is responsible for copper distribution in rice
- Nramp5 is a major transporter responsible for manganese and cadmium uptake in rice
- A zinc finger transcription factor ART1 regulates multiple genes implicated in aluminum tolerance in rice
- A transporter at the node responsible for intervascular transfer of silicon in rice
- Identification and characterization of maize and barley Lsi2-like silicon efflux transporters reveals a distinct silicon uptake system from that in rice
- A bacterial-type ABC transporter is involved in aluminum tolerance in rice

Plant Physiology Papers

- A member of the Heavy Metal P-Type ATPase OsHMA5 is involved in xylem loading of copper in rice
- TWIN SISTER OF FT, GIGANTEA, and CONSTANS have a positive but indirect effect on blue light-induced stomatal opening in Arabidopsis
- Preferential delivery of zinc to developing tissues in rice is mediated by P-Type Heavy Metal ATPase OsHMA2
- Functional characterization of a silicon transporter gene implicated in silicon distribution in barley
- Up-regulation of a magnesium transporter gene OsMGT1 is required for conferring aluminum tolerance in rice

continued on next page

BACK TO CONTENTS

Jian Feng Ma *continued from page 6*

- OsYSL6 is involved in the detoxification of excess manganese in rice
- High-resolution secondary ion mass spectrometry reveals the contrasting subcellular distribution of arsenic and silicon in rice roots
- Identification of a cis-acting element of ART1, a C2H2-type zinc-finger transcription factor for aluminum tolerance in rice
- Knockout of a bacterial-type ATP-binding cassette transporter gene, AtSTAR1, results in increased aluminum sensitivity in Arabidopsis
- Involvement of silicon influx transporter OsNIP2;1 in selenite uptake in rice
- The rice aquaporin Lsi1 mediates uptake of methylated arsenic species
- OsFRDL1 is a citrate transporter required for efficient translocation of iron in rice

BACK TO CONTENTS

Kazuki Saito

The Plant Cell, Plant Physiology

Kazuki Saito is deputy director of the RIKEN Center for Sustainable Resource Science, where he is also group director of the Metabolomics Research Group. He is also a professor in the Graduate School of Pharmaceutical Sciences at Chiba University.

As an expert in plant metabolomics and functional genomics, Kazuki has contributed to a number of journals, conferences, and advisory boards. He was awarded the Prize for Science and Technology (Research Category) by the Minister of Education, Culture, Sports, Science and Technology, Japan, in 2010, and named a highly cited researcher by Thomson Reuters in 2014 in the Plant and Animal Science field.

Kazuki's current research aims to understand the mechanism and regulation of plant metabolism through functional genomics approaches and subsequently to apply the obtained knowledge to biotechnology.

The Plant Cell Papers

- Lysine decarboxylase catalyzes the first step of quinolizidine alkaloid biosynthesis and coevolved with alkaloid production in leguminosae
- Triterpene functional genomics in licorice for identification of CYP72A154 involved in the biosynthesis of glycyrrhizin
- Pause-and-Stop: The effects of osmotic stress on cell proliferation during early leaf development in Arabidopsis and a role for ethylene signaling in cell cycle arrest
- Members of the LBD family of transcription factors repress anthocyanin synthesis and affect additional nitrogen responses in Arabidopsis
- A Chloroplastic UDP-Glucose Pyrophosphorylase from Arabidopsis is the committed enzyme for the first step of sulfolipid biosynthesis
- Disruption of Adenosine-5'-Phosphosulfate Kinase in Arabidopsis reduces levels of sulfated secondary metabolites

Plant Physiology Papers

- Exploring tomato gene functions based on coexpression modules using graph clustering and differential coexpression approaches
- Metabolomics of a Single Vacuole Reveals Metabolic Dynamism in an alga Chara australis
- Application of gene targeting to designed mutation breeding of high-tryptophan rice
- AtMetExpress development: a phytochemical atlas of Arabidopsis development
- Metabolic pathways involved in cold acclimation identified by integrated analysis of metabolites and transcripts regulated by DREB1A and DREB2A

BACK TO CONTENTS

Hitoshi Sakakibara

The Plant Cell, Plant Physiology

Hitoshi Sakakibara received his doctor of agriculture from the Graduate School of Agricultural Sciences, Nagoya University. He is currently group director, Plant Productivity Systems Research Group, RIKEN Center for Sustainable Resource Science, where his group conducts studies on uptake and signaling of nitrogen, action mechanisms of phytohormones, and mechanisms of metal tolerance and accumulation to aim for development of innovation technology for low-input production of plants by saving nitrogen and water, and recovery and recycling of metals. The group also conducts studies for discovery of novel signaling molecules and key genes for plant productivity by using hormonome platform.

Hitoshi was awarded the J.S.P.P. Young Investigator Award (Japanese Society of Plant Physiologists, 2004), the Olchemim Award (Olchemim Co. Ltd, 2009), the JSPS Prize (Japanese Society for the Promotion of Science, 2010), and the Kihara Memorial Foundation Special Award (2010).

The Plant Cell Papers

- WUSCHEL-RELATED HOMEOBOX4 is involved in meristem maintenance and is negatively regulated by the CLE gene FCP1 in rice
- The Arabidopsis nitrate transporter NRT2.4 plays a double role in roots and shoots of nitrogen-starved plants
- The COP1 Ortholog PPS regulates the juvenile–adult and vegetative–reproductive phase changes in rice
- Analysis of cytokinin mutants and regulation of cytokinin metabolic genes reveals important regulatory roles of cytokinins in drought, salt and abscisic acid responses, and abscisic acid biosynthesis
- LIGHT-REGULATED WD1 and PSEUDO-RESPONSE REGULATOR9 form a positive feedback regulatory loop in the Arabidopsis circadian clock
- PSEUDO-RESPONSE REGULATORS 9, 7, and 5 are transcriptional repressors in the Arabidopsis circadian clock
- Functional analyses of LONELY GUY cytokinin-activating enzymes reveal the importance of the direct activation pathway in Arabidopsis

Plant Physiology Papers

- Cytokinin activity of cis-zeatin and phenotypic alterations induced by overexpression of putative cis-Zeatin-O-glucosyltransferase in rice
- Agrobacterium tumefaciens tumor morphology root plastid localization and preferential usage of hydroxylated prenyl donor is important for efficient gall formation
- Genome-wide direct target analysis reveals a role for SHORT-ROOT in root vascular patterning through cytokinin homeostasis

continued on next page

BACK TO CONTENTS

Hitoshi Sakakibara *continued from page 9*

- WAVY LEAF1, an ortholog of Arabidopsis HEN1, regulates shoot development by maintaining microRNA and trans-acting small interfering RNA accumulation in rice
- Involvement of auxin and brassinosteroid in the regulation of petiole elongation under the shade
- Studies of aberrant phyllotaxy1 mutants of maize indicate complex interactions between auxin and cytokinin signaling in the shoot apical meristem

BACK TO CONTENTS

Kazuo Shinozaki

The Plant Cell, Plant Physiology

Kazuo Shinozaki has been director of the RIKEN Center for Sustainable Resource Science since 2013. His main research area is functional genomics in plant environmental stress response and tolerance. He earned his PhD at Nagoya University and was appointed research associate of the National Institute of Genetics. He became an associate professor at Nagoya University, where he determined the nucleotide sequence of the tobacco chloroplast genome in 1986. He was appointed chief scientist of the Plant Molecular Biology Laboratory, RIKEN, in 1989, undertaking pioneering research on the regulatory gene network governing plant abiotic stress responses in Arabidopsis. He became project director of the Plant Functional Genomics Group at RIKEN Genomic Sciences Center in 1999 and was appointed director of the RIKEN Plant Science Center in 2005. He has been a highly cited scientist in the Plant and Animal Science section of the Web of Science since 2007.

The Plant Cell Papers

- Osmotic stress responses and plant growth controlled by potassium transporters in Arabidopsis
- Arabidopsis GROWTH-REGULATING FACTOR7 functions as a transcriptional repressor of abscisic acid– and osmotic stress–responsive genes, including DREB2A
- Analysis of cytokinin mutants and regulation of cytokinin metabolic genes reveals important regulatory roles of cytokinins in drought, salt and abscisic acid responses, and abscisic acid biosynthesis
- TCP transcription factors regulate the activities of ASYMMETRIC LEAVES1 and miR164, as well as the auxin response, during differentiation of leaves in Arabidopsis
- Pentatricopeptide repeat proteins with the DYW motif have distinct molecular functions in RNA editing and RNA cleavage in Arabidopsis chloroplasts

Plant Physiology Papers

- OsTZF1, a CCCH-tandem zinc finger protein, confers delayed senescence and stress tolerance in rice by regulating stress-related genes
- GmDREB2A;2, a canonical DEHYDRATION-RESPONSIVE ELEMENT-BINDING PROTEIN2-type transcription factor in soybean, is posttranslationally regulated and mediates -dependent gene expression
- Cooperative function of PLDδ and PLDα1 in abscisic acid-induced stomatal closure in Arabidopsis
- SPINDLY, a negative regulator of gibberellic acid signaling, is involved in the plant abiotic stress response
- Arabidopsis Cys2/His2 zinc-finger proteins AZF1 and AZF2 negatively regulate abscisic acid-repressive and auxin-inducible genes under abiotic stress conditions

continued on next page

BACK TO CONTENTS

Kazuo Shinozaki *continued from page 11*

- MCA1 and MCA2 that mediate Ca^{2+} uptake have distinct and overlapping roles in Arabidopsis
- The phytochrome-interacting factor PIF7 negatively regulates DREB1 expression under circadian control in Arabidopsis
- Metabolic pathways involved in cold acclimation identified by integrated analysis of metabolites and transcripts regulated by DREB1A and DREB2A
- TriFLDB: a database of clustered full-length coding sequences from triticeae with applications to comparative grass genomics
- STOP1 regulates multiple genes that protect Arabidopsis from proton and aluminum toxicities

BACK TO CONTENTS

Naoki Yamaji

The Plant Cell, Plant Physiology

Naoki Yamaji is currently associate professor at the Institute of Plant Science and Resources, Okayama University, Japan. He holds a PhD in Plant Molecular Biology from Kagawa University, Japan.

Naoki's research focuses on two topics: plant tolerance to ion aluminum toxicity in acidic soils, and silicon transport from roots to leaves. Regarding aluminum toxicity, Yamaji and his collaborators identified a key transcription factor, *ART1*, which governs the expression of aluminum response genes in rice. Among the downstream tolerance mechanisms impacted by *ART1* expression is the unique bacterial-type ABC transporter complex, STAR1-STAR2, which contributes significantly to aluminum tolerance.

Yamaji's recent work on mineral uptake and distribution has highlighted the importance of intervascular transport in shoot nodes. In particular, he identified Lsi6, a silicic acid channel in rice, as the first example of a transporter involved in intervascular transfer of nutrients in nodes. In addition to his work on silicic acid transport, Yamaji and his collaborators have, to date, also identified transporters involved in the preferential distribution of Zn, Cd, Mn and Cu.

The Plant Cell Papers

- YSL16 is a phloem-localized transporter of the copper-nicotianamine complex that is responsible for copper distribution in rice
- Nramp5 is a major transporter responsible for manganese and cadmium uptake in rice
- A zinc finger transcription factor ART1 regulates multiple genes implicated in aluminum tolerance in rice
- A transporter at the node responsible for intervascular transfer of silicon in rice
- Identification and characterization of maize and barley Lsi2-like silicon efflux transporters reveals a distinct silicon uptake system from that in rice
- A bacterial-type ABC transporter is involved in aluminum tolerance in rice

Plant Physiology Papers

- A member of the Heavy Metal P-Type ATPase OsHMA5 is involved in xylem loading of copper in rice
- Preferential delivery of zinc to developing tissues in rice is mediated by P-Type Heavy Metal ATPase OsHMA2
- Functional characterization of a silicon transporter gene implicated in silicon distribution in barley
- Up-regulation of a magnesium transporter gene OsMGT1 is required for conferring aluminum tolerance in rice

continued on next page

BACK TO CONTENTS

Naoki Yamaji *continued from page 13*

- OsYSL6 is involved in the detoxification of excess manganese in rice
- Identification of a Cis-Acting Element of ART1, a C2H2-type zinc-finger transcription factor for aluminum tolerance in rice
- Knockout of a bacterial-type ATP-binding cassette transporter gene, AtSTAR1, results in increased aluminum sensitivity in Arabidopsis
- Involvement of silicon influx transporter OsNIP2;1 in selenite uptake in rice

BACK TO CONTENTS

Dabing Zhang

The Plant Cell, Plant Physiology

Dabing Zhang is currently vice dean of the School of Life Sciences and Biotechnology, Shanghai Jiao Tong University (SJTU). He has made remarkable contributions in the biological study of the reproduction and development of rice that have been widely recognized and highly praised by his counterparts worldwide. His research revealed important mechanisms of rice inflorescence, floral organ, and pollen development. That work has had great significance in protecting food safety around the globe. His group discovered pathways such as the regulatory cascade consisting of three basic helix-loop-helix transcription factors – TDR INTERACTING PROTEIN2, Tapetum Degeneration Retardation (TDR), ETERNAL TAPETUM 1 – in controlling anther morphogenesis.

Dabing has been selected for various honors, including distinguished professor at SJTU (2008 to present) and Yangtse River Scholar of Ministry of Education (2009 to present). In 2004 and 2013, he was awarded the Shanghai Nature and Science Peony Prize. He holds a PhD in plant molecular genetics from Shanghai Institute of Plant Physiology (SIPP), Chinese Academy of Sciences (CAS) and he was awarded an honorary doctorate of sciences from the University of Adelaide in 2014.

The Plant Cell Papers

- Functional analysis of all AGAMOUS subfamily members in rice reveals their roles in reproductive organ identity determination and meristem determinacy
- Rice MADS6 interacts with the floral homeotic genes SUPERWOMAN1, MADS3, MADS58, MADS13, and DROOPING LEAF in specifying floral organ identities and meristem fate
- Defective Pollen Wall is required for anther and microspore development in rice and encodes a fatty acyl carrier protein reductase
- Rice MADS3 regulates ROS homeostasis during late anther development
- RICE MORPHOLOGY DETERMINANT encodes the Type II Formin FH5 and regulates rice morphogenesis
- Carbon Starved Anther encodes a MYB domain protein that regulates sugar partitioning required for rice pollen development
- The ABORTED MICROSPORES regulatory network is required for postmeiotic male reproductive development in Arabidopsis thaliana
- Cytochrome P450 family member CYP704B2 Catalyzes the ω -Hydroxylation of fatty acids and is required for anther cutin biosynthesis and pollen exine formation in rice

Plant Physiology Papers

- Rice GLYCOSYLTRANSFERASE1 encodes a glycosyltransferase essential for pollen wall formation

continued on next page

BACK TO CONTENTS

Dabing Zhang *continued from page 15*

- ANAP: an integrated knowledge base for Arabidopsis protein interaction network analysis
- Transcriptional regulation of Arabidopsis MIR168a and ARGONAUTE1 homeostasis in abscisic acid and abiotic stress responses
- Male Sterile2 encodes a plastid-localized fatty acyl carrier protein reductase required for pollen exine development in Arabidopsis
- PERSISTENT TAPETAL CELL1 encodes a PHD-finger protein that is required for tapetal cell death and pollen development in rice
- Genetic interaction of OsMADS3, DROOPING LEAF, and OsMADS13 in specifying rice floral organ identities and meristem determinacy
- OsC6, encoding a lipid transfer protein, is required for postmeiotic anther development in rice
- The SEPALLATA-like gene OsMADS34 is required for rice inflorescence and spikelet development
- RETARDED PALEA1 controls palea development and floral zygomorphy in rice

BACK TO CONTENTS

Christine Beveridge

The Plant Cell, Plant Physiology

Christine Beveridge studied plant development for her PhD at the University of Tasmania and continued her work at the Institut National de la Recherche Agronomique (INRA), Versailles, and then at The University of Queensland, where she currently leads the Plant Development Lab (part of the School of Biological Sciences). She is president of the International Plant Growth Substances Association (IPGSA, 2013–2016) and fellow of the Australian Academy of Sciences.

Christine's main area of interest is the role plant hormones and other mobile chemicals play in the regulation and coordination of plant development. Her major contribution has been on the plant hormone strigolactone and on the process of shoot branching. Her recent work has introduced the concept that sugars, presumably sucrose, act as a long-distance signal in axillary bud release.

The Plant Cell Papers

- Computational modeling and molecular physiology experiments reveal new insights into shoot branching in pea

Plant Physiology Papers

- Strigolactones stimulate internode elongation independently of gibberellins
- Strigolactones are involved in root response to low phosphate conditions in Arabidopsis
- The Arabidopsis ortholog of rice DWARF27 acts upstream of MAX1 in the control of plant development by strigolactones
- Strigolactones suppress adventitious rooting in Arabidopsis and pea
- Antagonistic action of strigolactone and cytokinin in bud outgrowth control
- Pea has its tendrils in branching discoveries spanning a century from auxin to strigolactones
- Interactions between auxin and strigolactone in shoot branching control
- Strigolactone acts downstream of auxin to regulate bud outgrowth in pea and Arabidopsis
- Roles for auxin, cytokinin, and strigolactone in regulating shoot branching

BACK TO CONTENTS

Philip Brewer

Plant Physiology

Philip Brewer completed his PhD on a gene that controls Arabidopsis floral organ formation and patterning in the lab of David Smyth, who is one of the pioneers of Arabidopsis developmental genetics. Prior to that, Philip was a secondary school teacher. After his PhD work at Monash University, he worked as a postdoc unraveling the connection between PIN proteins and auxin transport in the lab of Jiri Friml at Tuebingen University in Germany. He then returned to Australia to work as a postdoc in the lab of Christine Beveridge at the University of Queensland. He was part of a team who discovered strigolactones as a novel plant hormone class that inhibits lateral branching, and is now focused on gene discovery in the strigolactone pathway, other plant processes that are regulated by strigolactones, how the different types of strigolactones are made in plants, and the crosstalk between auxin and strigolactones.

Philip hopes that by studying the actions of plant hormones on meristematic regions of plants, we can understand how plant growth can be manipulated, which will provide us with new knowledge and tools to adapt and optimize plant productivity.

Plant Physiology Papers

- Strigolactones are involved in root response to low phosphate conditions in Arabidopsis
- The Arabidopsis ortholog of rice DWARF27 acts upstream of MAX1 in the control of plant development by strigolactones
- Strigolactones suppress adventitious rooting in Arabidopsis and pea
- Strigolactone acts downstream of auxin to regulate bud outgrowth in pea and Arabidopsis

BACK TO CONTENTS

Matthew Gilliham

The Plant Cell, Plant Physiology

Matthew Gilliham is an Australian Research Council (ARC) future fellow and a chief investigator of the ARC Centre of Excellence in Plant Energy Biology within the School of Agriculture, Food and Wine, University of Adelaide, Australia.

Matthew's research focuses on characterizing salinity tolerance mechanisms in crop and model plants, especially those related to membrane transport of Na^+ and Cl^-; the regulation of membrane transport systems by plant energy status, and C:N balance; the mechanisms of cell-specific nutrient storage; and the use of knowledge gained from the above in breeding programs to improve crop nutrient use efficiency and abiotic stress tolerance.

Matthew earned his BSc (Hons) in ecology at the University of Lancaster and his PhD in plant science from the University of Cambridge, both in the United Kingdom.

The Plant Cell Papers

- Cell-specific vacuolar calcium storage mediated by CAX1 regulates apoplastic calcium concentration, gas exchange, and plant productivity in Arabidopsis
- Shoot Na^+ exclusion and increased salinity tolerance engineered by cell type–specific alteration of Na^+ transport in Arabidopsis

Plant Physiology Papers

- Channel-like characteristics of the low-affinity barley phosphate transporter PHT1;6 when expressed in Xenopus oocytes
- The role of plasma membrane intrinsic protein aquaporins in water transport through roots: diurnal and drought stress responses reveal different strategies between isohydric and anisohydric cultivars of grapevine

BACK TO CONTENTS

Harvey Millar

The Plant Cell, Plant Physiology

Harvey Millar is the director of the ARC Centre of Excellence in Plant Energy Biology in Australia and an ARC Future Fellow at The University of Western Australia, Perth. He earned his PhD in biochemistry and molecular biology from the Australian National University in Canberra and held postdoctoral research fellows in the Department of Plant Sciences at the University of Oxford, UK, and in the School of Chemistry and Biochemistry at The University of Western Australia.

His research focuses on plant proteomics and plant respiration. Using rice, wheat, barley, and Arabidopsis, he has provided insight into mitochondrial biogenesis and function, the mitochondrial proteome and genome, mitochondrial transport, and the proteomics of stress responses and protein turnover in plants. The long-term goal of this research is to improve the energy efficiency of plants by modifying their metabolism and respiration.

Harvey's honors and awards include ISI Highly Cited Researcher; Thomson Reuters ISI – Plant and Animal Sciences; ASPB's Charles Albert Shull Award; the Fenner Medal for Biology, Australian Academy of Science; the Australian Science Minister's Prize for Life Scientist of the Year; the Premier's Prize for Early Career Achievement in Science; and the Peter Goldacre Medal, Australian Society of Plant Scientists. Harvey is a member of the editorial board of *The Plant Cell* and *The Arabidopsis Book* (TAB), among other journals.

The Plant Cell Papers

- TCP transcription factors link the regulation of genes encoding mitochondrial proteins with the circadian clock in *Arabidopsis thaliana*
- Phage-type RNA polymerase RPOTmp performs gene-specific transcription in mitochondria of *Arabidopsis thaliana*
- Exploring the function-location nexus: using multiple lines of evidence in defining the subcellular location of plant proteins

Plant Physiology Papers

- Loss of Lon1 in Arabidopsis changes the mitochondrial proteome leading to altered metabolite profiles and growth retardation without an accumulation of oxidative damage
- Nucleotide and RNA metabolism prime translational initiation in the earliest events of mitochondrial biogenesis during Arabidopsis germination
- Multiple lines of evidence localize signaling, morphology, and lipid biosynthesis machinery to the mitochondrial outer membrane of Arabidopsis
- Differential molecular responses of rice and wheat coleoptiles to anoxia reveal novel metabolic adaptations in amino acid metabolism for tissue tolerance

continued on next page

BACK TO CONTENTS

Harvey Millar *continued from page 20*

- MASCP Gator: an aggregation portal for the visualization of Arabidopsis proteomics data
- Mitochondrial malate dehydrogenase lowers leaf respiration and alters photorespiration and plant growth in Arabidopsis
- Analysis of the rice mitochondrial carrier family reveals anaerobic accumulation of a basic amino acid carrier involved in arginine metabolism during seed germination
- Divalent metal ions in plant mitochondria and their role in interactions with proteins and oxidative stress-induced damage to respiratory function
- Remodeled respiration in ndufs4 with low phosphorylation efficiency suppresses Arabidopsis germination and growth and alters control of metabolism at night
- Defining core metabolic and transcriptomic responses to oxygen availability in rice embryos and young seedlings
- Refining the definition of plant mitochondrial presequences through analysis of sorting signals, N-terminal modifications, and cleavage motifs
- Experimental analysis of the rice mitochondrial proteome, its biogenesis, and heterogeneity
- Mapping metabolic and transcript temporal switches during germination in rice highlights specific transcription factors and the role of RNA instability in the germination process
- Differential response of gray poplar leaves and roots underpins stress adaptation during hypoxia

BACK TO CONTENTS

Reena Narsai

The Plant Cell, Plant Physiology

Reena Narsai was awarded her PhD with distinction from The University of Western Australia in late 2010. She then did postdoctoral research at the ARC Centre of Excellence in Plant Energy Biology and Centre for Computational Systems Biology at The University of Western Australia until the end of 2013. In 2014, she began work as a research fellow within the Centre for Agribioscience at La Trobe University, where she is currently based.

Reena's work investigates the molecular responses during seed germination in rice and Arabidopsis. Her research has revealed some of the earliest molecular events occurring during germination, unveiling a link between mitochondrial biogenesis and the progression of seed germination and identifying genes that are only transiently expressed for a brief period to drive germination in the plant life cycle. Additionally, her work in rice has uncovered the role of oxygen in the molecular events occurring during seed germination.

The Plant Cell Papers

- Dual location of the mitochondrial preprotein transporters B14.7 and Tim23-2 in Complex I and the TIM17:23 Complex in Arabidopsis links mitochondrial activity and biogenesis.

Plant Physiology Papers

- AtWRKY40 and AtWRKY63 Modulate the Expression of Stress-Responsive Nuclear Genes Encoding Mitochondrial and Chloroplast Proteins
- Identification of a dual-targeted protein belonging to the mitochondrial carrier family that is required for early leaf development in rice
- Nucleotide and RNA metabolism prime translational initiation in the earliest events of mitochondrial biogenesis during Arabidopsis germination
- Multiple lines of evidence localize signaling, morphology, and lipid biosynthesis machinery to the mitochondrial outer membrane of Arabidopsis
- In depth temporal transcriptome profiling reveals a crucial developmental switch with roles for RNA processing and organelle metabolism that are essential for germination in Arabidopsis
- Analysis of the rice mitochondrial carrier family reveals anaerobic accumulation of a basic amino acid carrier involved in arginine metabolism during seed germination
- Physiological and transcriptome analysis of iron and phosphorus interaction in rice seedlings
- Defining core metabolic and transcriptomic responses to oxygen availability in rice embryos and young seedlings

continued on next page

BACK TO CONTENTS

Reena Narsai *continued from page 22*

- Experimental analysis of the rice mitochondrial proteome, its biogenesis, and heterogeneity
- Mapping metabolic and transcript temporal switches during germination in rice highlights specific transcription factors and the role of RNA instability in the germination process.

BACK TO CONTENTS

Barry Pogson

The Plant Cell, Plant Physiology

Barry Pogson is deputy director of the ARC Centre of Excellence in Plant Energy Biology; senior editor, *The Plant Cell*; deputy editor *Science Advances* and professor of plant biology at The Australian National University. He has conducted pioneering work on signaling between chloroplasts and nuclei. Among his heralded discoveries are a chloroplast-to-nucleus signaling pathway that underlies drought tolerance and an epigenetic regulator of carotenoid accumulation.

He is at the forefront of genetic investigations into carotenoid biosynthesis and chloroplast retrograde signaling and their impacts on plant biology and human nutrition. A particular emphasis is on how the energy organelles sense the environment and initiate plant responses to coordinate growth, development, and acclimation to abiotic stress. Barry and members of his group have received national awards for their research and teaching, including the Fenner Medal (Australian Academy of Science) and the Peter Goldacre Medal (Australian Society of Plant Scientists).

The Plant Cell Papers

- Evidence for a SAL1-PAP chloroplast retrograde pathway that functions in drought and high light signaling in Arabidopsis
- The cytoskeleton and the peroxisomal-targeted SNOWY COTYLEDON3 Protein are required for chloroplast development in Arabidopsis
- Arabidopsis tRNA adenosine deaminase arginine edits the wobble nucleotide of chloroplast tRNA^{Arg}(ACG) and is essential for efficient chloroplast translation
- Exploring the function-location nexus: using multiple lines of evidence in defining the subcellular location of plant proteins
- Regulation of carotenoid composition and shoot branching in Arabidopsis by a chromatin modifying histone methyltransferase, SDG8

Plant Physiology Papers

- A novel proteinase, SNOWY COTYLEDON4, is required for photosynthetic acclimation to higher light intensities in Arabidopsis
- Decreased photochemical efficiency of photosystem ii following sunlight exposure of shade-grown leaves of avocado: because of, or in spite of, two kinetically distinct xanthophyll cycles?
- Lutein from deepoxidation of lutein epoxide replaces zeaxanthin to sustain an enhanced capacity for nonphotochemical chlorophyll fluorescence quenching in avocado shade leaves in the dark
- Remodeled respiration in ndufs4 with low phosphorylation efficiency suppresses Arabidopsis germination and growth and alters control of metabolism at night
- De novo synthesis and degradation of Lx and V Cycle pigments during shade and sun acclimation in avocado leaves

BACK TO CONTENTS

Ian Small

The Plant Cell, Plant Physiology

Ian Small's PhD at Edinburgh University (awarded in 1988) was followed by a career with France's National Agronomy Research Institute (INRA). He was awarded a Western Australia State Premier's Research Fellowship and moved to Perth to become the director of the Australian Research Council Centre of Excellence in Plant Energy Biology early in 2006. Ian was named Western Australia Scientist of the Year in 2014 and elected a fellow of the Australian Academy of Science in 2015. His research has focused on mitochondrial and chloroplast genomes, their expression, and their role in energy production and signaling within plants. He is perhaps best known for the discovery and characterization of the pentatricopeptide repeat (PPR) family of proteins, a huge family of RNA-binding proteins involved in controlling organelle gene expression. His current research builds on the discovery of how these proteins recognize nucleic acid sequences to design custom RNA processing tools.

The Plant Cell Papers

- Arabidopsis chloroplast RNA binding proteins CP31A and CP29A associate with large transcript pools and confer cold stress tolerance by influencing multiple chloroplast RNA processing steps
- Two interacting proteins are necessary for the editing of the NdhD-1 Site in Arabidopsis plastids
- Mutations in an Arabidopsis mitochondrial transcription termination factor–related protein enhance thermotolerance in the absence of the major molecular chaperone HSP101
- An Arabidopsis dual-localized pentatricopeptide repeat protein interacts with nuclear proteins involved in gene expression regulation
- The cytoskeleton and the peroxisomal-targeted SNOWY COTYLEDON3 protein are required for chloroplast development in Arabidopsis
- A study of new Arabidopsis chloroplast RNA editing mutants reveals general features of editing factors and their target sites
- Phage-Type RNA polymerase RPOTmp performs gene-specific transcription in mitochondria of *Arabidopsis thaliana*
- Arabidopsis tRNA adenosine deaminase arginine edits the wobble nucleotide of chloroplast tRNA^{Arg}(ACG) and is essential for efficient chloroplast translation
- Pentatricopeptide repeat proteins with the DYW motif have distinct molecular functions in RNA editing and RNA cleavage in Arabidopsis chloroplasts

Plant Physiology Papers

- Nucleotide and RNA metabolism prime translational initiation in the earliest events of mitochondrial biogenesis during Arabidopsis germination
- Remodeled respiration in ndufs4 with low phosphorylation efficiency suppresses Arabidopsis germination and growth and alters control of metabolism at night

BACK TO CONTENTS

Nicolas Taylor

The Plant Cell, Plant Physiology

Nicolas Taylor earned his MSc from Massey University (1999, New Zealand) and his PhD in plant biochemistry from The University of Western Australia (2004). He worked as a postdoc (2005–2006) at Oxford University before he moved to the ARC Centre of Excellence in Plant Energy Biology (Perth, Western Australia) in 2006. He is currently an ARC future fellow at the ARC Centre of Excellence in Plant Energy Biology and the School of Chemistry and Biochemistry at The University of Western Australia.

Nic's research focuses on understanding the metabolic mechanisms that underpin thermal and salinity stress/acclimation in both Arabidopsis and wheat. His areas of expertise include protein and metabolite mass spectrometry and the integration of proteomic and metabolic data into metabolic networks.

The Plant Cell Papers

- Arabidopsis tRNA adenosine deaminase arginine edits the wobble nucleotide of chloroplast tRNA^{Arg}(ACG) and is essential for efficient chloroplast translation
- The pentatricopeptide repeat gene OTP43 is required for trans-splicing of the mitochondrial nad1 intron 1 in Arabidopsis thaliana

Plant Physiology Papers

- Selected reaction monitoring to determine protein abundance in Arabidopsis using the Arabidopsis proteotypic predictor
- Nucleotide and RNA metabolism prime translational initiation in the earliest events of mitochondrial biogenesis during Arabidopsis germination
- Multiple lines of evidence localize signaling, morphology, and lipid biosynthesis machinery to the mitochondrial outer membrane of Arabidopsis
- Differential molecular responses of rice and wheat coleoptiles to anoxia reveal novel metabolic adaptations in amino acid metabolism for tissue tolerance
- Analysis of the rice mitochondrial carrier family reveals anaerobic accumulation of a basic amino acid carrier involved in arginine metabolism during seed germination
- Disruption of ptLPD1 or ptLPD2, genes that encode isoforms of the plastidial lipoamide dehydrogenase, confers arsenate hypersensitivity in Arabidopsis
- Divalent metal ions in plant mitochondria and their role in interactions with proteins and oxidative stress-induced damage to respiratory function
- Refining the definition of plant mitochondrial presequences through analysis of sorting signals, n-terminal modifications, and cleavage motifs
- Experimental analysis of the rice mitochondrial proteome, its biogenesis, and heterogeneity

BACK TO CONTENTS

Stephen Tyerman

The Plant Cell, Plant Physiology

Stephen Tyerman has researched nutrition, salinity, and water relations in plants. He has received several awards for his plant physiology research and was elected as a fellow of the Australian Academy of Science in 2003. He is currently head of the Department of Plant Science at the University of Adelaide and a chief investigator in the Australian Research Council Centre of Excellence in Plant Energy Biology, running a node of the Centre at the University of Adelaide. Steve earned his BSc (Hons) and his PhD from the University of Sydney. He is an associate editor for *Plant Cell and Environment* and *Functional Plant Biology*. He has also served as associate editor for *Plant Physiology*.

The Plant Cell Papers

- Cell-specific vacuolar calcium storage mediated by CAX1 regulates apoplastic calcium concentration, gas exchange, and plant productivity in Arabidopsis

Plant Physiology Papers

- Transposon-mediated alteration of TaMATE1B expression in wheat confers constitutive citrate efflux from root apices
- Boron toxicity tolerance in barley through reduced expression of the multifunctional aquaporin HvNIP2;1
- Channel-like characteristics of the low-affinity barley phosphate transporter PHT1;6 when expressed in xenopus oocytes
- Roles of morphology, anatomy, and aquaporins in determining contrasting hydraulic behavior of roots
- The role of plasma membrane intrinsic protein aquaporins in water transport through roots: diurnal and drought stress responses reveal different strategies between isohydric and anisohydric cultivars of grapevine

BACK TO CONTENTS

Olivier Van Aken

The Plant Cell, Plant Physiology

Olivier Van Aken obtained his PhD at Ghent University (Belgium) in the Flemish Institute for Biotechnology (VIB, Plant Systems Biology). He then moved to the ARC Centre of Excellence in Plant Energy Biology at The University of Western Australia, where he obtained an ARC Australian postdoctoral fellowship in 2010 and became research assistant professor in 2012.

Olivier's research is focused on how mitochondria and chloroplasts impact on environmental stress sensing and resistance. He is particularly interested in how these energy organelles operate as hubs during retrograde signaling and in the underlying transcriptional network. His work has resulted in the identification of several genes with roles in drought and pathogen resistance.

The Plant Cell Papers

- A membrane-bound NAC transcription factor, ANAC017, mediates mitochondrial retrograde signaling in Arabidopsis
- The membrane-bound NAC transcription factor ANAC013 functions in mitochondrial retrograde regulation of the oxidative stress response in Arabidopsis
- TCP transcription factors link the regulation of genes encoding mitochondrial proteins with the circadian clock in Arabidopsis thaliana
- Perturbation of indole-3-butyric acid homeostasis by the UDP-glucosyltransferase UGT74E2 modulates Arabidopsis architecture and water stress tolerance

Plant Physiology Papers

- AtWRKY40 and AtWRKY63 modulate the expression of stress-responsive nuclear genes encoding mitochondrial and chloroplast proteins
- Developmental stage specificity and the role of mitochondrial metabolism in the response of Arabidopsis leaves to prolonged mild osmotic stress
- The transcription factor ABI4 is a regulator of mitochondrial retrograde expression of alternative oxidase1a

BACK TO CONTENTS

James Whelan

The Plant Cell, Plant Physiology

James Whelan obtained his BSc and PhD degrees from University College Dublin, then spent five years as a postdoctoral fellow at the Australian National University before being appointed as a lecturer at The University of Western Australia in 1995, where he stayed until his appointment at La Trobe University in 2013 as a professor of AgriBioscience. He also holds a foreign expert professorship at Zheijang University, China, and an honorary doctorate from Stockholm University. He played an important role in establishing the Australian Research Council (ARC) Centre of Excellence in Plant Energy Biology and is currently codirector of AgriBio at La Trobe University.

Jim's research investigates mitochondrial biogenesis and the role of mitochondrial signaling in plant stress responses. His research has uncovered the fundamental science behind regulation of mitochondrial signaling and interactions between mitochondrial and chloroplast retrograde signaling. Research on mitochondrial biogenesis has uncovered a previously unknown role for mitochondria in defining the timing of germination.

The Plant Cell Papers

- Spatio-temporal transcript profiling of rice roots and shoots in response to phosphate starvation and recovery
- A membrane-bound NAC transcription factor, ANAC017, mediates mitochondrial retrograde signaling in Arabidopsis
- The membrane-bound NAC transcription factor ANAC013 functions in mitochondrial retrograde regulation of the oxidative stress response in Arabidopsis
- Mitochondrial targeting of the Arabidopsis F1-ATPase γ-subunit via multiple compensatory and synergistic presequence motifs
- Dual location of the mitochondrial preprotein transporters B14.7 and Tim23-2 in Complex I and the TIM17:23 Complex in Arabidopsis links mitochondrial activity and biogenesis
- Evidence for a SAL1-PAP chloroplast retrograde pathway that functions in drought and high light signaling in Arabidopsis
- TCP transcription factors link the regulation of genes encoding mitochondrial proteins with the circadian clock in *Arabidopsis thaliana*
- Phage-type RNA polymerase RPOTmp performs gene-specific transcription in mitochondria of *Arabidopsis thaliana*
- Exploring the function-location nexus: using multiple lines of evidence in defining the subcellular location of plant proteins

Plant Physiology Papers

- AtWRKY40 and AtWRKY63 modulate the expression of stress-responsive nuclear genes encoding mitochondrial and chloroplast proteins

continued on next page

BACK TO CONTENTS

James Whelan *continued from page 29*

- Identification of a dual-targeted protein belonging to the mitochondrial carrier family that is required for early leaf development in rice
- Acquisition, conservation, and loss of dual-targeted proteins in land plants
- Nucleotide and RNA metabolism prime translational initiation in the earliest events of mitochondrial biogenesis during Arabidopsis germination
- Multiple lines of evidence localize signaling, morphology, and lipid biosynthesis machinery to the mitochondrial outer membrane of Arabidopsis
- In-Depth temporal transcriptome profiling reveals a crucial developmental switch with roles for RNA processing and organelle metabolism that are essential for germination in Arabidopsis
- Analysis of the rice mitochondrial carrier family reveals anaerobic accumulation of a basic amino acid carrier involved in arginine metabolism during seed germination
- Physiological and transcriptome analysis of iron and phosphorus interaction in rice seedlings
- Defining core metabolic and transcriptomic responses to oxygen availability in rice embryos and young seedlings
- Refining the definition of plant mitochondrial presequences through analysis of sorting signals, N-terminal modifications, and cleavage motifs
- The transcription factor ABI4 is a regulator of mitochondrial retrograde expression of ALTERNATIVE OXIDASE1a
- Mitochondrial and nuclear localization of a novel pea thioredoxin: identification of its mitochondrial target proteins
- Experimental analysis of the rice mitochondrial proteome, its biogenesis, and heterogeneity
- Mapping metabolic and transcript temporal switches during germination in rice highlights specific transcription factors and the role of RNA instability in the germination process
- Differential response of gray poplar leaves and roots underpins stress adaptation during hypoxia

BACK TO CONTENTS

Carlos Ballare

Plant Physiology

Carlos L. Ballaré is professor of plant biology at the University of Buenos Aires and San Martín National University (Buenos Aires) and a senior scientist with the National Research Council of Argentina (CONICET). He completed his MSc and PhD degrees at the University of Buenos Aires and at Oregon State University, respectively, and was a postdoctoral scholar at Utah State University.

His laboratory has conducted pioneering research on the role of photoreceptors in regulating plant responses to the proximity of neighbors and on the effects of ultraviolet radiation on plants and terrestrial ecosystems. At present, the Ballaré lab uses a combination of genetic, physiological, and genomic and biochemical tools to understand the mechanisms by which photoreceptors regulate plant immunity against pathogens and herbivores.

Carlos has received a number of awards including recognition as one of the 50 Latin American leaders for the new millennium by CNN and Time, a Guggenheim Fellowship, and most recently, the Konex Merit Prize in 2013, awarded by the Konex Foundation, as one of the top five Argentine researchers in the discipline of "Biology and Ecology" in the last decade. He has served on the editorial boards of several journals, including *Plant Physiology*. He is presently editor-in-chief of *Oecologia* and, as part of his outreach activity, is a member of the Environmental Effects Assessment Panel of the United Nations Environment Programme.

Plant Physiology Papers

- Canopy light and plant health
- Low red/far-red ratios reduce arabidopsis resistance to botrytis cinerea and jasmonate responses via a COI1-JAZ10-dependent, salicylic acid-independent mechanism
- Jasmonate-dependent and -independent pathways mediate specific effects of solar ultraviolet B radiation on leaf phenolics and antiherbivore defense

BACK TO CONTENTS

José López Bucio

Plant Physiology

José López Bucio undertook his early studies at the Universidad Michoacana de San Nicolas de Hidalgo, where he completed a BSc in biology. He then went on to a PhD in the Department of Genetic Engineering at the Irapuato Unit of the Centre for Research and Advanced Studies (CINVESTAV), where he remained as a research professor after completing his studies. In 2002, he spent time at the Rice University in Texas as a visiting professor in the Department of Biochemistry and Cell Biology. He left CINVESTAV in 2004 to become a professor and researcher in the Institute of Chemical and Biological Research at the Universidad Michoacana de San Nicolas de Hidalgo. His current areas of interest include plant responses to bacterial quorum-sensing signals, plant nutrition, and hormonal regulation of root system architecture.

Among other honors and awards, José has earned the Arturo Rosenblueth prize for the best PhD thesis and the Marcos Moshinsky Fellowship, the prize of the Mexican Academy of Sciences for young scientists. He is currently a member of the National System of Researchers in México.

Plant Physiology Papers

- Characterization of drr1, an alkamide-resistant mutant of Arabidopsis, reveals an important role for small lipid amides in lateral root development and plant senescence
- Trichoderma virens, a plant beneficial fungus, enhances biomass production and promotes lateral root growth through an auxin-dependent mechanism in Arabidopsis

BACK TO CONTENTS

Jorge Casal

The Plant Cell, Plant Physiology

Jorge Casal undertook his early studies at the University of Buenos Aires (UBA), where he completed his MSc in 1987, before moving to the University of Leicester (UK) where he completed his PhD in 1989. He is now professor at UBA, a senior research investigator of the National Research Council of Argentina at Instituto de Investigaciones Fisiológicas y Ecológicas Vinculadas a la Agricultura, and the head of laboratory at Instituto Leloir, Buenos Aires, Argentina. His research interests include the signaling network involved in plant responses to light signals and its functional implications in crops.

Jorge has been the recipient of several academic awards, including Diploma of the Konex Foundation (2003), a grant from the Guggenheim Foundation (2002), the Lorenzo Parodi Award (1986–1988), the medal of the Josefina Prats Foundation (2005), and the Georg Forster Research Award of the Humboldt Foundation (2014).

He is an associate editor of *The Plant Journal* and *Plant Molecular Biology* and is a member of the editorial boards of *BMC Plant Biology* and *Trends in Plant Science.*

The Plant Cell Papers

- Heat shock–induced fluctuations in clock and light signaling enhance Phytochrome B–mediated Arabidopsis deetiolation

Plant Physiology Papers

- Abscisic acid regulates axillary bud outgrowth responses to the ratio of red to far-red light
- Stem transcriptome reveals mechanisms to reduce the energetic cost of shade-avoidance responses in tomato
- Phototropins but not cryptochromes mediate the blue light-specific promotion of stomatal conductance, while both enhance photosynthesis and transpiration under full sunlight
- Cryptochrome as a sensor of the blue/green ratio of natural radiation in Arabidopsis
- Phytochrome regulation of branching in Arabidopsis
- Phytochrome B enhances photosynthesis at the expense of water-use efficiency in Arabidopsis

BACK TO CONTENTS

Hexon Angel Contreras-Cornejo

Plant Physiology

Hexon Angel Contreras-Cornejo graduated with a PhD in experimental biology from Universidad Michoacana de San Nicolás de Hidalgo in 2015 and has already earned a number of honors and awards. He has conducted research on the role of beneficial rizospheric fungi on plant growth and defense responses against pathogens using a combination of classical genetics, genomics, biochemistry, and physiology responses to discover mechanisms that *Trichoderma* spp. regulate in the plant model *Arabidopsis thaliana*. He is a posdoctoral fellowship in the Universidad Nacional Autónoma de México and is interested in elucidating the ecological function of *Trichoderma* spp. in the rhizosphere. His current research activities include metabolic profiling and physiological responses in plants.

Plant Physiology Papers

- Trichoderma virens, a plant beneficial fungus, enhances biomass production and promotes lateral root growth through an auxin-dependent mechanism in Arabidopsis

BACK TO CONTENTS

Noelia Foresi

The Plant Cell

Noelia Foresi graduated from the National University of Mar del Plata, Argentina, with a PhD in biological sciences in 2013.She then held a series of teaching positions at the National University of Mar del Plata.She has presented research works at several national and international conferences, including the annual meeting of the Brazilian Society for Biochemistry and Molecular Biology. She is an assistant researcher in the CONICET – IIB (the National Scientific and Technical Research Council) and has been working in Lamattina's group for the last eight years. Lamattina's group is a pioneer and leader in the study of nitric oxide function in plants.

Noelia is now actively working on the study of new forms of nitric oxide synthases present in photosynthetic microorganisms, with an emphasis on the biotechnological potential of these enzymes to improve plant tolerance to stress.

The Plant Cell Papers

- Characterization of a nitric oxide synthase from the plant kingdom: NO generation from the green alga Ostreococcus tauri is light irradiance and growth phase dependent

BACK TO CONTENTS

Xavier Jordana

The Plant Cell, Plant Physiology

Xavier Jordana is full professor in the Department of Molecular Genetics and Microbiology, Pontificia Universidad Catolica de Chile. He earned his PhD from the University of Chile and was a postdoctoral fellow at the Institute of Molecular and Cell Biology at CNRS in Strasbourg, France. He began to work on plant biology in 1988, and his research interests and specializations are in plant molecular biology, gene expression, plant mitochondria, editing of RNA, transfer of genes from the mitochondrion to the nucleus, and the role of energy metabolism during plant development.

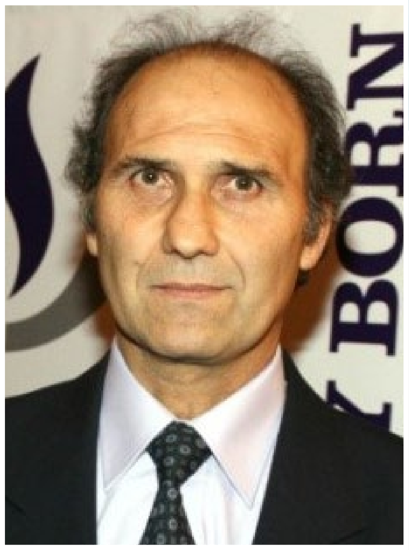
The Plant Cell Papers

- Antisense inhibition of the iron-sulphur subunit of succinate dehydrogenase enhances photosynthesis and growth in tomato via an organic acid–mediated effect on stomatal aperture

Plant Physiology Papers

- A deficiency in the flavoprotein of Arabidopsis mitochondrial Complex II results in elevated photosynthesis and better growth in nitrogen-limiting conditions
- A nuclear gene encoding the iron-sulfur subunit of mitochondrial Complex II is regulated by B3 domain transcription factors during seed development in Arabidopsis

BACK TO CONTENTS



Lorenzo Lamattina

The Plant Cell

Lorenzo Lamattina graduated from the National University of Lomas de Zamora, Argentina, with a degree in rural engineering. He went on to study at the National University of Mar del Plata, where he received his PhD in biological sciences in 1987. He did his postdoctoral training at IBMP (Institut de Biologie Moléculaire des Plantes) at the University of Strasbourg in France, where he studied the structure and expression of the mitochondrial DNA of plants.

He is now a full-time professor of cellular and molecular biology at the National University of Mar del Plata, and a senior investigator at CONICET (The National Scientific and Technical Research Council). His main areas of research include the physiology and molecular biology of plants, the biology of nitric oxide, and stress physiology.

He won the 2013 Konex award in biochemistry and molecular biology, the Bunge y Born award in plant biology in 2006 and the John Simon Guggenheim Foundation award in 2005 for his work on nítric oxide-mediated processes in plants.

The Plant Cell Papers

- Characterization of a nitric oxide synthase from the plant kingdom: NO generation from the green alga Ostreococcus tauri is light irradiance and growth phase dependent

BACK TO CONTENTS

Antonio Leon-Reyes

The Plant Cell, Plant Physiology

Antonio Leon-Reyes originally studied at Universidad San Francisco de Quito in Ecuador, where he obtained a BSc in agribusiness engineering and chemistry in 1999. He worked as technical manager of cut flowers crops, being responsible for pathogen and insect control, soil–plant nutrition, and postharvest management at several flower companies. He then completed his MSc in plant breeding and genetic resources at Wageningen University before obtaining a PhD in plant–microbe–interactions at Utrecht University, working under the direction of Prof. Corne Pieterse in the Netherlands in 2009.

Antonio has held research positions at Utrecht University (the Netherlands), Gent University (Belgium), and Universidad San Francisco de Quito, and teaching positions in Ecuador at Universidad de las Fuerzas Armadas–ESPE, Universidad Central del Ecuador, and Universidad San Francisco de Quito. Since January 2010, he has been a professor of agriculture and food science at Universidad San Francisco de Quito. His main research interest is strengthening the plant immune system by using elicitors to bust systemic resistance and find parameters to control mineral nutrition to increase the plant's self-defense. He has participated in several major conferences and published in many high-ranking international journals.

Plant Cell Papers

- Salicylic acid suppresses jasmonic acid signaling downstream of SCFCOI1-JAZ by targeting GCC promoter motifs via transcription factor ORA59

Plant Physiology Papers

- Ethylene modulates the role of NONEXPRESSOR OF PATHOGENESIS-RELATED GENES1 in cross talk between salicylate and jasmonate signaling

BACK TO CONTENTS

Ladaslav Sodek

Plant Physiology

Ladaslav Sodek graduated in biochemistry from the University of Sheffield in 1963 and earned a PhD in agricultural chemistry from the University of London (Wye College) in 1968. He spent two years (1968–1970) on a postdoctoral fellowship at the University of Illinois and sabbaticals at Rothamsted Experimental Station (1977–1978) and Lancaster University (1989–1990). He has been a professor at the State University of Campinas since 1975. His research emphasis is in plant biochemistry, acting on the following topics: soy, fixation of nitrogen, nitrogen metabolism, and stress (especially hypoxia).

Plant Physiology Papers

- Glycolysis and the tricarboxylic acid cycle are linked by alanine aminotransferase during hypoxia induced by waterlogging of Lotus japonicus
- Thiamin confers enhanced tolerance to oxidative stress in Arabidopsis

BACK TO CONTENTS

María Eugenia Zanetti

The Plant Cell, Plant Physiology

María Eugenia Zanetti obtained her PhD at the National University of Mar del Plata (Argentina) in 2002. Afterward, she joined the laboratory of Julia Bailey-Serres at the University of California, Riverside, as a postdoctoral researcher, where she conducted seminal research on the affinity purification of "translatomes" from specific cell types in plants. María Eugenia is currently a professor and researcher at the National University of La Plata and CONICET (Argentina). Her main interest is to understand the molecular mechanisms underlying the root nodule symbiosis established between legume plants and nitrogen fixing rhizobium bacteria. Her research is focused on the characterization of transcriptional gene regulatory networks governed by the NF-Y and GRAS class of transcription factors during root nodule symbiosis. In addition, she is interested in understanding how post-transcriptional events, including both translational control and small RNA mediated effects, contribute to the regulation of gene expression during symbiosis.

The Plant Cell Papers

- A C subunit of the plant nuclear factor NF-Y required for rhizobial infection and nodule development affects partner selection in the common bean-Rhizobium etli symbiosis
- A small GTPase of the Rab family is required for root hair formation and pre-infection stages in the common bean-rhizobium symbiotic association

Plant Physiology Papers

- Cross-kingdom comparison of transcriptomic adjustments to low oxygen stress highlights conserved and plant-specific responses.

BACK TO CONTENTS

Ian Baldwin

The Plant Cell, Plant Physiology

Ian Baldwin graduated with a PhD in chemical ecology from Cornell University, Ithaca, New York, Section of Neurobiology and Behavior in 1989. He was an assistant (1989), associate (1993), and full professor (1996) in the Department of Biology at SUNY Buffalo. In 1996, Ian became the founding director of the Max Planck Institute for Chemical Ecology, where he currently heads the Department of Molecular Ecology. In 1999, he was appointed honorary professor at Friedrich Schiller University in Jena, Germany. In 2002, Ian founded the International Max Planck Research School at the Max Planck Institute in Jena.

His scientific work is devoted to understanding the traits that allow plants to survive in the real world. To achieve this, he has developed a molecular toolbox for the native tobacco, *Nicotiana attenuata* (coyote tobacco), and a graduate program that trains "genome-enabled field biologists" to combine genomic and molecular genetic tools with field work to understand the genes that matter for plant–herbivore, –pollinator, –plant, –microbial interactions in nature. He has been a driver behind the open access publication efforts of the Max Planck Society and is a member of the National Academy of Sciences, the German Academy of Sciences Leopoldina, and the European Molecular Biology Organization (EMBO).

The Plant Cell Papers

- Dimethyl disulfide produced by the naturally associated bacterium *Bacillus* sp B55 promotes *Nicotiana attenuata* growth by enhancing sulfur nutrition
- A self-regulatory circuit of CIRCADIAN CLOCK-ASSOCIATED1 underlies the circadian clock regulation of temperature responses in Arabidopsis
- Nicotiana attenuata LECTIN RECEPTOR KINASE1 suppresses the insect-mediated inhibition of induced defense responses during Manduca sexta herbivory
- Serine protease inhibitors specifically defend Solanum nigrum against generalist herbivores but do not influence plant growth and development
- Jasmonate and ppHsystemin regulate key malonylation steps in the biosynthesis of 17-hydroxygeranyllinalool diterpene glycosides, an abundant and effective direct defense against herbivores in Nicotiana attenuate

Plant Physiology Papers, including:

- The HERBIVORE ELICITOR-REGULATED1 gene enhances abscisic acid levels and defenses against herbivores in Nicotiana attenuata plants
- Deciphering herbivory-induced gene-to-metabolite dynamics in Nicotiana attenuata tissues using a multifactorial approach
- Alternative oxidase in resistance to biotic stresses: Nicotiana attenuata AOX contributes to resistance to a pathogen and a piercing-sucking insect but not Manduca sexta larvae

continued on next page

BACK TO CONTENTS

Ian Baldwin *continued from page 41*

- HSPRO controls early Nicotiana attenuata seedling growth during interaction with the fungus Piriformospora indica
- Environmental stresses of field growth allow cinnamyl alcohol dehydrogenase-deficient Nicotiana attenuata plants to compensate for their structural deficiencies
- Silencing Nicotiana attenuata calcium-dependent protein kinases, CDPK4 and CDPK5, strongly up-regulates wound- and herbivory-induced jasmonic acid accumulations
- NaJAZh regulates a subset of defense responses against herbivores and spontaneous leaf necrosis in Nicotiana attenuata plants
- 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
- MYB8 controls inducible phenolamide levels by activating three novel hydroxycinnamoyl-coenzyme A:Polyamine transferases in Nicotiana attenuate
- Ectopic expression of AtJMT in Nicotiana attenuata: creating a metabolic sink has tissue-specific consequences for the jasmonate metabolic network and silences downstream gene expression
- Lipase activity in insect oral secretions mediates defense responses in Arabidopsis
- EOBII controls flower opening by functioning as a general transcriptomic switch
- Pithy protection: Nicotiana attenuata's jasmonic acid-mediated defenses are required to resist stem-boring weevil larvae
- Variation in antiherbivore defense responses in synthetic Nicotiana allopolyploids correlates with changes in uniparental patterns of gene expression
- Jasmonic acid and ethylene modulate local responses to wounding and simulated herbivory in Nicotiana attenuata leaves
- Silencing NaTPI expression increases nectar germin, nectarins, and hydrogen peroxide levels and inhibits nectar removal from plants in nature
- Nicotiana attenuata SIPK, WIPK, NPR1, and fatty acid-amino acid conjugates participate in the induction of jasmonic acid biosynthesis by affecting early enzymatic steps in the pathway
- Different lepidopteran elicitors account for cross-talk in herbivory-induced phytohormone signaling
- Silencing the hydroxyproline-rich glycopeptide systemin precursor in two accessions of Nicotiana attenuata alters flower morphology and rates of self-pollination
- Molecular interactions between the specialist herbivore Manduca sexta (Lepidoptera, Sphigidae) and its natural host Nicotiana attenuata. VIII. An unbiased GCxGC-ToFMS analysis of the plant's elicited volatile emissions

BACK TO CONTENTS

Wout Boerjan

The Plant Cell, Plant Physiology

Boerjan Wout earned his PhD in plant biotechnology from the University of Ghent, Belgium, and is currently an associate professor at the university and group leader at the VIB Department of Plant Systems Biology and Bioinformatics, where he leads the Bio-Energy Group with the primary focus of understanding the biosynthesis of plant cell walls to provide the fundamental knowledge necessary to design plant cell walls that are easier to process into simple sugars.

His research is heavily supported by metabolomics, and his efforts will underpin the transition from a fossil-based to a sustainable bio-economy. Boerjan is a member of the international Academy of Wood Science, associate editor of *Bioenergy Research*, advisory board member of several international projects and regular organizer of international congresses. In 2009, he was named Forest Biotechnologist of the Year by the International Institute of Forest Biotechnology.

The Plant Cell Papers

- Protein–Protein and Protein–Membrane associations in the lignin pathway
- A systems biology view of responses to lignin biosynthesis perturbations in Arabidopsis
- Syringyl lignin is unaltered by severe sinapyl alcohol dehydrogenase suppression in tobacco
- Perturbation of Indole-3-Butyric acid homeostasis by the UDP-Glucosyltransferase UGT74E2 modulates Arabidopsis architecture and water stress tolerance

Plant Physiology Papers

- Lignification in sugarcane: biochemical characterization, gene discovery, and expression analysis in two genotypes contrasting for lignin content
- Impact of the absence of stem-specific β-glucosidases on lignin and monolignols
- Natural hypolignification is associated with extensive oligolignol accumulation in flax stems
- Mass spectrometry-based sequencing of lignin oligomers
- Modeling lignin polymerization. I. simulation model of dehydrogenation polymers
- Sequencing around 5-Hydroxyconiferyl alcohol-derived units in caffeic acid O-methyltransferase-deficient poplar lignins

BACK TO CONTENTS

Chris Carrie

The Plant Cell, Plant Physiology

Chris Carrie received his bachelor's degree from the University of Western Australia in 2005. He then went on to obtain his PhD in 2011 working at the ARC Centre of Excellence in Plant Biology located at the University of Western Australia. In 2012 he moved to the Ludwig-Maximilians-Universität Munich (Germany) after being awarded a prestigious Alexander von Humboldt Fellowship. Chris is now a postdoc in the group of Prof. Jürgen Soll in Munich and is studying how plant mitochondria import and assemble their proteins.

The Plant Cell Papers

- Dual location of the mitochondrial preprotein transporters B14.7 and Tim23-2 in Complex I and the TIM17:23 Complex in Arabidopsis links mitochondrial activity and biogenesis

Plant Physiology Papers

- Identification of a dual-targeted protein belonging to the mitochondrial carrier family that is required for early leaf development in rice
- Acquisition, conservation, and loss of dual-targeted proteins in land plants
- Nucleotide and RNA metabolism prime translational initiation in the earliest events of mitochondrial biogenesis during Arabidopsis germination
- Multiple lines of evidence localize signaling, morphology, and lipid biosynthesis machinery to the mitochondrial outer membrane of Arabidopsis
- In-depth temporal transcriptome profiling reveals a crucial developmental switch with roles for RNA processing and organelle metabolism that are essential for germination in Arabidopsis

BACK TO CONTENTS

Lieven De Veylder

The Plant Cell, Plant Physiology

Lieven De Veylder is a principal investigator in the Plant Systems Biology Department of Ghent University–VIB, Belgium, where he leads the Cell Cycle Group. The group aims to understand how cell cycle control genes drive plant cell division and elucidate how cell division control interacts with different aspects of plant development, such as morphogenesis, architecture, and growth rate. In particular, the team aims to understand how plants control their exit from the cell cycle.

The Plant Cell Papers

- AUREOCHROME1a-Mediated induction of the diatom-specific Cyclin dsCYC2 controls the onset of cell division in diatoms (Phaeodactylum tricornutum)
- Evidence for a role of Arabidopsis CDT1 proteins in gametophyte development and maintenance of genome integrity
- Arabidopsis ULTRAVIOLET-B-INSENSITIVE4 maintains cell division activity by temporal inhibition of the anaphase-promoting complex/cyclosome
- Auxin-dependent cell cycle reactivation through transcriptional regulation of Arabidopsis E2Fa by lateral organ boundary proteins
- The Arabidopsis thaliana checkpoint kinase WEE1 protects against premature vascular differentiation during replication stress
- Functional modules in the Arabidopsis core cell cycle binary protein–protein interaction network
- Control of cell proliferation, organ growth, and DNA damage response operate independently of dephosphorylation of the Arabidopsis Cdk1 Homolog CDKA;1

Plant Physiology Papers

- Multiple functions of kip-related Protein5 connect endoreduplication and cell elongation
- New insights into the control of endoreduplication: endoreduplication could be driven by organ growth in Arabidopsis leaves
- Light-dependent regulation of DEL1 is determined by the antagonistic action of E2Fb and E2Fc
- Model-based analysis of Arabidopsis leaf epidermal cells reveals distinct division and expansion patterns for pavement and guard cells
- CDKB1;1 forms a functional complex with CYCA2;3 to suppress endocycle onset
- Unraveling transcriptional control in Arabidopsis using cis-Regulatory elements and coexpression networks
- Eternal youth, the fate of developing Arabidopsis leaves upon Rhodococcus fascians infection

BACK TO CONTENTS

Alisdair Fernie

The Plant Cell, Plant Physiology

Alisdair Fernie is a research group leader at the Max Planck Institute of Molecular Plant Physiology, Golm, Germany. His work involves carrying out detailed analysis of the chemical composition of crop species, with a particularly focus on tomato fruits across populations displaying broad genetic divergence. His current research activities include metabolic profiling and genome sequencing in Solanaceous species, analytical tool development for the manipulation of the dominant fluxes of carbon metabolism, and better understanding of the compartmentation of plant energy metabolism.

Alisdair has an undergraduate degree (BSc Honours) from Sheffield University, U.K., and later studied at the University of Oxford.

The Plant Cell Papers, including:

- Metabolic fluxes in an illuminated Arabidopsis rosette
- Antisense inhibition of the 2-Oxoglutarate dehydrogenase complex in tomato demonstrates its importance for plant respiration and during leaf senescence and fruit maturation
- Vitamin deficiencies in humans: can plant science help?
- Recommendations for reporting metabolite data
- Antisense inhibition of the iron-sulphur subunit of succinate dehydrogenase enhances photosynthesis and growth in tomato via an organic acid–mediated effect on stomatal aperture
- Malate plays a crucial role in starch metabolism, ripening, and soluble solid content of tomato fruit and affects postharvest softening
- Identification of the 2-Hydroxyglutarate and Isovaleryl-CoA dehydrogenases as alternative electron donors linking lysine catabolism to the electron transport chain of Arabidopsis mitochondria

Plant Physiology Papers, including:

- Alteration of the interconversion of pyruvate and malate in the plastid or cytosol of ripening tomato fruit invokes diverse consequences on sugar but similar effects on cellular organic acid, metabolism, and transitory starch accumulation
- Decreasing the mitochondrial synthesis of malate in potato tubers does not affect plastidial starch synthesis, suggesting that the physiological regulation of ADPglucose Pyrophosphorylase is context dependent
- Integrative comparative analyses of transcript and metabolite profiles from pepper and tomato ripening and development stages uncovers species-specific patterns of network regulatory behavior

continued on next page

BACK TO CONTENTS

Alistdair Fernie *continued from page 46*

- Tomato fruit photosynthesis is seemingly unimportant in primary metabolism and ripening but plays a considerable role in seed development
- Targeted enhancement of Glutamate-to-γ-Aminobutyrate conversion in Arabidopsis seeds affects carbon-nitrogen balance and storage reserves in a development-dependent manner
- Toward the storage metabolome: profiling the barley vacuole
- Analysis of a range of catabolic mutants provides evidence that Phytanoyl-Coenzyme a does not act as a substrate of the electron-transfer flavoprotein/electron-transfer flavoprotein:ubiquinone oxidoreductase complex in Arabidopsis during dark-induced senescence
- Systems biology of tomato fruit development: combined transcript, protein, and metabolite analysis of tomato transcription factor (nor, rin) and ethylene receptor (Nr) mutants reveals novel regulatory interactions
- Targeting mitochondrial metabolism and machinery as a means to enhance photosynthesis
- The influence of fruit load on the tomato pericarp metabolome in a Solanum chmielewskii introgression line population
- RNA interference of LIN5 in tomato confirms its role in controlling brix content, uncovers the influence of sugars on the levels of fruit hormones, and demonstrates the importance of sucrose cleavage for normal fruit development and fertility
- Decreased Mitochondrial Activities of Malate Dehydrogenase and Fumarase in Tomato Lead to Altered Root Growth and Architecture via Diverse Mechanisms

BACK TO CONTENTS

Wilhelm Gruissem

The Plant Cell, Plant Physiology

Wilhelm Gruissem has been professor of plant biotechnology at ETH Zurich (Swiss Federal Institute of Technology) since 2000. Previously, he was appointed as professor at the University of California at Berkeley in 1983, where he chaired the Department of Plant and Microbial Biology from 1993 to 1998. From 2006 to 2010, he served as president of the European Plant Science Organization (EPSO) and since 2011 has been president of the Global Plant Council.

In addition to his research on systems approaches, Willi directs a biotechnology program on trait improvement in cassava, rice, and wheat. In 2008, he founded Nebion, a company known for the internationally successful Genevestigator database. He is an elected fellow of AAAS and ASPB, editor-in-chief of *Plant Molecular Biology*, and a member of several editorial and advisory boards. He is coeditor of the acclaimed book *Biochemistry and Molecular Biology of Plants* with Bob Buchanan and Russell Jones, and has received several awards for his biotechnology work, including the 2013 Sheng Fa Yang award.

The Plant Cell Papers

- Plastid proteome assembly without Toc159: photosynthetic protein import and accumulation of N-acetylated plastid precursor proteins
- Arabidopsis RETINOBLASTOMA-RELATED is required for stem cell maintenance, cell differentiation, and lateral organ production

Plant Physiology Papers

- Measuring Arabidopsis chromatin accessibility using DNase I-Polymerase chain reaction and DNase I-Chip assays
- The Arabidopsis Rho of plants GTPase AtROP6 functions in developmental and pathogen response pathways
- MASCP Gator: an aggregation portal for the visualization of Arabidopsis proteomics data
- A gain-of-function mutation of Arabidopsis CRYPTOCHROME1 promotes flowering
- Probing the reproducibility of leaf growth and molecular phenotypes: a comparison of three Arabidopsis accessions cultivated in ten laboratories
- AGRONOMICS1: a new resource for Arabidopsis transcriptome profiling
- Large-scale Arabidopsis phosphoproteome profiling reveals novel chloroplast kinase substrates and phosphorylation networks

BACK TO CONTENTS

Rüdiger Hell

The Plant Cell, Plant Physiology

Rüdiger Hell earned his PhD in botany from the University of Cologne and was a postdoctoral fellow with the University of California, Berkeley. He is currently professor of molecular biology of plants and director of the Metabolomics Core Technology Platform at the Centre for Organismal Studies, Ruprecht-Karls-Universitaet Heidelberg, Germany.

His fields of interest are the regulation of sulfur metabolism, redox control, subcellular transport, plant mineral nutrition, abiotic stress, and more recently N-terminal acetylation of proteins. Rüdiger is active in teaching plant molecular biology, physiology and biotechnology at undergraduate and postgraduate levels.

Rüdiger's activities in the scientific community include service as a member of the Board of Directors of HBIGS Excellence Graduate School at Heidelberg University and speaking engagements with the Plant Biotechnology Group of the German Society for Biochemistry and Molecular Biology.

The Plant Cell Papers

- Vacuolar Nicotianamine has critical and distinct roles under iron deficiency and for zinc sequestration in Arabidopsis
- Evidence for a SAL1-PAP chloroplast retrograde pathway that functions in drought and high light signaling in Arabidopsis
- Sulfite reductase defines a newly discovered bottleneck for assimilatory sulfate reduction and is essential for growth and development in Arabidopsis thaliana
- Dynamic plastid redox signals integrate gene expression and metabolism to induce distinct metabolic states in photosynthetic acclimation in Arabidopsis
- Disruption of Adenosine-5′-Phosphosulfate Kinase in Arabidopsis reduces levels of sulfated secondary metabolites

Plant Physiology Papers

- Successful fertilization requires the presence of at least one major O-Acetylserine(thiol)lyase for cysteine synthesis in pollen of Arabidopsis
- Recycling of methylthioadenosine is essential for normal vascular development and reproduction in Arabidopsis
- The seed composition of arabidopsis mutants for the group 3 sulfate transporters indicates a role in sulfate translocation within developing seeds
- The analysis of Arabidopsis nicotianamine synthase mutants reveals functions for nicotianamine in seed iron loading and iron deficiency responses

BACK TO CONTENTS

Dirk Inzé

The Plant Cell, Plant Physiology

Dirk Inzé is a Belgian molecular biologist and professor at Ghent University (Belgium). He is currently scientific director of the Vlaams Instituut voor Biotechnologie Department of Plant Systems Biology. Under his directorship, the VIB, which currently employs 300 people, became one of the world's leading centers for advanced plant sciences.

His research interest is on the molecular networks underpinning yield and organ growth, both under standard as well as mild drought stress conditions in Arabidopsis and the C_4 crop maize. He is a member of the European Molecular Biology Organisation (EMBO), and in 2005 he was awarded the Francqui Prize on Biological and Medical Sciences for his research on plant systems biology.

In 2012, he became the chair of the Life Science Committee of the important science policy organization Science Europe. Additionally, he has served on numerous scientific committees, editorial boards, and science advisory boards and has been an invited speaker at more than 150 internationally renowned conferences.

The Plant Cell Papers

- The potential of text mining in data integration and network biology for plant research: a case study on Arabidopsis
- AUREOCHROME1a-mediated induction of the diatom-specific cyclin dsCYC2 controls the onset of cell division in diatoms (Phaeodactylum tricornutum)
- Tackling drought stress: RECEPTOR-LIKE KINASES present new approaches
- Pause-and-Stop: the effects of osmotic stress on cell proliferation during early leaf development in Arabidopsis and a role for ethylene signaling in cell cycle arrest
- Perturbation of Indole-3-Butyric Acid homeostasis by the UDP-Glucosyltransferase UGT74E2 modulates Arabidopsis architecture and water stress tolerance
- Functional modules in the Arabidopsis core cell cycle binary protein–protein interaction network
- A population genomics study of the Arabidopsis core cell cycle genes shows the signature of natural selection

Plant Physiology Papers

- The agony of choice: how plants balance growth and survival under water-limiting conditions
- ETHYLENE RESPONSE FACTOR6 acts as a central regulator of leaf growth under water-limiting conditions in Arabidopsis

continued on next page

BACK TO CONTENTS

Dirk Inzé *continued from page 50*

- DELLA signaling mediates stress-induced cell differentiation in Arabidopsis leaves through modulation of anaphase-promoting complex/cyclosome activity
- Model-based analysis of Arabidopsis leaf epidermal cells reveals distinct division and expansion patterns for pavement and guard cells
- Combining enhanced root and shoot growth reveals cross talk between pathways that control plant organ size in Arabidopsis
- VirtualLeaf: An open-source framework for cell-based modeling of plant tissue growth and development
- SHORT-ROOT and SCARECROW regulate leaf growth in arabidopsis by stimulating S-Phase progression of the cell cycle
- Mass spectrometry-based sequencing of lignin oligomers
- Increased leaf size: different means to an end
- Systematic localization of the arabidopsis core cell cycle proteins reveals novel cell division complexes
- Developmental stage specificity and the role of mitochondrial metabolism in the response of Arabidopsis leaves to prolonged mild osmotic stress
- CDKB1;1 forms a functional complex with CYCA2;3 to suppress endocycle onset

BACK TO CONTENTS

Dario Leister

The Plant Cell, Plant Physiology

Dario Leister is a professor of plant molecular biology at Ludwig-Maximilians-Universitat in Munich. His lab is engaged in the regulation of photosynthesis and the integration of photosynthetic processes in the eukaryotic cell, focusing on intracellular signal transduction, posttranslational protein modification, thylakoid biogenesis, and synthetic biology. Dario is also head of the Copenhagen Plant Science Center in Denmark. He holds a PhD in genetics from the Max Planck Institute for Plant Breeding Research.

The Plant Cell Papers

- The PHOTOSYNTHESIS AFFECTED MUTANT68–LIKE protein evolved from a PSII assembly factor to mediate assembly of the chloroplast NAD(P)H dehydrogenase complex in Arabidopsis
- Arabidopsis CURVATURE THYLAKOID1 proteins modify thylakoid architecture by inducing membrane curvature
- The Arabidopsis thylakoid protein PAM68 is required for efficient D1 biogenesis and photosystem II assembly
- Redox regulation of the NPR1-TGA1 system of Arabidopsis thaliana by nitric oxide
- Dynamic plastid redox signals integrate gene expression and metabolism to induce distinct metabolic states in photosynthetic acclimation in Arabidopsis
- Arabidopsis STN7 kinase provides a link between short- and long-term photosynthetic acclimation

Plant Physiology Papers

- Transcriptomic analysis of the role of carboxylic acids in metabolite signaling in Arabidopsis leaves
- Intracompartmental and intercompartmental transcriptional networks coordinate the expression of genes for organellar functions

BACK TO CONTENTS

Karin Ljung

The Plant Cell, Plant Physiology

Having earned a PhD from the Swedish University of Agricultural Sciences (SLU), Umea, Sweden, Karin Ljung is now based at Umea Plant Science Centre (UPSC), Department of Forest Genetics and Plant Physiology. UPSC is an internationally recognized research collaboration between Umea University and SLU, working with plant and forest biology and biotechnology (www.upsc.se).

Karin's research is focused on the mechanisms and processes regulating plant growth and development. She is particularly interested in the role of plant growth regulating substances in primary and secondary root development and in understanding how a plant coordinates the growth of its aerial parts with its root system.

The Plant Cell Papers

- Regulation of auxin homeostasis and gradients in Arabidopsis roots through the formation of the Indole-3-Acetic Acid Catabolite 2-Oxindole-3-Acetic Acid
- Soluble carbohydrates regulate auxin biosynthesis via PIF proteins in Arabidopsis
- Fruit growth in Arabidopsis occurs via DELLA-Dependent and DELLA-independent gibberellin responses
- The Arabidopsis YUCCA1 flavin monooxygenase functions in the Indole-3-Pyruvic Acid branch of auxin biosynthesis
- Cytokinin regulation of auxin synthesis in Arabidopsis involves a homeostatic feedback loop regulated via auxin and cytokinin signal transduction
- Interplay between the NADP-linked thioredoxin and glutathione systems in Arabidopsis auxin signaling
- An auxin gradient and maximum in the Arabidopsis root apex shown by high-resolution cell-specific analysis of IAA distribution and synthesis

Plant Physiology Papers

- An endogenous carbon-sensing pathway triggers increased auxin flux and hypocotyl elongation
- SHORT-ROOT regulates primary, lateral, and adventitious root development in Arabidopsis
- Auxin metabolism and function in the multicellular brown alga Ectocarpus siliculosus

BACK TO CONTENTS

Staffan Persson

The Plant Cell, Plant Physiology

Staffan Persson received his doctorate degree from Lund University (Sweden)/North Carolina State University (USA) in late 2003, and then did a postdoc at the Carnegie Institution of Washington at Stanford. He was a Max Planck research group leader at the Max Planck Institute for Molecular Plant Physiology, Germany, between 2008 and 2014.

Staffan has recently accepted a professor position and chair in plant cell biology at the University of Melbourne, where he started in early 2015 at the School of Bioscience and will be affiliated with the ARC Centre of Excellence for Plant Cell Walls. Additionally, Staffan serves on the editorial boards of several international journals and is a Changjiang scholar and visiting professor at the HZAU Agricultural University, China.

Staffan's research group investigates plant cell walls with a focus on the communication between the cell wall and the cell, trafficking of the cellulose synthase to and from the plasma membrane, and the influence of cellulose deposition on cell and organ shape.

The Plant Cell Papers

- Phosphatidylinositol 4,5-Bisphosphate influences PIN polarization by controlling clathrin-mediated membrane trafficking in Arabidopsis
- Downregulation of the δ-Subunit reduces mitochondrial ATP synthase levels, alters respiration, and restricts growth and gametophyte development in Arabidopsis
- CHITINASE-LIKE1/POM-POM1 and its homolog CTL2 are glucan-interacting proteins important for cellulose biosynthesis in Arabidopsis
- POM-POM2/CELLULOSE SYNTHASE INTERACTING1 is essential for the functional association of cellulose synthase and microtubules in Arabidopsis
- Live cell imaging reveals structural associations between the actin and microtubule cytoskeleton in Arabidopsis
- PlaNet: Combined sequence and expression comparisons across plant networks derived from seven species

Plant Physiology Papers

- Patterning and lifetime of plasma membrane-localized cellulose synthase is dependent on actin organization in arabidopsis interphase cells
- Toward the storage metabolome: profiling the barley vacuole

continued on next page

BACK TO CONTENTS

Staffan Persson *continued from page 54*

- Subfunctionalization of cellulose synthases in seed coat epidermal cells mediates secondary radial wall synthesis and mucilage attachment
- TRICHOME BIREFRINGENCE and its homolog AT5G01360 encode plant-specific DUF231 proteins required for cellulose biosynthesis in Arabidopsis
- Tricarboxylic acid cycle activity regulates tomato root growth via effects on secondary cell wall production
- Assembly of an interactive correlation network for the arabidopsis genome using a novel heuristic clustering algorithm

BACK TO CONTENTS

Bahtijor Rasulov

Plant Physiology

Bahtijor Rasulov earned his PhD (1983) and of doctor of sciences degrees (1993) at the Institute of Physiology and Genetics, Tajik Academy of Sciences. He worked at the institute as a researcher and later as the head of Physiology and Biochemistry of Cotton Plants laboratory. He led several large-scale projects on endogenous and exogenous mechanisms of regulation of photosynthesis and productivity of cotton. From 1998 to 2001, he participated in the European Union Inco Copernicus program, joining the efforts of Tajik, Estonian, Finnish, and Italian researchers to study the mechanisms affecting silver birch growth at elevated levels of CO_2 and ozone. He has led the construction of over 10 unique gas-exchange systems for different Estonian, U.S. and Swedish laboratories. Within past 7 years, his research interests include regulation of isoprenoid metabolism and its functional connections with plant photosynthesis. His scientific contributions were awarded with the science prize for young researchers by the Tajik Academy of Sciences (1983) and the mark of honor by the University of Tartu (2010).

Papers

- Induction of a Longer Term Component of Isoprene Release in Darkened Aspen Leaves: Origin and Regulation under Different Environmental Conditions
- Temperature Response of Isoprene Emission in Vivo Reflects a Combined Effect of Substrate Limitations and Isoprene Synthase Activity: A Kinetic Analysis
- Evidence That Light, Carbon Dioxide, and Oxygen Dependencies of Leaf Isoprene Emission Are Driven by Energy Status in Hybrid Aspen
- Postillumination Isoprene Emission: In Vivo Measurements of Dimethylallyldiphosphate Pool Size and Isoprene Synthase Kinetics in Aspen Leaves

BACK TO CONTENTS

Pedro L. Rodriguez

The Plant Cell, Plant Physiology

Pedro L. Rodriguez is a staff scientist with the Spanish Research Council (CSIC). He received his PhD in biochemistry and molecular biology from the Autonoma University of Madrid and carried out postdoctoral work at the ETH Zurich and TU Munich. Pedro's research has focused on abscisic acid biosynthesis and signaling. He is group leader of a team at Instituto de Biologia Molecular y Celular de Plantas (IBMCP), Valencia, Spain. This institute is located at the campus of the Technical University of Valencia, where he also collaborates in postgraduate teaching.

His research is currently focused on the role played by PYR/PYL/RCAR ABA receptors, protein phosphatases type 2C, and SnRK2 kinases as regulators of ABA signaling, with emphasis on the biotechnological potential of the pathway to improve plant tolerance to drought. His group has identified and characterized key genes involved in the ABA biosynthetic and signal transduction pathways.

The Plant Cell Papers

- ABI1 and PP2CA phosphatases are negative regulators of Snf1-related protein Kinase1 signaling in Arabidopsis
- The SWI2/SNF2 chromatin remodeling ATPase BRAHMA represses abscisic acid responses in the absence of the stress stimulus in Arabidopsis
- Arabidopsis PYR/PYL/RCAR receptors play a major role in quantitative regulation of stomatal aperture and transcriptional response to abscisic acid
- Protein phosphatases 2C regulate the activation of the Snf1-related Kinase OST1 by abscisic acid in Arabidopsis

Plant Physiology Papers

- The PYL4 A194T mutant uncovers a key role of PYR1-LIKE4/PROTEIN PHOSPHATASE 2CA interaction for abscisic acid signaling and plant drought resistance
- PYR/RCAR receptors contribute to ozone-, reduced air humidity-, darkness-, and CO2-induced stomatal regulation
- PYRABACTIN RESISTANCE1-LIKE8 plays an important role for the regulation of abscisic acid signaling in root
- Selective inhibition of clade a phosphatases Type 2C by PYR/PYL/RCAR abscisic acid receptors
- Modulation of abscisic acid signaling in vivo by an engineered receptor-insensitive protein phosphatase Type 2C Allele
- Triple loss of function of protein phosphatases Type 2C leads to partial constitutive response to endogenous abscisic acid
- The short-rooted phenotype of the brevis radix mutant partly reflects root abscisic acid hypersensitivity

BACK TO CONTENTS

Nils Stein

The Plant Cell, Plant Physiology

Nils Stein earned his PhD in genetics at the University of Hohenheim (1997, Stuttgart, Germany). He worked as a postdoc (1998–2001) at Zurich University, Switzerland, before he moved in 2001 to the Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben. Since 2007, Nils has led the genome diversity group of the Genebank department. The main research focus is on structural, functional, and comparative genome analysis in Triticeae species like barley, wheat, and rye, with special emphasis on barley.

Nils is co-coordinator of the European Triticeae Genomics Initiative (ETGI) and since 2008 has chaired the International Barley Genome Sequencing Consortium (IBSC). In 2010 he was awarded the Günter und Anna Wricke Forschungspreis in applied genetics and breeding research for his contributions in cereal genome analysis.

The Plant Cell Papers

- Reticulate evolution of the rye genome
- Frequent gene movement and pseudogene evolution is common to the large and complex genomes of wheat, barley, and their relatives
- Unlocking the barley genome by chromosomal and comparative genomics

Plant Physiology Papers

- A sequence-ready physical map of barley anchored genetically by two million single-nucleotide polymorphisms
- Genetic dissection of barley morphology and development
- Gene content and virtual gene order of barley chromosome 1H
- Analysis of intraspecies diversity in wheat and barley genomes identifies breakpoints of ancient haplotypes and provides insight into the structure of diploid and hexaploid triticeae gene pools

BACK TO CONTENTS

York-Dieter Stierhof

The Plant Cell

York-Dieter Stierhof is the head of the central facility for electron microscopy at the Center for Plant Molecular Biology ZMBP at the University of Tübingen. He studied biology at the University of Tübingen and got his PhD in zoology/parasitology. During his PhD he examined hepatitis A virus infected cells. In 1989, he moved to the Max Planck Institute for Biology in Tübingen as head of the electron microscopy facility, where he focused on bacteriophage structure; protein export in *E. coli;* and ultrastructural and immunohistochemical analysis of trypanosomes, leishmania cells, and infected tissue. In 2000, York-Dieter moved to the ZMBP, where he set up a central facility for electron microscopy. He established improved and new embedding techniques for cryofixed plant tissues in order to improve preservation of ultrastructure and antigenicity and to enhance the sensitivity of immunolabeling techniques.

In 2009 (Martin, C., Happy Birthday to *The Plant Cell.* Plant Cell **21:** 1–2), *The Plant Cell* selected the paper Dettmer et al. (2006) as one of the five best Plant Cell articles of the past 20 years (Dettmer, J., Hong-Hermesdorf, A., Stierhof, Y.-D., and Schumacher, K. 2006. Vacuolar H+-ATPase Activity Is Required for Endocytic and Secretory Trafficking in Arabidopsis. Plant Cell **18:** 715–730). In 2014, Thomson Reuters selected York-Deiter as a highly cited researcher in the field of animal and plant science (articles ranking among the top 1% of the most cited in the respective field; h-index: 55).

Papers

- MTV1 and MTV4 encode plant-specific ENTH and ARF GAP proteins that mediate clathrin-dependent trafficking of vacuolar cargo from the *trans*-golgi network
- The Deubiquitinating Enzyme AMSH3 is required for intracellular trafficking and vacuole biogenesis in *Arabidopsis thaliana*
- Endocytic and secretory traffic in Arabidopsis merge in the trans-golgi network/early endosome, an independent and highly dynamic organelle
- Heat Shock Protein Cognate 70-4 and an E3 Ubiquitin Ligase, CHIP, mediate plastid-destined precursor degradation through the ubiquitin-26s proteasome system in Arabidopsis
- Pausing of golgi bodies on microtubules regulates secretion of cellulose synthase complexes in Arabidopsis

BACK TO CONTENTS

Mark Stitt

The Plant Cell, Plant Physiology

Mark Stitt studied natural sciences at the University of Cambridge, UK, and went on to earn a PhD at the University of Gottingen in Germany. He held the Fiebiger Professorship for Plant Biochemistry at Bayreuth University and later became director of the Botany Institute at Heidelberg University. Today he is one of the directors at the Max Planck Institute of Molecular Plant Physiology, Golm, and honorary professor at the University of Potsdam.

His main area of interest is the regulation of plant metabolism – in particular how the carbon signaling mediated by trehalose-6-phosphate and other mechanisms interacts with clock- and light-signaling to pace metabolism, growth, and development against the carbon supply in a fluctuating environment. He also develops methods to quantify flux in metabolism and structural cellular components, and he applies the systems approaches to the study of metabolism and growth.

The Plant Cell Papers

- Systems-level analysis of nitrogen starvation–induced modifications of carbon metabolism in a *Chlamydomonas reinhardtii* starchless mutant
- Metabolic fluxes in an illuminated Arabidopsis rosette
- Metabolism and growth in Arabidopsis depend on the daytime temperature but are temperature-compensated against cool nights
- Malate plays a crucial role in starch metabolism, ripening, and soluble solid content of tomato fruit and affects postharvest softening
- Network analysis of enzyme activities and metabolite levels and their relationship to biomass in a large panel of Arabidopsis accessions

Plant Physiology Papers

- Feedback inhibition of starch degradation in Arabidopsis leaves mediated by Trehalose 6-phosphate
- Diurnal changes of polysome loading track sucrose content in the rosette of wild-type Arabidopsis and the starchless pgm mutant
- Impact of the carbon and nitrogen supply on relationships and connectivity between metabolism and biomass in a broad panel of Arabidopsis accessions
- On the discordance of metabolomics with proteomics and transcriptomics: coping with increasing complexity in logic, chemistry, and network interactions scientific correspondence
- Tomato fruit photosynthesis is seemingly unimportant in primary metabolism and ripening but plays a considerable role in seed development

continued on next page

BACK TO CONTENTS

Mark Stitt *continued from page 60*

- Identification of enzyme activity quantitative trait loci in a *Solanum lycopersicum* × *Solanum pennellii* introgression line population
- Fine quantitative trait loci mapping of carbon and nitrogen metabolism enzyme activities and seedling biomass in the maize IBM mapping population
- Arabidopsis plants acclimate to water deficit at low cost through changes of carbon usage: an integrated perspective using growth, metabolite, enzyme, and gene expression analysis
- Increased leaf size: different means to an end
- Robin: an intuitive wizard application for R-Based expression microarray quality assessment and analysis
- Enzyme activity profiles during fruit development in tomato cultivars and Solanum pennellii
- Multilevel analysis of primary metabolism provides new insights into the role of potassium nutrition for glycolysis and nitrogen assimilation in Arabidopsis roots

BACK TO CONTENTS

Ronan Sulpice

The Plant Cell, Plant Physiology

Ronan Sulpice has been a lecturer in the School of Natural Sciences at NUI Galway (Ireland) since 2012 and is head of the Plant Systems Biology lab, a member of the Plant & AgriBiosciences Research Centre and the Ryan Institute. After obtaining his PhD in Rennes (France) at the end of 2000, he spent two years as a postdoctoral fellow at the National Institute for Basic Biology (Okazaki, Japan), then moved to TU Munich before joining the Max Planck Institute of Plant Molecular Physiology (Potsdam, Germany) in 2004.

Ronan is interested in elucidating how photosynthetic organisms respond and adapt to their environment, especially at the metabolic level, and how the costs of adapting to a changing environment might feedback on the growth and performance of the organism. In order to identify the specific and ubiquitous mechanisms potentially involved, a broad range of photosynthetic organisms are investigated, from Cyanobacteria and micro- and macro-algae up to higher plants of agricultural interest.

The Plant Cell Papers

- Metabolism and growth in Arabidopsis depend on the daytime temperature but are temperature-compensated against cool nights
- Network analysis of enzyme activities and metabolite levels and their relationship to biomass in a large panel of Arabidopsis accessions

Plant Physiology Papers

- Diurnal changes of polysome loading track sucrose content in the rosette of wild-type Arabidopsis and the starchless pgm mutant
- Impact of the carbon and nitrogen supply on relationships and connectivity between metabolism and biomass in a broad panel of arabidopsis accessions
- The influence of fruit load on the tomato pericarp metabolome in a Solanum chmielewskii introgression line population
- Arabidopsis plants acclimate to water deficit at low cost through changes of carbon usage: an integrated perspective using growth, metabolite, enzyme, and gene expression analysis
- Increased leaf size: different means to an end
- Metabolic networks: how to identify key components in the regulation of metabolism and growth
- Multilevel analysis of primary metabolism provides new insights into the role of potassium nutrition for glycolysis and nitrogen assimilation in Arabidopsis roots

BACK TO CONTENTS

Takayuki Tohge

The Plant Cell, Plant Physiology

Takayuki Tohge is a research project leader at the Max Planck Institute of Molecular Plant Physiology, Golm, Germany. He received a BSc and an MSc in pharmaceutical science from Kanazawa University and a PhD from Chiba University. After completing his PhD, he participated in establishing the plant metabolomics research group at the RIKEN Institute in Japan for two years and then later joined the Max Planck Institute of Molecular Plant Physiology. From 2008 to 2010, he held an Alexander von Humboldt Fellowship. He was a Thomson Reuters highly cited researcher from 2002 to 2012.

Takayuki's research focuses on elucidation of genes involved in plant secondary metabolism, especially phenylpropanoids in Arabidopsis, tomato, tobacco, maize, and rice in order to enable biosynthesis-based cross-species comparison for understanding chemical diversity in plant secondary metabolism.

The Plant Cell Papers

- Arabidopsis BPM Proteins function as substrate adaptors to a CULLIN3-Based E3 Ligase to affect fatty acid metabolism in plants
- Metabolic fluxes in an illuminated Arabidopsis rosette
- Antisense inhibition of the 2-Oxoglutarate Dehydrogenase Complex in tomato demonstrates its importance for plant respiration and during leaf senescence and fruit maturation
- JUNGBRUNNEN1, a reactive oxygen species–Responsive NAC Transcription Factor, regulates longevity in Arabidopsis
- Tissue- and cell-type specific transcriptome profiling of expanding tomato fruit provides insights into metabolic and regulatory specialization and cuticle formation
- Identification of genes in the phenylalanine metabolic pathway by ectopic expression of a MYB transcription factor in tomato fruit
- PlaNet: Combined sequence and expression comparisons across plant networks derived from seven species
- Antisense inhibition of the Iron-Sulphur Subunit of Succinate Dehydrogenase enhances photosynthesis and growth in tomato via an organic acid–mediated effect on stomatal aperture
- Identification of the 2-Hydroxyglutarate and Isovaleryl-CoA Dehydrogenases as alternative electron donors linking lysine catabolism to the electron transport chain of Arabidopsis mitochondria
- Members of the LBD family of transcription factors repress anthocyanin synthesis and affect additional nitrogen responses in Arabidopsis

continued on next page

BACK TO CONTENTS

Takayuki Tohge *continued from page 63*

Plant Physiology Papers

- Conserved changes in the dynamics of metabolic processes during fruit development and ripening across species
- DELLA-interacting SWI3C core subunit of switch/sucrose nonfermenting chromatin remodeling complex modulates gibberellin responses and hormonal cross talk in Arabidopsis
- Comprehensive dissection of spatiotemporal metabolic shifts in primary, secondary, and lipid metabolism during developmental senescence in Arabidopsis
- Tomato fruit photosynthesis is seemingly unimportant in primary metabolism and ripening but plays a considerable role in seed development
- Toward the storage metabolome: Profiling the barley vacuole
- Analysis of a Range of Catabolic Mutants Provides Evidence That Phytanoyl-Coenzyme A Does Not Act as a Substrate of the Electron-Transfer Flavoprotein/Electron-Transfer Flavoprotein:Ubiquinone Oxidoreductase Complex in Arabidopsis during Dark-Induced Senescence
- Systems biology of tomato fruit development: combined transcript, protein, and metabolite analysis of tomato transcription factor (nor, rin) and ethylene receptor (Nr) mutants reveals novel regulatory interactions
- Characterization of the branched-chain amino acid aminotransferase enzyme family in tomato

BACK TO CONTENTS

Bart P.H.J. Thomma

The Plant Cell, Plant Physiology

Bart Thomma earned his doctorate in 2000 from the Katholieke Universiteit Leuven in Belgium and is currently professor and head of department at the Laboratory of Phytopathology of Wageningen University.

Bart's areas of expertise are microbiology, mycology, plant diseases, plant pathogenic fungi, and plant and crop protection, with emphasis on fungal plant pathogens and vascular wilt diseases caused by *Verticillium* spp. Additionally, he is a board member of The Royal Netherlands Society of Plant Pathology (KNPV), senior editor *Molecular Plant Pathology*, associate editor *PLoS Pathogens*, associate editor *Molecular Plant–Microbe Interactions*, and editor *FEMS Microbiology Reviews*.

The Plant Cell Papers

- Effector-mediated suppression of chitin-triggered immunity by *Magnaporthe oryzae* is necessary for rice blast disease
- Of PAMPs and effectors: the blurred PTI-ETI dichotomy

Plant Physiology Papers

- Endoplasmic reticulum-quality control chaperones facilitate the biogenesis of Cf receptor-like proteins involved in pathogen resistance of tomato
- Interfamily transfer of tomato Ve1 mediates *Verticillium* resistance in Arabidopsis
- Analysis of two in planta expressed LysM effector homologs from the fungus *Mycosphaerella graminicola* reveals novel functional properties and varying contributions to virulence on wheat
- Differential tomato transcriptomic responses induced by pepino mosaic virus isolates with differential aggressiveness
- Functional analyses of the CLAVATA2-like proteins and their domains that contribute to CLAVATA2 specificity
- Genetic dissection of *Verticillium* wilt resistance mediated by Tomato Ve1

BACK TO CONTENTS

Björn Usadel

The Plant Cell, Plant Physiology

Björn Usadel studied biochemistry in Berlin and New York. He went on to pursue a PhD at the Max Planck Institute of Molecular Plant Physiology and Potsdam University with Markus Pauly. Afterward he worked with Mark Stitt on carbon metabolism, high throughput data analysis, and omics data visualization. Today Björn is a professor at RWTH Aachen University and a director at "Forschungszentrum Jülich."

His main areas of interest include carbon metabolism, plant seed mucilage and cell walls, big data and databases, data visualization, and bridging high throughput omics data to phenotyping efforts. He provides several tools such as MapMan, RobiNA, Mercator, and trimmomatic to the community.

The Plant Cell Papers

- Evolution of a complex locus for terpene biosynthesis in Solanum
- Antisense inhibition of the 2-Oxoglutarate dehydrogenase complex in tomato demonstrates its importance for plant respiration and during leaf senescence and fruit maturation
- The interconversion of UDP-Arabinopyranose and UDP-Arabinofuranose is indispensable for plant development in Arabidopsis
- PlaNet: Combined sequence and expression comparisons across plant networks derived from seven species
- Antisense inhibition of the iron-sulphur subunit of succinate dehydrogenase enhances photosynthesis and growth in tomato via an organic acid–mediated effect on stomatal aperture
- Network analysis of enzyme activities and metabolite levels and their relationship to biomass in a large panel of Arabidopsis accessions
- An *Orange Ripening* mutant links plastid NAD(P)H dehydrogenase complex activity to central and specialized metabolism during tomato fruit maturation
- Regulatory features underlying pollination-dependent and -independent tomato fruit set revealed by transcript and primary metabolite profiling

Plant Physiology Papers

- Diurnal changes of polysome loading track sucrose content in the rosette of wild-type Arabidopsis and the Starchless *pgm* Mutant
- Demethylesterification of cell wall pectins in arabidopsis plays a role in seed germination
- Identification of enzyme activity quantitative trait loci in a *Solanum lycopersicum* × *Solanum pennellii* introgression line population

continued on next page

BACK TO CONTENTS

Björn Usadel *continued from page 66*

- Systems biology of tomato fruit development: combined transcript, protein, and metabolite analysis of tomato transcription factor (*nor, rin*) and ethylene receptor (*Nr*) mutants reveals novel regulatory interactions
- Assembly of an interactive correlation network for the arabidopsis genome using a novel heuristic clustering algorithm
- RNA interference of LIN5 in tomato confirms its role in controlling brix content, uncovers the influence of sugars on the levels of fruit hormones, and demonstrates the importance of sucrose cleavage for normal fruit development and fertility
- Mapping metabolic and transcript temporal switches during germination in rice highlights specific transcription factors and the role of RNA instability in the germination process

BACK TO CONTENTS

Detlef Weigel

The Plant Cell, Plant Physiology

Detlef Weigel was introduced to plant genetics during his postdoctoral work with Elliot Meyerowitz at Caltech. After nine years on the faculty of the Salk Institute for Biological Studies, La Jolla, California, he moved to the Max Planck Institute for Developmental Biology, Germany, where he is director of the Department of Molecular Biology. His lab is studying questions at the interface of plant biology, developmental genetics, and evolutionary genomics.

Detlef has been the recipient of many honors, including ASPB's Charles Albert Shull Award (2001), the Gottfried Wilhelm Leibniz Prize of the Deutsche Forschungsgemeinschaft (2007), and the Otto Bayer Award (2010). He is a member of the U.S. and German National Academies of Sciences, the Royal Society of London, and the European Molecular Biology Organization, where he currently serves as chair of council. He was a coeditor of *The Plant Cell* from 1996 to 2005.

The Plant Cell Papers

- Prediction of regulatory interactions from genome sequences using a biophysical model for the Arabidopsis LEAFY transcription factor
- Negative regulation of anthocyanin biosynthesis in Arabidopsis by a miR156-targeted SPL transcription factor
- The role of the Arabidopsis morning loop components CCA1, LHY, PRR7, and PRR9 in temperature compensation
- MicroRNA gene evolution in Arabidopsis lyrata and *Arabidopsis thaliana*
- The *NGATHA* genes direct style development in the Arabidopsis gynoecium

Plant Physiology Papers

- Tissue-specific silencing of Arabidopsis *SU(VAR)3-9 HOMOLOG8* by miR171a*
- Natural variation in arabidopsis: from molecular genetics to ecological genomics
- Genome-wide comparison of nucleotide-binding site-leucine-rich repeat-encoding genes in Arabidopsis
- Evolution of the *S*-Locus region in Arabidopsis relatives
- Increased leaf size: different means to an end
- Probing the reproducibility of leaf growth and molecular phenotypes: a comparison of three Arabidopsis accessions cultivated in ten laboratories
- AGRONOMICS1: A new resource for Arabidopsis transcriptome profiling

BACK TO CONTENTS

Markus Wirtz

The Plant Cell, Plant Physiology

Markus Wirtz is a group leader with the Centre for Organismal Studies, Ruprecht-Karls-Universität Heidelberg. His areas of expertise are the role of sulfur metabolism in oxidative stress defense and development, relevance of cysteine synthesis for glutathione turnover, subcellular compartmentalization of stress-responses, retrograde signaling, and post-translational modifications of sulfur metabolism related proteins.

The Plant Cell Papers

- Vacuolar Nicotianamine has critical and distinct roles under iron deficiency and for zinc sequestration in Arabidopsis
- Evidence for a SAL1-PAP chloroplast retrograde pathway that functions in drought and high light signaling in Arabidopsis
- Sulfite reductase defines a newly discovered bottleneck for assimilatory sulfate reduction and is essential for growth and development in *Arabidopsis thaliana*
- Dynamic plastid redox signals integrate gene expression and metabolism to induce distinct metabolic states in photosynthetic acclimation in Arabidopsis
- Disruption of adenosine-5´-phosphosulfate kinase in Arabidopsis reduces levels of sulfated secondary metabolites

Plant Physiology Papers

- Successful fertilization requires the presence of at least one major O-Acetylserine(thiol)lyase for cysteine synthesis in pollen of Arabidopsis
- Targeted systems biology profiling of tomato fruit reveals coordination of the yang cycle and a distinct regulation of ethylene biosynthesis during postclimacteric ripening
- Recycling of methylthioadenosine is essential for normal vascular development and reproduction in Arabidopsis
- The seed composition of Arabidopsis mutants for the group 3 sulfate transporters indicates a role in sulfate translocation within developing seeds
- The analysis of Arabidopsis nicotianamine synthase mutants reveals functions for nicotianamine in seed iron loading and iron deficiency responses

BACK TO CONTENTS

Asaph Aharoni

Plant Physiology, The Plant Cell

Asaph Aharoni is an associate professor in the Department of Plant and Environmental Sciences of the Weizmann Institute of Science in Israel. He earned his MSC at the Hebrew University of Jerusalem and his PhD from Wageningen University, Netherlands.

Asaph's research interests center on uncovering the molecular mechanisms underlying the biosynthesis and regulation of metabolic pathways in plants. His lab combines cutting-edge metabolomics with molecular genetics and computational biology to study secondary/specialized metabolism and its interface with primary metabolism in plant development and stress.

He has been the former chair of the Israel Society of Mass Spectrometry and a member of the Israel Analytical Chemistry Society's executive committee. Asaph serves as review editor for *The Plant Journal*. He has been the recipient of a number of awards, including The European Research Council (ERC) grant for starting independent investigators, the James Heineman Research Award for Biological and Biomedical Research, the Weizmann Institute Scientific Council Prize (Levinson Prize in Biology), and the Yigal Alon Fellowship award by the Council for Higher Education in Israel.

Plant Physiology Papers

- The Arabidopsis DCR encoding a soluble BAHD acyltransferase is required for cutin polyester formation and seed hydration properties

The Plant Cell Papers

- Orchestration of thiamin biosynthesis and central metabolism by combined action of the thiamin pyrophosphate riboswitch and the circadian clock in Arabidopsis
- GLYCOALKALOID METABOLISM1 is required for steroidal alkaloid glycosylation and prevention of phytotoxicity in tomato
- Tissue- and cell-type specific transcriptome profiling of expanding tomato fruit provides insights into metabolic and regulatory specialization and cuticle formation
- An orange ripening mutant links plastid NAD(P)H dehydrogenase complex activity to central and specialized metabolism during tomato fruit maturation

BACK TO CONTENTS

Synan AbuQamar

Plant Physiology, The Plant Cell

Having earned a PhD from the Department of Botany and Plant Pathology at Purdue University, Synan AbuQamar is now based at the United Arab Emirates University (UAEU), Department of Biology, as an associate professor in the area of plant molecular genetics and plant biotechnology. Synan's research focuses on functional genomics of plant defense responses to necrotrophic fungi and cross-talk between signal transduction pathways in response to biotic and abiotic stresses. He has authored a number of scientific articles and has recently been recognized by UAEU for his achievement in publication in the top 10% of journals in 2013.

Synan is an editorial member and expert reviewer for several reputable journals. He is also a member of the scientific board of Khalifa Center for Biotechnology and Genetic Engineering and serves on the technical committee of the Abu Dhabi Plant Genetic Resources Centre.

Plant Physiology Papers

- Polyamines attenuate ethylene-mediated defense responses to abrogate resistance to botrytis cinerea in tomato
- The Arabidopsis mitochondria-localized pentatricopeptide repeat protein PGN functions in defense against necrotrophic fungi and abiotic stress tolerance
- The Arabidopsis RESURRECTION1 Gene Regulates a Novel Antagonistic Interaction in Plant Defense to Biotrophs and Necrotrophs

The Plant Cell Papers

- HISTONE MONOUBIQUITINATION1 interacts with a subunit of the mediator complex and regulates defense against necrotrophic fungal pathogens in Arabidopsis

BACK TO CONTENTS

Idan Efroni

The Plant Cell

Idan Efroni has received his PhD from the Weizmann Institute in Israel in 2010. He then went on to work as a postdoctoral fellow at New York University using single-cell profiling to undercover the mechanisms of root regeneration. He is due to open his own independent lab at the Hebrew University in early 2016.

Idan is interested in understanding the principles of plant developmental plasticity at the cellular and organismal level. He also develops tools for the construction of synthetic and designer promoters. A programmer at heart, he works at the intersection of bioinformatics, Arabidopsis and tomatoes.

The Plant Cell Papers

- The Arabidopsis O-linked N-acetylglucosamine transferase SPINDLY interacts with class I TCPs to facilitate cytokinin responses in leaves and flowers
- Differentiating Arabidopsis shoots from leaves by combined YABBY activities
- Morphogenesis of simple and compound leaves: a critical review
- The NGATHA distal organ development genes are essential for style specification in Arabidopsis

BACK TO CONTENTS

Yuval Eshed

Plant Physiology, The Plant Cell

Yuval Eshed received his BSc in horticulture (1989) and was awarded a PhD from the Hebrew University's Faculty of Agriculture in 1996. From 1996 to 2001, he worked as a postdoctoral fellow at the University of California, Davis. In 2001, he returned to Israel and joined the Weizmann Institute. Yuval's research team addresses variations in the architecture of shoots of the model plants *Arabidopsis thaliana* and tomato. Because plant architecture is critical for optimal productivity, their findings may offer new means by which to optimize shoot organization, thereby improving plant growth and productivity. The team has focused on plant meristems, examining how external cues or internal conditions lead to a developmental change in the SAM behavior. The group studies the impact of systemic growth hormones, florigen, auxin, and cytokinin on the shoot apical meristem and on the materialization of cryptic potentials — for example, the formation of tubers by tomato buds. Today, the group focuses on the way side shoots respond to specific signals in a different way from the main shoot.

Plant Physiology Papers

- Flexible tools for gene expression and silencing in tomato

The Plant Cell Papers

- Failure of the Tomato trans-acting short interfering RNA program to regulate AUXIN RESPONSE FACTOR3 and ARF4 underlies the wiry leaf syndrome
- The Arabidopsis O-Linked N-Acetylglucosamine transferase SPINDLY interacts with Class I TCPs to facilitate cytokinin responses in leaves and flowers
- Differentiating Arabidopsis shoots from leaves by combined YABBY activities
- The NGATHA distal organ development genes are essential for style specification in Arabidopsis

BACK TO CONTENTS

Menachem Moshelion

Plant Physiology

Menachem Moshelion completed his PhD at the Hebrew University of Jerusalem in 2001, after which he undertook postdoctorate studies in Louvain-la-Neuve, Belgium. In 2004, he returned to the Hebrew University of Jerusalem to become a lecturer in the Institute of Plant Sciences and Genetics in Agriculture. He is currently an associate professor at the Faculty of Agriculture of the Hebrew University of Jerusalem and runs a laboratory focusing on molecular mechanisms controlling whole plant–water relations.

Plant Physiology Papers

- The role of tobacco Aquaporin1 in improving water use efficiency, hydraulic conductivity, and yield production under salt stress
- The pitfalls of transgenic selection and new roles of AtHXK1: a high level of AtHXK1 expression uncouples hexokinase1-dependent sugar signaling from exogenous sugar

BACK TO CONTENTS

Naomi Ori

Plant Physiology, The Plant Cell

Naomi Ori is currently associate professor of plant sciences at The Robert H. Smith Institute of Plant Sciences and Genetics in Agriculture, at the Faculty of Agriculture, Food and Environment of the Hebrew University, Rehovot, Israel, a position which she has held since 2011. Her main research interest is in plant developmental genetics, and she is currently involved in research projects on compound leaf development and the role of hormones in leaf development.

Plant Physiology Papers

- Release of apical dominance in potato tuber is accompanied by programmed cell death in the apical bud meristem
- Differential effects of prenylation and S-Acylation on Type I and II ROPS membrane interaction and function

The Plant Cell Papers

- A role for APETALA1/FRUITFULL transcription factors in tomato leaf development
- Programmed cell death occurs asymmetrically during abscission in tomato
- Cytokinin regulates compound leaf development in tomato
- Stage-specific regulation of Solanum lycopersicum leaf maturation by Class 1 KNOTTED1-LIKE HOMEOBOX proteins

BACK TO CONTENTS

Nir Sade

Plant Physiology

Nir Sade received his BSc (cum laude), MSc (summa cum laude) and PhD degrees from the Department of Plant Genetics, The Hebrew University of Jerusalem (adviser Dr. Menachem Moshelion). His research areas of interest are plant water channels (AQP) and their effect on abiotic and biotic stress resistance. During work on his PhD, he received several awards for his plant physiology research. He is currently a postdoc at the Plant Science Department at the University of Davis, California, in Professor Eduardo Blumwald's lab.

Plant Physiology Papers

- The role of Tobacco Aquaporin1 in improving water use efficiency, hydraulic conductivity, and yield production under salt stress

BACK TO CONTENTS

Alexander Vainstein

Plant Physiology, The Plant Cell

Prof. Alexander Vainstein was born in Tbilisi, Georgia. He immigrated to Israel at the age of 20, a few months before receiving his MSc degree in physics. In Israel, he shifted disciplines and received his PhD in biology from the Hebrew University of Jerusalem. His postdoctoral studies at UCLA led to an interest in plant molecular biology, eventually resulting in his current professorial tenure at the Hebrew University's Robert H. Smith Faculty of Agriculture, Food and Environment.

Alexander is the incumbent of the Wolfson Family Chair in Floriculture and served as a visiting professor at USDA and SUNY. He has published more than 130 scientific papers and books, developed six patents, and has served as head of the Hebrew University Graduate Horticulture Program, Graduate Plant Sciences Program, and Graduate Biotechnology Program; head of The Institute of Plant Sciences and Genetics in Agriculture, Hebrew University of Jerusalem; and president of the Israeli Society of Plant Sciences.

Plant Physiology Papers

- Nontransgenic genome modification in plant cells

The Plant Cell Papers

- The R2R3-MYB–like regulatory factor EOBI, acting downstream of EOBII, regulates scent production by activating ODO1 and Structural scent-related genes in petunia
- EOBII, a gene encoding a flower-specific regulator of phenylpropanoid volatiles' biosynthesis in petunia

BACK TO CONTENTS

Julia Bailey-Serres

The Plant Cell, Plant Physiology

Julia Bailey-Serres is professor of genetics, director of the Center for Plant Cell Biology, and a member of the Institute for Integrative Genome Biology at the University of California, Riverside. She earned her PhD from the University of Edinburgh. Her accomplishments include the pioneering of methods for profiling the "translatomes" of discrete cell types of plants and identification of a homeostatic sensor of oxygen deprivation in plants. Her team's research at UCR has deciphered the functions of SUB1A, the transcription factor that allows rice to survive complete submergence under water, which scientists at the International Rice Research Institute (IRRI) used to create the now widely grown flood-tolerant rice variety Swarna-Sub1.

Currently, she and her researchers are investigating the molecular and physiological processes that enable plants to tolerate or survive stresses such as flooding or drought. In 2010, Julia became a fellow of the American Society of Plant Biologists, and in 2011, she was elected secretary.

The Plant Cell Papers

- Two Rumex species from contrasting hydrological niches regulate flooding tolerance through distinct mechanisms
- The submergence tolerance regulator SUB1A mediates crosstalk between submergence and drought tolerance in rice

Plant Physiology Papers

- Characteristics and significance of intergenic polyadenylated RNA transcription in Arabidopsis
- The submergence tolerance Gene *SUB1A* delays leaf senescence under prolonged darkness through hormonal regulation in rice
- Posttranscriptional control of photosynthetic mRNA decay under stress conditions requires 3' and 5' untranslated regions and correlates with differential polysome association in rice
- Cross-kingdom comparison of transcriptomic adjustments to low-oxygen stress highlights conserved and plant-specific responses
- The submergence tolerance regulator *Sub1A* mediates stress-responsive expression of *AP2/ERF* transcription factors

BACK TO CONTENTS

Philip Benfey

The Plant Cell

Philip Benfey is an HHMI Investigator and the Paul Kramer Professor of Biology at Duke University. His research focuses on plant developmental genetics and genomics. Philip is a fellow of the American Association for the Advancement of Science and a member of the U.S. National Academy of Sciences. He received his PhD from Harvard University and a DEUG (Diplome d'Etudes Universitaire Generale) from the University of Paris. He cofounded a spin-off company, GrassRoots Biotechnology, which was sold to a large multinational. He now leads a new company, Hi Fidelity Genetics, which applies sophisticated data analytics to plant breeding.

Papers

- The bHLH transcription factor POPEYE regulates response to iron deficiency in Arabidopsis roots
- An auxin gradient and maximum in the Arabidopsis root apex shown by high-resolution cell-specific analysis of IAA distribution and synthesis

BACK TO CONTENTS

Ray Bressan

The Plant Cell, Plant Physiology

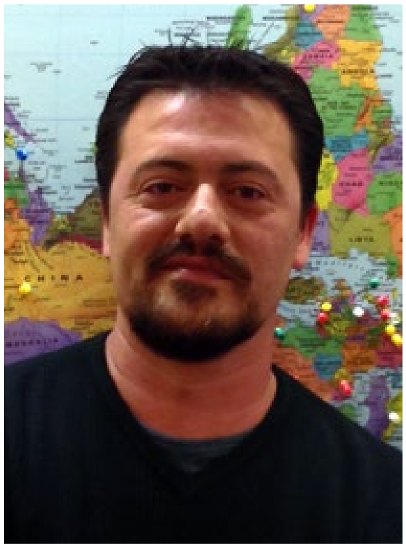
Ray Bressan is distinguished professor, College of Agriculture Purdue University. He earned his PhD in plant physiology from Colorado State University. He holds an Alumni Achievement Award from Illinois State University and the Herbert Newby McCoy Award (1995) from Purdue. His area of expertise is molecular genetics. Ray has used various genetic approaches to identify genes involved in adaptations to stresses and has extensively used insertion mutagenesis and other techniques to determine important genetic components of adaptation.

The Plant Cell Papers

- A Vacuolar β-Glucosidase Homolog that possesses glucose-conjugated abscisic acid hydrolyzing activity plays an important role in osmotic stress responses in Arabidopsis
- Auxin-mediated ribosomal biogenesis regulates vacuolar trafficking in Arabidopsis

Plant Physiology Papers

- CYCLIN H;1 regulates drought stress responses and blue light-induced stomatal opening by inhibiting reactive oxygen species accumulation in Arabidopsis
- Regulation of *miR399f* Transcription by AtMYB2 affects phosphate starvation responses in Arabidopsis
- Arabidopsis *ECERIFERUM9* involvement in cuticle formation and maintenance of plant water status
- TsHKT1;2, a HKT1 homolog from the extremophile Arabidopsis relative *Thellungiella salsuginea*, shows K^+ specificity in the presence of NaCl
- The *glossyhead1* Allele of *ACC1* reveals a principal role for multidomain acetyl-coenzyme a carboxylase in the biosynthesis of cuticular waxes by Arabidopsis
- Genome structures and halophyte-specific gene expression of the extremophile *Thellungiella parvula* in comparison with *Thellungiella salsuginea* (*Thellungiella halophila*) and Arabidopsis
- Specific domain structures control abscisic acid-, salicylic acid-, and stress-mediated SIZ1 phenotypes
- Loss of halophytism by interference with SOS1 expression
- The Arabidopsis *RESURRECTION1* gene regulates a novel antagonistic interaction in plant defense to biotrophs and necrotrophs



BACK TO CONTENTS

David Casero

The Plant Cell, Plant Physiology

David Casero is an assistant researcher in the Department of Pathology and Laboratory Medicine, UCLA. He earned his BS in theoretical physics and PhD in applied mathematics at Complutense University in Spain.

David conducted postdoctoral research in Matteo Pellegrini's group (UCLA). His research was to exploit the then-emerging next generation sequencing (NGS) technologies to define the transcriptional landscape of the model *Chlamydomonas reinhardtii* and other algal organisms. Built upon a synergistic collaboration with Sabeeha Merchant, he played a central role in a large-scale community effort for the application and analysis of NGS data in systems biology of algae.

He is now actively working on the analysis of sequencing data for the annotation and characterization of different families of RNAs, with a focus on non-coding RNAs and their relevance in plant, tumor, and stem cell biology.

The Plant Cell Papers

- Systems-level analysis of nitrogen starvation-induced modifications of carbon metabolism in a *Chlamydomonas reinhardtii* starchless mutant
- COPPER RESPONSE REGULATOR1-Dependent and -Independent responses of the *Chlamydomonas reinhardtii* transcriptome to dark anoxia
- Systems and *trans*-system level analysis identifies conserved iron deficiency responses in the plant lineage
- Activation of the carbon concentrating mechanism by CO2 deprivation coincides with massive transcriptional restructuring in *Chlamydomonas reinhardtii*
- Transcriptome-wide changes in *Chlamydomonas reinhardtii* gene expression regulated by carbon dioxide and the CO_2-concentrating mechanism regulator *CIA5/CCM1*
- Transcriptome sequencing identifies SPL7-regulated copper acquisition genes *FRO4/FRO5* and the copper dependence of iron homeostasis in Arabidopsis
- Systems biology approach in *Chlamydomonas* reveals connections between copper nutrition and multiple metabolic steps
- RNA-seq analysis of sulfur-deprived *Chlamydomonas* cells reveals aspects of acclimation critical for cell survival

BACK TO CONTENTS

Zhixiang Chen

The Plant Cell, Plant Physiology

Zhixiang Chen was recently recognized by Thomson Reuters as one of the world's most influential scientific minds in 2014. He earned his MS in plant genetics and breeding from Cornell University and his PhD in biochemistry and molecular biology from the University of Nebraska–Lincoln in 1990. Currently, Zhixiang is a professor in the Department of Botany and Plant Pathology, Purdue University, and an adjunct professor with the College of Agriculture and Biotechnology at Zhejiang University in China.

His area of expertise is the molecular and cellular basis of plant responses to biotic and abiotic stresses. Earlier research in his laboratory focused on the role of salicylic acid, WRKY transcription factors, and RNA silencing in signal transduction and regulation of gene expression during plant defense against microbial pathogens. More recent research has expanded to the role of vesicle trafficking, including autophagy and multivesicular bodies in broad plant stress responses.

The Plant Cell Papers

- Arabidopsis sigma factor binding proteins are activators of the WRKY33 transcription factor in plant defense
- *cis*- and *trans*-regulation of miR163 and target genes confers natural variation of secondary metabolites in two Arabidopsis species and their Allopolyploids
- Phosphorylation of a WRKY transcription factor by two pathogen-responsive MAPKs drives phytoalexin biosynthesis in Arabidopsis

Plant Physiology Papers

- Structural and functional analysis of VQ motif-containing proteins in Arabidopsis as interacting proteins of WRKY transcription factors
- Functional analysis of the Arabidopsis *PAL* gene family in plant growth, development, and response to environmental stress
- Apyrase (nucleoside triphosphate-diphosphohydrolase) and extracellular nucleotides regulate cotton fiber elongation in cultured ovules
- Reactive oxygen species are involved in brassinosteroid-induced stress tolerance in cucumber

BACK TO CONTENTS

Jerry Cohen

The Plant Cell, Plant Physiology

Jerry Cohen is distinguished graduate teaching professor and holds the Bailey Endowed Chair in the Department of Horticultural Science and is a member of the Microbial and Plant Genomics Institute, University of Minnesota. Jerry received his BS in microbiology from the University of California, Riverside, his MS in plant physiology from San Diego State University, and his PhD in plant biochemistry from Michigan State University (1979). He has been a fellow of ASPB since 2008 and is past president of the International Plant Growth Substances Association.

While his lab is probably best known for studies of auxin metabolism, its current research aims to understand the basic biology of plant growth, signaling systems that regulate growth and development, and plant responses to biological and physical stresses. The group focuses on the application of modern biochemical analysis supplemented by metabolomics and proteomic systems biology approaches to look at complex biological processes.

The Plant Cell Papers

- Multiple facets of Arabidopsis seedling development require indole-3-butyric acid–derived auxin
- *vanishing tassel2* encodes a grass-specific tryptophan aminotransferase required for vegetative and reproductive development in maize
- *Arabidopsis ASA1* is important for jasmonate-mediated regulation of auxin biosynthesis and transport during lateral root formation

Plant Physiology Papers

- ROOT ULTRAVIOLET B-SENSITIVE1/WEAK AUXIN RESPONSE3 is essential for polar auxin transport in Arabidopsis
- Transport of indole-3-butyric acid and indole-3-acetic acid in Arabidopsis hypocotyls using stable isotope labeling
- Low-Fluence red light increases the transport and biosynthesis of auxin
- Conversion of endogenous indole-3-butyric acid to indole-3-acetic acid drives cell expansion in Arabidopsis seedlings
- Arabidopsis *IAR4* modulates auxin response by regulating auxin homeostasis

BACK TO CONTENTS

Richard Dixon

The Plant Cell, Plant Physiology

Richard Dixon, distinguished research professor, University of North Texas, earned his M.A. in biochemistry, PhD in botany, and a doctor of science from the University of Oxford. He is a member of the U.S. National Academy of Sciences and a fellow of the National Academy of Inventors and the American Association for the Advancement of Science, and he has been named by the Institute for Scientific Information (ISI) as one of the most highly cited authors in plant and animal science. He serves on the editorial boards of five international journals.

His research interests center on the biochemistry, molecular biology, and metabolic engineering of plant natural product pathways and their implications for agriculture and human health, and the engineering of lignocellulosic biomass for the improvement of forage and bioenergy feedstocks. Rick will serve the Society as president in 2015–2016.

The Plant Cell Papers

- A genomics approach to deciphering lignin biosynthesis in switchgrass
- *LACCASE* is necessary and nonredundant with *PEROXIDASE* for lignin polymerization during vascular development in Arabidopsis
- Coexistence but independent biosynthesis of catechyl and guaiacyl/syringyl lignin polymers in seed coats
- MATE2 mediates vacuolar sequestration of flavonoid glycosides and glycoside malonates in *Medicago truncatula*
- Genomic and coexpression analyses predict multiple genes involved in triterpene saponin biosynthesis in *Medicago truncatula*
- MATE transporters facilitate vacuolar uptake of Epicatechin 3'-*O*-Glucoside for proanthocyanidin biosynthesis in *Medicago truncatula* and Arabidopsis

Plant Physiology Papers

- Functional characterization of proanthocyanidin pathway enzymes from tea and their application for metabolic engineering
- Characterization of an isoflavonoid-specific prenyltransferase from *Lupinus albus*
- TrichOME: A comparative omics database for plant trichomes
- Integrated metabolite and transcript profiling identify a biosynthetic mechanism for hispidol in *Medicago truncatula* cell cultures
- A WD40 repeat protein from *Medicago truncatula* is necessary for tissue-specific anthocyanin and proanthocyanidin biosynthesis but not for trichome development
- Divergent regulation of terpenoid metabolism in the trichomes of wild and cultivated tomato species

BACK TO CONTENTS

Axel Elling

The Plant Cell

Axel Elling is a plant nematologist at Bayer CropScience. The team he oversees integrates cutting-edge molecular biology, biochemistry, and genomics tools to strategically address fundamental challenges posed by economically relevant plant-parasitic nematodes. Axel held a faculty position in the Department of Plant Pathology at Washington State University. He obtained his doctorate at Iowa State University under the guidance of Thomas Baum and completed his postdoctoral training with Xing Wang Deng at Yale University.

He is an editor for the *Journal of Nematology*, executive board member of the Society of Nematologists, and councilor for the International Federation of Nematology Societies. He recently completed terms as associate editor for *Phytopathology* and *Plant Disease*.

Axel holds a patent on transgenic potato lines with RNA interference-mediated resistance against root-knot nematodes and received the Schroth Faces of the Future in Nematology Award from the American Phytopathological Society.

Papers

- Global epigenetic and transcriptional trends among two rice subspecies and their reciprocal hybrids
- Dynamic landscapes of four histone modifications during deetiolation in Arabidopsis
- Genome-wide and organ-specific landscapes of epigenetic modifications and their relationships to mRNA and small RNA transcriptomes in maize

BACK TO CONTENTS

Takeshi Fukao

The Plant Cell, Plant Physiology

Takeshi Fukao is currently assistant professor in the Department of Crop and Soil Environmental Sciences at Virginia Tech. Takeshi earned his BS in plant breeding from Kyoto Prefectural University, his MS in agronomy and horticultural sciences from Kyoto University, and his PhD in molecular and environmental plant sciences from Texas A&M University (2002). Prior to his position at Virginia Tech, Takeshi was a postdoctoral researcher and assistant specialist in the Department of Botany and Plant Sciences at the University of California, Riverside.

His laboratory at Virginia Tech focuses on elucidation of the regulatory mechanisms underlying response and tolerance to submergence, drought, and nutrient deficiency in rice, soybean, and wheat, aiding in the improvement of stress tolerance in the major crop species.

The Plant Cell Papers

- The Submergence Tolerance Regulator SUB1A Mediates Crosstalk between Submergence and Drought Tolerance in Rice

Plant Physiology Papers

- The submergence tolerance Gene *SUB1A* delays leaf senescence under prolonged darkness through hormonal regulation in rice
- Cross-Kingdom comparison of transcriptomic adjustments to low-oxygen stress highlights conserved and plant-specific responses
- The submergence tolerance regulator *Sub1A* mediates stress-responsive expression of *AP2/ERF* transcription factors

BACK TO CONTENTS

Sheng Yang He

The Plant Cell, Plant Physiology

Sheng Yang He grew up in rural China and obtained a BS in in plant protection from Zhejiang University and a PhD in plant pathology from Cornell University. Today, he is a Howard Hughes Medical Institute–Gordon and Betty Moore Foundation investigator. He is also a university distinguished professor of plant biology at Michigan State University. In 2011, Sheng Yang was selected as a AAAS Fellow, and in 2014, he was recognized as a Thomson Reuters Highly Cited Researcher in plant and animal science.

Sheng Yang is currently studying the molecular interplay between microbial pathogenesis and host immunity, with a focus on understanding how pathogens employ the type III secretion system and toxins to manipulate plant cellular functions, such as innate immunity, vesicle traffic, jasmonate signaling, and stomatal closure, to induce disease susceptibility. One new line of research is aimed at thwarting critical pathogen virulence factors to inhibit disease development.

The Plant Cell Papers

- Mitogen-Activated protein kinases 3 and 6 are required for full priming of stress responses in *Arabidopsis thaliana*

Plant Physiology Papers

- Negative feedback control of jasmonate signaling by an alternative splice variant of JAZ10
- A critical role of *STAYGREEN*/Mendel's *I* Locus in controlling disease symptom development during *Pseudomonas syringae* pv *tomato* infection of Arabidopsis
- A prominent role of the flagellin feceptor FLAGELLIN-SENSING2 in mediating stomatal response to *Pseudomonas syringae* pv *tomato* DC3000 in Arabidopsis
- Type III protein secretion in plant pathogenic bacteria
- Subcellular localization and functional analysis of the Arabidopsis GTPase RabE

BACK TO CONTENTS

Rossana Henriques

The Plant Cell

Rossana Henriques, is a career track fellow at the Centre for Research in Agricultural Genomics in Barcelona. She was recently awarded a Ramón y Cajal Tenure Track contract as well as a Career Integration Grant. She is interested in the circadian regulation of growth signaling pathways as well as the identification and characterization of circadian-regulated long non-coding RNAs. Rossana was a research associate and postdoctoral fellow at Rockefeller University's Laboratory of Plant Molecular Biology in New York, where she focused on posttranslational regulation within the light signaling pathway and the circadian clock. She also worked as postdoctoral fellow at Royal Holloway, University of London, on the signaling pathways connecting cell growth and cell division in Arabidopsis.

Rossana earned her MSc in biology from the Universidade de Coimbra and her PhD in molecular biology from the Universidade de Lisboa in collaboration with the Max Planck Institute for Plant Breeding Research in Cologne.

Papers

- Arabidopsis PHYTOCHROME INTERACTING FACTOR proteins promote phytochrome B polyubiquitination by COP1 E3 ligase in the nucleus
- PSEUDO-RESPONSE REGULATORS 9, 7, and 5 are transcriptional repressors in the Arabidopsis circadian clock
- F-Box proteins FKF1 and LKP2 act in concert with ZEITLUPE to control Arabidopsis clock progression
- FAR-RED ELONGATED HYPOCOTYL1 and FHY1-LIKE associate with the Arabidopsis transcription factors LAF1 and HFR1 to transmit phytochrome A signals for inhibition of hypocotyl elongation

BACK TO CONTENTS

Yidong Liu

The Plant Cell

Yidong Liu, senior research specialist, Department of Biochemistry, University of Missouri, Christopher S. Bond Life Sciences Center, earned her BS in biology from Nanjing University in China and her MS degree in plant biology from the University of Texas at Austin. Working as the lab manager in Dr. Shuqun Zhang's lab, her recent research has been focused on the functions of mitogen-activated protein kinase (MAPK) cascades in plant defense responses such as pathogen-induced ethylene biosynthesis and phytoalexin induction.

Papers

- Phosphorylation of an ERF transcription factor by Arabidopsis MPK3/MPK6 regulates plant defense gene induction and fungal resistance
- A MAPK cascade downstream of ERECTA receptor-like protein kinase regulates Arabidopsis inflorescence architecture by promoting localized cell proliferation
- Phosphorylation of a WRKY transcription factor by two pathogen-responsive MAPKs drives phytoalexin biosynthesis in Arabidopsis
- Ethylene-induced stabilization of ETHYLENE INSENSITIVE3 and EIN3-LIKE1 is mediated by proteasomal degradation of EIN3 binding F-Box 1 and 2 that requires EIN2 in Arabidopsis
- Mitogen-Activated Protein Kinases 3 and 6 are required for full priming of stress responses in *Arabidopsis thaliana*

BACK TO CONTENTS

Sabeeha Merchant

The Plant Cell, Plant Physiology

Sabeeha Merchant is professor of biochemistry and Director of the DOE–Institute for Genomics and Proteomics at the University of California, Los Angeles. She completed her bachelor's and PhD degrees at the University of Wisconsin–Madison and was a postdoctoral scholar at Harvard University.

She has conducted seminal research on the role of metals in regulating the biosynthesis and assembly of metalloproteins in photosynthetic eukaryotes, and she pioneered discoveries in the assembly of metalloenzymes and the regulated biogenesis of major complexes of the photosynthetic apparatus in green algae. At present the Merchant group uses a combination of classical genetics, genomics, and biochemistry to discover mechanisms of trace metal homeostasis in Chlamydomonas.

Sabeeha has earned a number of honors and awards including the NIH Research Career Development Award, ULCA Faculty Career Development Award, ASPB Charles Albert Shull Award, UCLA Herber Newby McCoy Award, NAS Gilbert Morgan Smith Medal, ASPB Charles F. Kettering Award, Humboldt Forschungspreis (Alexander von Humboldt Foundation), and Darbaker Prize from the Botanical Society of America. She is an external scientific member of the Max Planck Institute of Molecular Plant Physiology, Potsdam-Golm; a fellow of the Guggenheim Foundation, AAAS, and ASPB; and an elected member of the U.S. National Academy of Sciences and the American Academy of Arts and Sciences. She has been an editor of *Annual Review of Plant Biology* since 2005, and in 2015 became editor-in-chief of *The Plant Cell*.

The Plant Cell Papers

- Systems-Level analysis of nitrogen starvation–induced modifications of carbon metabolism in a *Chlamydomonas reinhardtii* starchless mutant
- COPPER RESPONSE REGULATOR1–Dependent and –Independent responses of the *Chlamydomonas reinhardtii* transcriptome to dark anoxia
- Systems and *Trans*-System level analysis identifies conserved iron deficiency responses in the plant lineage
- Fe sparing and Fe recycling contribute to increased superoxide dismutase capacity in iron-starved *Chlamydomonas reinhardtii*
- Transcriptome-Wide changes in *Chlamydomonas reinhardtii* gene expression regulated by carbon dioxide and the CO_2-concentrating mechanism regulator *CIA5/CCM1*
- Transcriptome sequencing identifies *SPL7*-regulated copper acquisition genes *FRO4/FRO5* and the copper dependence of iron homeostasis in Arabidopsis

continued on next page

BACK TO CONTENTS

Sabeeha Merchant *continued from page 90*

- Systems biology approach in *Chlamydomonas* reveals connections between copper nutrition and multiple metabolic steps
- The CRR1 nutritional copper sensor in *Chlamydomonas* contains two distinct metal-responsive domains
- RNA-Seq analysis of sulfur-deprived *Chlamydomonas* cells reveals aspects of acclimation critical for cell survival
- Two *Chlamydomonas* CTR copper transporters with a novel cys-met motif are localized to the plasma membrane and function in copper assimilation

Plant Physiology Papers

- The γ-Carbonic Anhydrase subcomplex of mitochondrial complex I is essential for development and important for photomorphogenesis of Arabidopsis

BACK TO CONTENTS

John Ohlrogge

The Plant Cell, Plant Physiology

John Ohlrogge's research has focused on fatty acid synthesis and lipid metabolic pathways. He has devoted his career toward research that could serve agriculture and societal needs. The talented members of his group have made discoveries critical to the understanding of lipid systems, including identification of mechanisms involved in the biochemical regulation of fatty acid synthesis; mapping the fluxes of carbon into seed oils; and deciphering the biosynthetic enzymes, genes, and pathways that build cutin and suberin lipid polymers. John has also coordinated the development of several community web databases focused on plant lipids.

He has served ASPB as both a monitoring editor and an associate editor of *Plant Physiology*. After postdoctoral training with Paul Stumpf at UC Davis, he spent seven years at the USDA before moving to Michigan State University, where he is now university distinguished professor in the Department of Plant Biology. In 2010, he received the Martin Gibbs Medal from ASPB.

The Plant Cell Papers

- Altered lipid composition and enhanced nutritional value of Arabidopsis leaves following introduction of an algal diacylglycerol acyltransferase 2
- *DGAT1* and *PDAT1* acyltransferases have overlapping functions in Arabidopsis triacylglycerol biosynthesis and are essential for normal pollen and seed development

Plant Physiology Papers

- Identification of a new class of lipid droplet-associated proteins in plants
- A land-plant-specific glycerol-3-phosphate acyltransferase family in Arabidopsis: substrate specificity, *sn*-2 preference, and evolution
- Identification of an Arabidopsis fatty alcohol:caffeoyl-coenzyme A acyltransferase required for the synthesis of alkyl hydroxycinnamates in root waxes
- Pleiotropic phenotypes of the *sticky peel* mutant provide new insight into the role of *CUTIN DEFICIENT2* in epidermal cell function in tomato
- Rapid kinetic labeling of Arabidopsis cell suspension cultures: implications for models of lipid export from plastids
- Identification of an Arabidopsis Feruloyl-Coenzyme A transferase required for suberin synthesis
- Turnover of fatty acids during natural senescence of Arabidopsis, *Brachypodium*, and switchgrass and in Arabidopsis β-Oxidation mutants
- Analysis of acyl fluxes through multiple pathways of triacylglycerol synthesis in developing soybean embryos

BACK TO CONTENTS

Eran Pichersky

The Plant Cell, Plant Physiology

Eran Pichersky is M. M. Martin Collegiate Professor at the University of Michigan. He earned his BSc with highest honors from the University of California, Berkeley. He received his PhD in genetics from the University of California, Davis, before undertaking postdoctoral work at Rockefeller University. He is a specialist in biochemistry and evolution of plant volatile metabolites.

His lab investigates the biochemical pathways involved in the production of plant volatiles, the enzymes that catalyze them, and the genes that encode these enzymes. Genetic engineering of plants with such genes could result in the introduction of new scents and flavors into various plant species.

Among other honors and awards, Eran received an Alexander von Humboldt Award for Senior U.S. Scientists and a Senior Fulbright Scholarship, both in 2000, and was elected a AAAS fellow in 2012.

The Plant Cell Papers

- Evolution of a complex locus for terpene biosynthesis in *Solanum*
- Contribution of CoA ligases to benzenoid biosynthesis in petunia flowers
- Emergent decarboxylase activity and attenuation of α/β-Hydrolase activity during the evolution of methylketone biosynthesis in tomato
- RNAi suppression of *Arogenate Dehydratase1* reveals that phenylalanine is synthesized predominantly via the arogenate pathway in petunia petals
- The small subunit of Snapdragon geranyl diphosphate synthase modifies the chain length specificity of tobacco geranylgeranyl diphosphate synthase in planta

Plant Physiology Papers

- Veratrole biosynthesis in white campion
- The tomato terpene synthase gene family
- Polymethylated myricetin in trichomes of the wild tomato species *Solanum habrochaites* and characterization of trichome-specific 3′/5′- and 7/4′-Myricetin *O*-Methyltransferases
- Comparative functional genomic analysis of *Solanum* glandular trichome types
- Enzymatic functions of wild tomato methylketone synthases 1 and 2
- A copal-8-ol diphosphate synthase from the angiosperm *Cistus creticus* subsp. *creticus* is a putative key enzyme for the formation of pharmacologically active, oxygen-containing labdane-type diterpenes

continued on next page

BACK TO CONTENTS

Eran Pichersky *continued from page 93*

- Multiple biochemical and morphological factors underlie the production of methylketones in tomato trichomes
- An aldehyde oxidase in developing seeds of Arabidopsis converts benzaldehyde to benzoic acid
- Biosynthesis of *t*-Anethole in anise: characterization of *t*-Anol/Isoeugenol synthase and an *O*-Methyltransferase specific for a C7-C8 propenyl side chain

BACK TO CONTENTS

John Ralph

The Plant Cell, Plant Physiology

John Ralph received his BSc (Hons) in chemistry at Canterbury University, NZ, and his PhD in chemistry/forestry at the University of Wisconsin–Madison. After serving as a research scientist for the Forest Research Institute in Rotorua, NZ, he became scientific head of the Research Laboratory for Nuclear Magnetic Resonance Spectroscopy in Chemistry at the University of California, Berkeley. John has been a research chemist with the USDA-ARS U.S. Dairy Forage Research Center in Madison, Wisconsin, with joint appointments in the Departments of Forestry and Biological Systems Engineering at the University of Wisconsin. Some seven years ago, he was appointed professor in the Department of Biochemistry at the university. He currently serves on the editorial boards for the journals *BioEnergy Research*, *J. Wood Chemistry and Technology*, *Holzforschung*, and *Journal of Science of Food and Agriculture*.

His research group is recognized for its highly collaborative work on lignin biosynthesis, including delineation of the pathways of monolignol synthesis, lignin chemistry, and lignin reactions. The group has also defined the chemical effects of perturbing lignin biosynthesis, and extensions of this work are aimed at redesigning lignins to be more readily degraded. For example, imbuing lignin with readily cleavable ester bonds in its backbone by lignifying using monolignol ferulate conjugates is looking particularly promising for developing plants with 'lignins designed for deconstruction' to simplify pulping and the conversion of lignocellulosics to liquid biofuels. Ralph was recognized by the Institute for Scientific Information as a highly cited author in the field of agricultural science. He is an elected fellow of AAAS.

The Plant Cell Papers

- Coexistence but independent biosynthesis of catechyl and guaiacyl/syringyl lignin polymers in seed coats
- An engineered Monolignol 4-*O*-Methyltransferase depresses lignin biosynthesis and confers novel metabolic capability in Arabidopsis
- Independent recruitment of an *O*-Methyltransferase for syringyl lignin biosynthesis in *Selaginella moellendorffii*
- Convergent evolution of syringyl lignin biosynthesis via distinct pathways in the Lycophyte *Selaginella* and flowering plants

Plant Physiology Papers

- Environmental stresses of field growth allow cinnamyl alcohol dehydrogenase-deficient *Nicotiana attenuata* plants to compensate for their structural deficiencies

continued on next page

BACK TO CONTENTS

John Ralph *continued from page 95*

- Molecular and biochemical basis for stress-induced accumulation of free and bound *p*-coumaraldehyde in cucumber
- Lignin composition and structure in young versus adult *Eucalyptus globulus* plants mass spectrometry-based sequencing of lignin oligomers
- Modeling lignin polymerization. I. simulation model of dehydrogenation polymers
- Sequencing around 5-hydroxyconiferyl alcohol-derived units in caffeic acid *O*-methyltransferase-deficient poplar lignins
- The effects on lignin structure of overexpression of ferulate 5-hydroxylase in hybrid poplar

BACK TO CONTENTS

Jocelyn K.C. Rose

The Plant Cell, Plant Physiology

Jocelyn K. C. Rose completed his undergraduate degree in biology at the University of Manchester, UK, before working at ICI Seeds (later Zeneca Plant Science and then Syngenta). He made the jump across the Atlantic to pursue his PhD at the University of California, Davis, studying mechanisms of cell wall disassembly during fruit ripening, and then moved to the Complex Carbohydrate Research Center, University of Georgia, where his postdoctoral research focused on cell wall proteins and plant-pathogen interactions.

Joss accepted a faculty position in the Department of Plant Biology at Cornell University, where he has continued his interest in plant wall research. Recently, his group has become particularly interested in the plant cuticle, a specialized hydrophobic cell wall. In 2010, he accepted the positions of director of the Institute of Biotechnology and director of the Center of Life Science Enterprise, one of New York State's Centers for Advanced Technology.

The Plant Cell Papers

- An ATP binding cassette transporter is required for cuticular wax deposition and desiccation tolerance in the moss *Physcomitrella patens*
- Tissue- and cell-type specific transcriptome profiling of expanding tomato fruit provides insights into metabolic and regulatory specialization and cuticle formation
- Malate plays a crucial role in starch metabolism, ripening, and soluble solid content of tomato fruit and affects postharvest softening
- Fleshy fruit expansion and ripening are regulated by the tomato *SHATTERPROOF* gene *TAGL1*
- Arabidopsis LTPG is a glycosylphosphatidylinositol-anchored lipid transfer protein required for export of lipids to the plant surface

Plant Physiology Papers

- The formation and function of plant cuticles
- Systems biology of tomato fruit development: combined transcript, protein, and metabolite analysis of tomato transcription factor (*nor, rin*) and ethylene receptor (*Nr*) mutants reveals novel regulatory interactions
- Two oxidosqualene cyclases responsible for biosynthesis of tomato fruit cuticular triterpenoids

BACK TO CONTENTS

Julian Schroeder

The Plant Cell, Plant Physiology

Julian Schroeder is Novartis chair and distinguished professor in the Division of Biological Sciences at the University of California San Diego and is director of the Plant Systems Biology NSF UCSD–Salk IGERT Graduate Training Program. He received his PhD working with Erwin Neher at the Max Planck Institute for Biophysical Chemistry in Göttingen, Germany.

Julian pioneered characterizations of plant ion channels, which led to models of their unique functions in plant biology. He also pioneered functional characterizations of genes encoding plant ion transport proteins and their roles in stress tolerance. He has received numerous awards, including the Presidential Young Investigator Award from NSF, the Charles Albert Shull Award from ASPB, the DFG Heinz-Maier-Leibnitz Research Prize, and the Blasker Award in Environmental Science and Engineering. He was named a highly cited researcher by the Institute for Scientific Information, received a Feodor-Lynen Fellowship from the Alexander von Humboldt Foundation as a postdoctoral scholar, and with collaborators shared the Cozzarelli Prize from PNAS (2010). He is an elected fellow of AAAS (2006) and was named Chinese Academy of Sciences International Professor (2009) and Churchill Overseas Fellow, Cambridge University (2014). He is currently ASPB president (2014–2015).

The Plant Cell Papers

- A genomic-scale artificial microRNA library as a tool to investigate the functionally redundant gene space in Arabidopsis
- Natural variation in small molecule–induced TIR-NB-LRR signaling induces root growth arrest via EDS1- and PAD4-Complexed R Protein VICTR in Arabidopsis
- The Arabidopsis nitrate transporter NRT1.8 functions in nitrate removal from the xylem sap and mediates cadmium tolerance

Plant Physiology Papers

- Regulation of drought tolerance by the F-Box Protein MAX2 in Arabidopsis
- Identification of cyclic GMP-activated nonselective Ca^{2+}-permeable cation channels and associated *CNGC5* and *CNGC6* genes in Arabidopsis guard cells
- PYR/RCAR receptors contribute to ozone-, reduced air humidity-, darkness-, and CO_2-induced stomatal regulation
- K^+ transport by the OsHKT2;4 transporter from rice with atypical Na^+ transport properties and competition in permeation of K^+ over Mg^{2+} and Ca^{2+} ions
- High-affinity K^+ transport in Arabidopsis: AtHAK5 and AKT1 are vital for seedling establishment and postgermination growth under low-potassium conditions
- Differential sodium and potassium transport selectivities of the rice OsHKT2;1 and OsHKT2;2 transporters in plant cells
- Triple loss of function of protein phosphatases type 2C leads to partial constitutive response to endogenous abscisic acid

BACK TO CONTENTS

Gary Stacey

Plant Physiology

Gary Stacey is an endowed professor of plant sciences and associate director of the National Center for Soybean Biotechnology at the University of Missouri–Columbia. He holds a joint appointment in the Division of Biochemistry. His research focuses generally on molecular aspects of plant–microbe interactions, including studies of the beneficial legume–rhizobium symbiosis and plant–fungal pathogen interactions. He has also been instrumental in the development of genomic resources for the study of soybean.

From 2010 to 2013, he was editor-in-chief of *Molecular Plant–Microbe Interactions*; he is a former associate editor of *Plant Physiology*. He chaired the ASPB Public Affairs Committee from 2006 to 2011. He is also currently chair of the Department of Energy, Biological and Environmental Research Advisory Committee. In 2008, he founded a not-for-profit corporation, Missouri Energy Initiative (MEI), a resource network for building partnerships to move Missouri forward in terms of energy information and solutions.

His awards include a research fellowship by the Alexander Von Humboldt Stiftung; the title of van der Klaauw Chair of Molecular Biology at the University of Leiden, Netherlands; the Chancellor's Award for Research and Creative Achievement at the University of Tennessee; the Distinguished Research Award in the College of Agriculture, Food and Natural Resources at the University of Missouri; and the Mumford Outstanding Faculty award from that college. In 2014, he was named a Curator's Professor by the University of Missouri. He is a fellow of AAAS, the American Academy of Microbiology, and ASPB.

Papers

- *Tnt1* Retrotransposon Mutagenesis: A tool for soybean functional fenomics
- 14-3-3 proteins SGF14c and SGF14l play critical roles during soybean nodulation
- LYK4, a lysin motif receptor-like kinase, is important for chitin signaling and plant innate immunity in Arabidopsis
- Identification of quantitative trait loci controlling gene expression during the innate immunity response of soybean
- Phenotypic and genomic analyses of a fast neutron mutant population resource in soybean
- Enzymatic activity of the soybean Ecto-Apyrase GS52 is essential for stimulation of nodulation
- Extracellular nucleotides elicit cytosolic free calcium oscillations in Arabidopsis
- Soybean metabolites regulated in root hairs in response to the symbiotic bacterium *Bradyrhizobium japonicum*

continued on next page

BACK TO CONTENTS

Gary Stacey *continued from page 99*

- Complete transcriptome of the soybean root hair cell, a single-cell model, and its alteration in response to *Bradyrhizobium japonicum* infection
- Large-scale analysis of putative soybean regulatory gene expression identifies a *Myb* gene involved in soybean nodule development
- Molecular and chromosomal evidence for allopolyploidy in soybean
- Establishment of a protein reference map for soybean root hair cells
- GS52 ecto-apyrase plays a critical role during soybean nodulation

BACK TO CONTENTS

Lloyd Sumner

The Plant Cell, Plant Physiology

Lloyd Sumner acquired his Ph.D. in analytical chemistry from Oklahoma State University in 1993. He joined the Samuel Roberts Noble Foundation in 1999, where he has risen to the rank of professor within the Plant Biology Division.

Lloyd has built a research program focused on the development and integration of large-scale biochemical profiling of plant metabolites, proteins, and transcripts (metabolomics, proteomics, and transcriptomics) for the discovery and characterization of the molecular and biochemical components related to plant specialized metabolism. He also applies these integrated omics technologies for greater biochemical insight into system responses to genetic and environmental perturbations. His research is or has been graciously supported by the Noble Foundation, NSF 2010, NSF MCB, NSF MRI, NSF-JST, NSF-IOS, and The Oklahoma Commission for the Advancement of Science and Technology.

Lloyd is currently a AAAS fellow, former treasurer and president of the Metabolomics Society, and president-elect of the Phytochemical Society of North America.

The Plant Cell Papers

- *STENOFOLIA* regulates blade outgrowth and leaf vascular patterning in *Medicago truncatula* and *Nicotiana sylvestris*
- MATE2 mediates vacuolar sequestration of flavonoid glycosides and glycoside malonates in *Medicago truncatula*
- Nonflowering plants possess a unique folate-dependent phenylalanine hydroxylase that is localized in chloroplasts
- Genomic and coexpression analyses predict multiple genes involved in triterpene saponin biosynthesis in *Medicago truncatula*

Plant Physiology Papers

- Functional characterization of proanthocyanidin pathway enzymes from tea and their application for metabolic engineering
- Influence of host chloroplast proteins on *Tobacco mosaic virus* accumulation and intercellular movement
- Characterization of an isoflavonoid-specific prenyltransferase from *Lupinus albus*
- A large-scale genetic screen in Arabidopsis to identify genes involved in pollen exine production
- The folylpolyglutamate synthetase plastidial isoform is required for postembryonic root development in Arabidopsis

continued on next page

BACK TO CONTENTS

Lloyd Sumner *continued from page 101*

- Soybean metabolites regulated in root hairs in response to the symbiotic bacterium *Bradyrhizobium japonicum*
- *LAP5* and *LAP6* encode anther-specific proteins with similarity to chalcone synthase essential for pollen exine development in Arabidopsis
- Integrated metabolite and transcript profiling identify a biosynthetic mechanism for hispidol in *Medicago truncatula* cell cultures
- A WD40 repeat protein from *Medicago truncatula* is necessary for tissue-specific anthocyanin and proanthocyanidin biosynthesis but not for trichome development

BACK TO CONTENTS

Yuhong Tang

The Plant Cell, Plant Physiology

Yuhong Tang received her bachelor's degree in biology from Beijing Normal University, a master's degree in genetics from the Institute of Genetics, Chinese Academy of Sciences, and her PhD in interdisciplinary genetics from Clemson University, South Carolina, where she was the recipient of the Wade Stackhouse Graduate Research Fellowship. Yuhong also holds a master's degree in computer science from the University of Oklahoma, Norman. Currently, she is Genomics Core Facility Manager at The Samuel Roberts Noble Foundation, where she works to establish and improve services in DNA sequencing and gene expression analysis for the Noble Foundation research community and its collaborators.

The Plant Cell Papers

- The *Trans*-acting short interfering RNA3 pathway and NO APICAL MERISTEM antagonistically regulate leaf margin development and lateral organ separation, as revealed by analysis of an *argonaute7/lobed leaflet1* mutant in *Medicago truncatula*
- A genomics approach to deciphering lignin biosynthesis in switchgrass
- Loss of abaxial leaf epicuticular wax in *Medicago truncatula irg1/palm1* mutants results in reduced spore differentiation of anthracnose and nonhost rust pathogens
- *STENOFOLIA* regulates blade outgrowth and leaf vascular patterning in *Medicago truncatula* and *Nicotiana sylvestris*
- MATE2 mediates vacuolar sequestration of flavonoid glycosides and glycoside malonates in *Medicago truncatula*
- Genomic and coexpression analyses predict multiple genes involved in triterpene saponin biosynthesis in *Medicago truncatula*

Plant Physiology Papers

- From model to crop: functional analysis of a *STAY-GREEN* Gene in the model legume *Medicago truncatula* and effective use of the gene for alfalfa improvement
- The folylpolyglutamate synthetase plastidial isoform is required for postembryonic root development in Arabidopsis
- Genomic inventory and transcriptional analysis of *Medicago truncatula* transporters
- TrichOME: A comparative omics database for plant trichomes
- A WD40 repeat protein from *Medicago truncatula* is necessary for tissue-specific anthocyanin and proanthocyanidin biosynthesis but not for trichome development

BACK TO CONTENTS

Barbara Valent

The Plant Cell

Barbara Valent, distinguished professor of plant pathology at Kansas State University, earned a PhD in biochemistry from the University of Colorado. She received an NIH National Research Service Award for postdoctoral training as a yeast molecular geneticist at Cornell University. While there, she began developing the rice blast fungus, *Magnaporthe oryzae,* as a model fungal plant pathogen.

Barbara joined the DuPont Company in 1985 to pursue rice blast research and develop novel control strategies for this pathogen, which remains a global threat to rice production. She rose to research fellow, the top scientific position within DuPont, before moving to Kansas State University in 2001.

Barbara is a Fellow of the American Phytopathological Society and of the American Association for the Advancement of Science. Career highlights include service on the Board of Trustees for the International Center of Tropical Agriculture in Cali, Colombia. Barbara's current research combines functional genomics with live cell microscopy to understand how specialized biotrophic hyphae invade living rice cells to cause blast disease. She has become a leader in research on wheat blast, a disease that recently emerged in South America and now threatens global wheat production.

Papers

- The *Magnaporthe oryzae* Effector AvrPiz-t targets the RING E3 Ubiquitin Ligase APIP6 to suppress pathogen-associated molecular pattern–triggered immunity in rice
- Translocation of *Magnaporthe oryzae* Effectors into rice cells and their subsequent cell-to-cell movement
- Interaction transcriptome analysis identifies *Magnaporthe oryzae* BAS1-4 as Biotrophy-Associated Secreted Proteins in rice blast disease
- The ER Chaperone LHS1 is involved in asexual development and rice infection by the blast fungus *Magnaporthe oryzae*

BACK TO CONTENTS

Ruth Welti

The Plant Cell, Plant Physiology

Ruth Welti, university distinguished professor of biology, Kansas State University, studies the chemistry and biochemistry of lipids. She is director and cofounder of the Kansas Lipidomics Research Center, which is used by scientists around the world as a resource for lipid analysis by mass spectrometry. She has been influential in introducing mass spectrometry as a tool for analysis of lipids, particularly to plant biologists. Ruth's research has appeared in more than 100 publications. Her current work is aimed at determining the role of lipid compositional alterations in the response of plants to environmental stresses such as temperature changes and exposure to pathogens.

Ruth received the Kansas Technology Enterprise Corporation Scholar award in 2006 and the Outstanding Senior Scientist Award from the Kansas State University chapter of Sigma Xi in 2008. She has served on five journal editorial boards, including the board of the *Journal of Biological Chemistry*. In 2012, she was named a fellow of the American Association for the Advancement of Science.

She received a doctorate in biological chemistry from Washington University in St. Louis and graduated with honors with a bachelor's degree in chemistry from the University of Connecticut. Before joining Kansas State University in 1985, she was a postdoctoral fellow and research assistant professor of biochemistry at the University of Kansas Medical Center.]

The Plant Cell Papers

- Patatin-related phospholipase pPLAIIIβ-induced changes in lipid metabolism alter cellulose content and cell elongation in Arabidopsis
- Nonspecific phospholipase C NPC4 promotes responses to abscisic acid and tolerance to hyperosmotic stress in Arabidopsis
- Overexpression of Arabidopsis Acyl-CoA binding protein ACBP3 promotes starvation-induced and age-dependent leaf senescence
- Phospholipase Dα1 and phosphatidic acid regulate NADPH oxidase activity and production of reactive oxygen species in aba-mediated stomatal closure in Arabidopsis

Plant Physiology Papers

- Patatin-related phospholipase pPLAIIIδ increases seed oil content with long-chain fatty acids in Arabidopsis
- Direct infusion mass spectrometry of oxylipin-containing arabidopsis membrane lipids reveals varied patterns in different stress responses
- Overexpression of Sinapine Esterase *BnSCE3* in oilseed rape seeds triggers global changes in seed metabolism

BACK TO CONTENTS

Klaas van Wijk

The Plant Cell, Plant Physiology

After completing his BSc and MSc at the Agricultural University Wageningen, Klaas van Wijk obtained a PhD at the University of Groningen (the Netherlands). This was then followed by postdocs at the Department of Biochemistry, Stockholm University, and at the Carnegie Institution at Stanford University. Klaas then became assistant professor in 1997 at the Department of Biochemistry, Stockholm University, and moved his lab in 2001 to Cornell University.

The van Wijk lab is focused on (1) bundle sheath and mesophyll cell specific differentiation of chloroplasts in leaves of the C^4 plant maize, (2) chloroplast biogenesis and protein homeostasis in *Arabidopsis thaliana*, with a focus on the Clp protease machinery, and (3) the function of thylakoid-associated proteolipoparticles and its highly specialized proteome. These research topics are tackled using a multidisciplinary approach, with emphasis on large-scale comparative proteomics and mass spectrometry, bioinformatics, and reverse genetics. Klaas has received the Melvin Calvin Award from the International Society for Photosynthesis Research (2004) and the Research Award from the Alexander von Humboldt Foundation (2012).

The Plant Cell Papers

- ClpS1 is a conserved substrate selector for the chloroplast Clp protease system in Arabidopsis
- Loss of plastoglobule kinases ABC1K1 and ABC1K3 causes conditional degreening, modified prenyl-lipids, and recruitment of the jasmonic acid pathway
- A plasmodesmata-localized protein mediates crosstalk between cell-to-cell communication and innate immunity in Arabidopsis
- Subunit stoichiometry, evolution, and functional implications of an asymmetric plant plastid ClpP/R protease complex in Arabidopsis
- APO1 promotes the splicing of chloroplast group II introns and harbors a plant-specific zinc-dependent RNA binding domain
- Structural and metabolic transitions of C_4 leaf development and differentiation defined by microscopy and quantitative proteomics in maize
- Subunits of the plastid ClpPR protease complex have differential contributions to embryogenesis, plastid biogenesis, and plant development in Arabidopsis

Plant Physiology Papers

- Modified Clp protease complex in the ClpP3 null mutant and consequences for chloroplast development and function in Arabidopsis
- Chloroplast RH3 DEAD Box RNA helicases in maize and Arabidopsis function in splicing of specific group II introns and affect chloroplast ribosome biogenesis

continued on next page

BACK TO CONTENTS

Klaas van Wijk *continued from page 106*

- The functional network of the Arabidopsis plastoglobule proteome based on quantitative proteomics and genome-wide coexpression analysis
- Nucleoid-enriched proteomes in developing plastids and chloroplasts from maize leaves: a new conceptual framework for nucleoid functions
- Plastid proteomics in higher plants: current state and future goals
- Reconstruction of metabolic pathways, protein expression, and homeostasis machineries across maize bundle sheath and mesophyll chloroplasts: large-scale quantitative proteomics using the first maize genome assembly

BACK TO CONTENTS

Zheng-Hua Ye

The Plant Cell, Plant Physiology

Zheng-Hua Ye earned his PhD in plant cell and molecular genetics from Washington University in 1994 under the guidance of Dr. Joseph E. Varner. He is currently a professor of plant biology at the University of Georgia. His research interests center on uncovering the molecular mechanisms underlying the biosynthesis of secondary cell walls and the transcriptional regulation of secondary cell wall biosynthesis in plants.

Zheng-Hua received the Sandy Beaver Excellence in Teaching award, University of Georgia, 2007, and was elected as a National Academies Education Fellow in the Life Sciences in 2014. He was selected as a highly cited researcher by Thomson Reuters (ranking among the top 1% most cited for their subject field [Plant and Animal Science] and year of publication [2002–2012]).

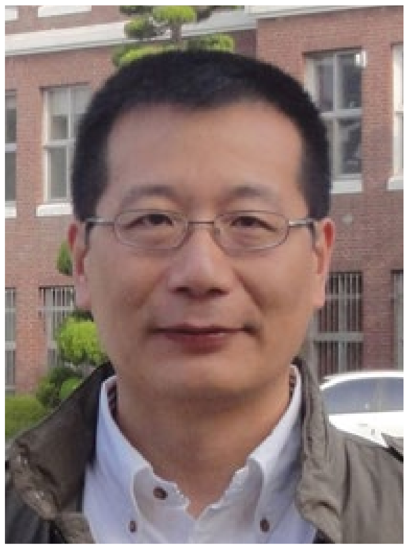
The Plant Cell Papers

- MYB58 and MYB63 are transcriptional activators of the lignin biosynthetic pathway during secondary cell wall formation in Arabidopsis

Plant Physiology Papers

- Dissection of the transcriptional program regulating secondary wall biosynthesis during wood formation in poplar
- The Arabidopsis family GT43 glycosyltransferases form two functionally non-redundant groups essential for the elongation of glucuronoxylan chain length
- Functional characterization of poplar wood-associated NAC domain transcription factors

BACK TO CONTENTS



Shuqun Zhang

The Plant Cell

Shuqun Zhang, professor of biochemistry, University of Missouri, Christopher S. Bond Life Sciences Center, earned his BS in biology from Nanjing University in China and his PhD in plant biology from the University of Texas. A fellow of AAAS, Shuqun received the National Science Foundation's Faculty Early Career Development (CAREER) award in 2002; a faculty fellowship, Department of Biochemistry, University of Missouri, in 2012, and the Distinguished Researcher Award, College of Agriculture, Food and Natural Resources, University of Missouri, in 2013.

Shuqun's primary research is aimed at understanding, at molecular and cellular levels, how mitogen-activated protein kinase (MAPK) signaling cascades regulate plant growth, development, and immunity downstream of cellular receptors/sensors.

Papers

- Phosphorylation of an ERF transcription factor by Arabidopsis MPK3/MPK6 regulates plant defense gene induction and fungal resistance
- A MAPK cascade downstream of ERECTA receptor-like protein kinase regulates Arabidopsis inflorescence architecture by promoting localized cell proliferation
- Phosphorylation of a WRKY transcription factor by two pathogen-responsive MAPKs drives phytoalexin biosynthesis in Arabidopsis
- Ethylene-Induced stabilization of ETHYLENE INSENSITIVE3 and EIN3-LIKE1 is mediated by proteasomal degradation of EIN3 Binding F-Box 1 and 2 that requires EIN2 in Arabidopsis
- Mitogen-Activated protein kinases 3 and 6 are required for full priming of stress responses in *Arabidopsis thaliana*

BACK TO CONTENTS

Ruiqin Zhong

The Plant Cell, Plant Physiology

Ruiqin Zhong is a senior research manager in Department of Plant Biology, University of Georgia. She earned her MS degree in molecular cell biology from School of Medicine, Washington University, working on the cellular basis of angiogenesis in human cells. In the past two decades, she has been working on the molecular mechanisms underlying plant vascular development and secondary wall biosynthesis and published over 70 research articles. Ruiqin is a highly cited researcher selected by Thomson Reuters (ranking among the top 1% most cited for their subject field [Plant and Animal Science] and year of publication [2002-2012]).

The Plant Cell Papers

- MYB58 and MYB63 are transcriptional activators of the lignin biosynthetic pathway during secondary cell wall formation in Arabidopsis
- MYB58 and MYB63 are transcriptional activators of the lignin biosynthetic pathway during secondary cell wall formation in Arabidopsis

Plant Physiology Papers

- The Arabidopsis family GT43 glycosyltransferases form two functionally nonredundant groups essential for the elongation of glucuronoxylan chain length
- Functional characterization of poplar wood-associated NAC domain transcription factors