

## Mary

### **Chloroplast Hsp70 isoform is required for age-dependent tissue preference of Bamboo mosaicvirus in mature *Nicotiana benthamiana* leaves**

[Mol Plant Microbe Interact.](#) 2017 May 1

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Plant viruses may exhibit age-dependent tissue preference in their hosts, but the underlying mechanism(s) are not well understood. In this study, we provide several lines of evidence to reveal the determining role of a protein of the *Nicotiana benthamiana* chloroplastHsp70 (NbcpHsp70) family, NbcpHsp70-2, involved in the preference of Bamboo mosaic virus (BaMV) to infect older tissues. NbcpHsp70 family proteins were identified in complexes pulled down with BaMV replicase as the bait. Among the isoforms of NbcpHsp70, only the specific silencing of NbcpHsp70-2 resulted in the significant decrease of BaMV RNA in *N. benthamiana* protoplasts, indicating NbcpHsp70-2 is involved in the efficient replication of BaMV RNA. We further identified the age-dependent import regulation signal in the transit peptide of NbcpHsp70-2 contains. Deletion, overexpression, and substitution experiments revealed that the signal in transit peptide of NbcpHsp70-2 is crucial for both the import of NbcpHsp70-2 into older chloroplasts and the preference of BaMV for infecting older leaves of *N. benthamiana*. Together, these data demonstrated that BaMV may exploit cellular age-dependent transportation mechanism to target a suitable environment for viral replication.

## Minsoo

1. Plant Cell. 2017 Apr 18. pii: tpc.00899.2016. doi: 10.1105/tpc.16.00899. [Epub

ahead of print]

The Mitochondrial DNA (mtDNA)-Associated Protein SWIB5 Influences mtDNA Architecture and Homologous Recombination.

Blomme J(1), Van Aken O(2), Van Leene J(1), Jégu T(3), De Rycke RM(4), De Bruyne M(1), Vercruysse J(1), Nolf J(1), Van Daele T(1), De Milde L(1), Vermeersch M(1), Colas des Francs-Small C(5), De Jaeger G(6), Benhamed M(7), Millar AH(8), Inzé D(9), Gonzalez N(1).

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In addition to the nucleus, mitochondria and chloroplasts in plant cells also contain genomes. Efficient DNA repair pathways are crucial in these organelles to fix damage resulting from endogenous and exogenous factors. Plant organellar genomes are complex compared to their animal counterparts and although several plant-specific mediators of organelle DNA repair have been reported, many regulators remain to be identified. Here, we show that a mitochondrial SWI/SNF (nucleosome remodeling) complex B protein, SWIB5, is capable of associating with mitochondrial DNA (mtDNA) in *Arabidopsis thaliana*. Gain- and loss-of-function mutants provided evidence for a role of SWIB5 in influencing mtDNA architecture and homologous recombination at specific intermediate-sized repeats both under normal and genotoxic conditions. SWIB5 interacts with other mitochondrial SWIB proteins. Gene expression and mutant phenotypic analysis of SWIB5 and SWIB family members suggests a link between organellar genome maintenance and cell proliferation. Taken together, our work presents a protein family that influences mtDNA architecture and homologous recombination in plants and suggests a link between organelle functioning and plant development.

2. Mol Cell. 2017 Apr 6;66(1):117-128.e5. doi: 10.1016/j.molcel.2017.02.016. Epub 2017 Mar 23.

Plasma Membrane CRPK1-Mediated Phosphorylation of 14-3-3 Proteins Induces Their Nuclear Import to Fine-Tune CBF Signaling during Cold Response.

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In plant cells, changes in fluidity of the plasma membrane may serve as the primary sensor of cold stress; however, the precise mechanism and how the cell transduces and fine-tunes cold signals remain elusive. Here we show that the cold-activated plasma membrane protein cold-responsive protein kinase 1 (CRPK1) phosphorylates 14-3-3 proteins. The phosphorylated 14-3-3 proteins shuttle from the cytosol to the nucleus, where they interact with and destabilize the key cold-responsive C-repeat-binding factor (CBF) proteins. Consistent with this, the *crpk1* and 14-3-3 $\kappa$  mutants show enhanced freezing tolerance, and transgenic plants overexpressing 14-3-3 $\lambda$  show reduced freezing tolerance. Further study shows that CRPK1 is essential for the nuclear translocation of 14-3-3 proteins and for 14-3-3 function in freezing tolerance. Thus, our study reveals that the CRPK1-14-3-3 module transduces the cold signal from the plasma membrane to the nucleus to modulate CBF stability, which ensures a faithfully adjusted response to cold stress of plants.

## Patrick

[Plant Physiology and Biochemistry 115 \(2017\) 354e359](#)

Evidence towards the involvement of nitric oxide in drought tolerance of sugarcane

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a b s t r a c t

Exogenous supply of nitric oxide (NO) increases drought tolerance in sugarcane plants. However, little is known about the role of NO produced by plants under water deficit. The aim of this study was to test the hypothesis that drought-tolerance in sugarcane is associated with NO production and metabolism, with the more drought-tolerant genotype presenting higher

NO accumulation in plant tissues. The sugarcane genotypes IACSP95-5000 (drought-tolerant) and IACSP97-7065 (drought-sensitive) were submitted to water deficit by adding polyethylene glycol (PEG-8000) in nutrient solution to reduce the osmotic potential to  $-0.4$  MPa. To evaluate short-time responses to water deficit, leaf and root samples were taken after 24 h under water deficit. The drought-tolerant genotype presented higher root extracellular NO content, which was accompanied by higher root nitrate reductase (NR) activity as compared to the drought-sensitive genotype under water deficit. In addition, the drought-tolerant genotype had higher leaf intracellular NO content than the drought-sensitive one. IACSP95-5000 exhibited decreases in root S-nitrosogluthione reductase (GSNOR) activity under water deficit, suggesting that S-nitrosogluthione (GSNO) is less degraded and that the drought-tolerant genotype has a higher natural reservoir of NO than the drought-sensitive one. Those differences in intracellular and extracellular NO contents and enzymatic activities were associated with higher leaf hydration in the drought-tolerant genotype as compared to the sensitive one under water deficit.

## 2.

Nitrosopersulfide (SSNO<sub>2</sub>) decomposes in the presence of sulfide, cyanide or glutathione to give HSNO/SNO<sub>2</sub>: consequences for the assumed role in cell signalling

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The emergence of hydrogen sulfide (H<sub>2</sub>S) as a new signalling molecule able to control vasodilation, neurotransmission and immune response, prompted questions about its possible cross-talk with the other gas transmitter, nitric oxide (NO). It has been shown that H<sub>2</sub>S reacts with NO and its metabolites and several potentially biologically active species have been identified. Thionitrous acid (HSNO) was proposed to be an intermediate product of the reaction of S-nitrosothiols with H<sub>2</sub>S capable of crossing the membranes and causing further trans-nitrosation of proteins. Alternatively, formation of nitrosopersulfide (SSNO<sub>2</sub>) has been proposed in this reaction. SSNO<sub>2</sub> was claimed to be particularly stable and inert to H<sub>2</sub>S, thiols and cyanides. It is suggested that this putative SSNO<sub>2</sub> slowly decomposes to give NO, HNO and polysulfides. However, the chemical studies with pure SSNO<sub>2</sub> salts showed some conflicting observations. In this study, we work with pure PNPbSSNO<sub>2</sub> to show that contrary to everything that is claimed for the yellow reaction product of GSNO with H<sub>2</sub>S, pure SSNO<sub>2</sub> decomposes readily in the presence of cyanide, H<sub>2</sub>S and glutathione to form SNO<sub>2</sub>. Based on literature overview and chemical data about the structures of HSNO/SNO<sub>2</sub> and SSNO<sub>2</sub> we discuss the biological role these two species could have.

## Keith

### Cell Stress Chaperones.

2017 Apr 7

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The structure and chaperone function of DmHsp22WT, a small Hsp of *Drosophila melanogaster* localized within mitochondria were examined. Mutations of conserved arginine mutants within the alpha-crystallin domain (ACD) domain (R105G, R109G, and R110G) were introduced, and their effects on oligomerization and chaperone function were assessed. Arginine to glycine mutations do not induce significant changes in tryptophan fluorescence, and the mutated proteins form oligomers that are of equal or smaller size than the wild-type protein. They all form oligomer with one single peak as determined by size exclusion chromatography. While all mutants demonstrate the same efficiency as the DmHsp22WT in a DTT-induced insulin aggregation assay, all are more efficient chaperones to prevent aggregation of malate dehydrogenase. Arginine mutants of DmHsp22 are efficient chaperones to retard aggregation of CS and Luc. In summary, this study shows that mutations of arginine to glycine in DmHsp22 ACD induce a number of structural changes, some of which differ from those described in mammalian sHsps. Interestingly, only the R110G-DmHsp22 mutant, and not the expected R109G equivalent to human R140-HspB1, R116-HspB4, and R120-HspB5, showed different structural properties compared with the DmHsp22WT.

**Key features of an Hsp70 chaperone allosteric landscape revealed by ion mobility native mass spectrometry and double electron-electron resonance.**

J Biol Chem. 2017 Apr 20

Lai AL<sup>1</sup>, Clerico EM<sup>2</sup>, Blackburn ME<sup>3</sup>, Patel NA<sup>4</sup>, Robinson CV<sup>4</sup>, Borbat PP<sup>1</sup>, Freed JH<sup>1</sup>, Gierasch LM<sup>5</sup>.

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Proteins are dynamic entities that populate conformational ensembles, and most functions of proteins depend on their dynamic character. Allostery, in particular, relies on ligand-modulated shifts in these conformational ensembles. Hsp70s are allosteric molecular chaperones with conformational landscapes that involve large rearrangements of their two domains (viz, the nucleotide-binding domain and substrate-binding domain) in response to adenine nucleotides and substrates. However, it remains unclear how the Hsp70 conformational ensemble is populated at each point of the allosteric cycle and how ligands control these populations. We have mapped the conformational species present under different ligand-binding conditions throughout the allosteric cycle of the E. coli Hsp70 DnaK by two complementary methods, ion mobility mass spectrometry and double electron-electron resonance. Our results obtained under biologically relevant ligand-bound conditions confirm the current picture derived from NMR and crystallographic data of domain docking upon ATP binding and undocking in response to ADP and substrate. Additionally, we find that the helical lid of DnaK is a highly dynamic unit of the structure in all ligand-bound states. Importantly, we demonstrate that DnaK populates a partially docked state in the presence of ATP and substrate and that this state represents an energy minimum on the DnaK allosteric landscape. Because Hsp70s are emerging as potential drug targets for many diseases, fully mapping an allosteric landscape of a molecular chaperone like DnaK will facilitate the development of small molecules that modulate Hsp70 function via allosteric mechanisms.

Elizabeth

### **The Plant Journal**

[Subunit-selective proteasome activity profiling uncovers uncoupled proteasome subunit activities during bacterial infections \(pages 418–430\)](#)

Johana C. Misas-Villamil, Aranka M. van der Burgh, Friederike Grosse-Holz, Marcel Bach-Pages, Judit Kovács, Farnusch Kaschani, Sören Schilasky, Asif E.K. Emon, Mark Ruben, Markus Kaiser, Hermen S. Overkleeft and Renier A.L. van der Hoorn

14 MAR 2017 | DOI: 10.1111/tpj.13494

Proteasome activity profiling with subunit-selective fluorescent probes is a robust way to display activities of  $\beta 1$  and  $\beta 5$  proteasome subunits in plants. We validate these next generation probes and use them to uncover that  $\beta 1$  and  $\beta 5$  activities are uncoupled upon *Pseudomonas syringae* infection.

### **Plant Cell Table of Contents for March 2017; Vol. 29, No. 3**

Transcriptome-Wide Mapping of RNA 5-Methylcytosine in Arabidopsis mRNAs and Noncoding RNAs

Rakesh David, Alice Burgess, Brian Parker, Jun Li, Kalinya Pulsford, Tennille Sibbritt, Thomas Preiss, and Iain Robert Searle

Plant Cell 2017 29: 445-460. First Published on January 6, 2017; doi:10.1105/tpc.16.00751  
<http://www.plantcell.org/content/29/3/445.abstract>

Transcriptome-wide quantitative mapping of 5-methylcytosine in Arabidopsis via RNA bisulfite sequencing reveals crucial links between this modification and cell division and plant stress pathways.

Cytokinin-Mediated Regulation of Reactive Oxygen Species Homeostasis Modulates Stomatal Immunity in Arabidopsis

Dominique Arnaud, Seungchul Lee, Yumiko Takebayashi, Daeseok Choi, Jaemyung Choi, Hitoshi Sakakibara, and Ildoo Hwang

Plant Cell 2017 29: 543-559. First Published on March 2, 2017; doi:10.1105/tpc.16.00583

**OPEN**

<http://www.plantcell.org/content/29/3/543.abstract>

Cytokinins stimulate stomatal immunity and plant resistance to bacteria by the ARR2-mediated transcriptional regulation of apoplastic peroxidase genes, which control ROS homeostasis in guard cells.

Dabbaghizadeh A, Finet S, Morrow G, Moutaoufik MT, Tanguay RM.

Oligomeric structure and chaperone-like activity of *Drosophila melanogaster* mitochondrial small heat shock protein Hsp22 and arginine mutants in the alpha-crystallin domain.

Cell Stress Chaperones. 2017 Apr 7;. [Epub ahead of print] PMID: 28389817 [PubMed - as supplied by publisher]

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Mol Cell. 2017 Apr 6;66(1):1-2. PMID: 28388436 [PubMed - in process]

### **Plant Cell Advance Publication**

Bound by Fate: Reactive Oxygen Species in Receptor-Like Kinase Signaling

Sachie Kimura, Cezary Waszczak, Kerri Hunter, and Michael Wrzaczek

Plant Cell 2017 tpc.16.00947; Advance Publication April 3, 2017; doi:10.1105/tpc.16.00947

**OPEN**

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## **Plant Cell**

Tissue-Specific Transcriptomics Reveals an Important Role of the Unfolded Protein Response in Maintaining Fertility upon Heat Stress in Arabidopsis

Shuang-Shuang Zhang, Hongxing Yang, Lan Ding, Ze-Ting Song, Hong Ma, Fang Chang, and Jian-Xiang Liu

Plant Cell 2017 tpc.16.00916; Advance Publication April 24, 2017; doi:10.1105/tpc.16.00916  
Elevated temperatures have a great impact on plant reproductive development and subsequent fruit and seed set, but the underlying molecular mechanisms are not well understood. We used transcriptome profiling to investigate the effect of heat stress on reproductive development of Arabidopsis (*Arabidopsis thaliana*) seedlings and observed distinct response patterns in vegetative vs. reproductive tissues. Exposure to heat stress affected reproductive developmental programs including early phases of anther/ovule development and meiosis. Also, genes participating in the unfolded protein response (UPR) were enriched in the reproductive tissue-specific genes that were up-regulated by heat. Moreover, we found that the UPR-deficient *bzip28 bzip60* double mutant was sensitive to heat stresses and had reduced silique length and fertility. Comparison of heat responsiveness wild-type vs. *bzip28 bzip60* plants identified 521 genes that were regulated by bZIP28 and bZIP60 upon heat stress during reproductive stages, most of which were non-canonical UPR genes. ChIP-Seq analyses revealed 133 likely direct targets of bZIP28 in Arabidopsis seedlings subjected to heat stress, including 27 genes that were also up-regulated by heat during reproductive development. Our results provide important insights into heat responsiveness in Arabidopsis reproductive tissues and demonstrate the protective roles of the UPR for maintaining fertility upon heat stress.

The Mitochondrial DNA (mtDNA)-Associated Protein SWIB5 Influences mtDNA Architecture and Homologous Recombination

Jonas Blomme, Olivier Van Aken, Jelle Van Leene, Teddy Jégu, Riet Maria De Rycke, Michiel De Bruyne, Jasmien Vercruyse, Jonah Nolf, Twiggy Van Daele, Liesbeth De Milde, Mattias Vermeersch, Catherine Colas des Francs-Small, Geert De Jaeger, Moussa Benhamed, A. Harvey Millar, Dirk Inzé, and Nathalie Gonzalez

Plant Cell 2017 tpc.16.00899; Advance Publication April 18, 2017; doi:10.1105/tpc.16.00899  
<http://www.plantcell.org/content/early/2017/04/18/tpc.16.00899.abstract>

In addition to the nucleus, mitochondria and chloroplasts in plant cells also contain genomes. Efficient DNA repair pathways are crucial in these organelles to fix damage resulting from endogenous and exogenous factors. Plant organellar genomes are complex compared to their animal counterparts and although several plant-specific mediators of organelle DNA repair have been reported, many regulators remain to be identified. Here, we show that a mitochondrial SWI/SNF (nucleosome remodeling) complex B protein, SWIB5, is capable of associating with mitochondrial DNA (mtDNA) in *Arabidopsis thaliana*. Gain- and loss-of-function mutants provided evidence for a role of SWIB5 in influencing mtDNA architecture and homologous recombination at specific intermediate-sized repeats both under normal and genotoxic conditions. SWIB5 interacts with other mitochondrial SWIB proteins. Gene expression and mutant phenotypic analysis of SWIB5 and SWIB family members suggests a link between organellar genome maintenance and cell proliferation. Taken together, our work presents a protein family that influences mtDNA architecture and homologous recombination in plants and suggests a link between organelle functioning and plant development.

Bound by Fate: The Role of Reactive Oxygen Species in Receptor-Like Kinase Signaling  
Sachie Kimura, Cezary Waszczak, Kerri Hunter, and Michael Wrzaczek

Plant Cell 2017 29: 638-654. First Published on April 3, 2017; doi:10.1105/tpc.16.00947 **OPEN**  
<http://www.plantcell.org/content/29/4/638.abstract>

Receptor-like kinases and reactive oxygen species are intricately entangled and have central roles in controlling many processes in plants, but their interaction is still insufficiently understood.

Lateral segregation of photosystem I in cyanobacterial thylakoids

Craig MacGregor-Chatwin, Melih Sener, Samuel F.H. Barnett, Andrew Hitchcock, Meghan C. Barnhart-Dailey, Karim Maghlaoui, James Barber, Jerilyn A Timlin, Klaus Schulten, and Christopher Neil Hunter

Plant Cell 2017 tpc.17.00071; Advance Publication March 31, 2017; doi:10.1105/tpc.17.00071  
**OPEN**

<http://www.plantcell.org/content/early/2017/03/31/tpc.17.00071.abstract>

Photosystem I (PSI) is the dominant photosystem in cyanobacteria and it plays a pivotal role in cyanobacterial metabolism. Despite its biological importance, the native organisation of PSI in cyanobacterial thylakoid membranes is poorly understood. Here, we use atomic force microscopy (AFM) to show that ordered, extensive macromolecular arrays of PSI complexes are present in thylakoids from *Thermosynechococcus* (T.) *elongatus*, *Synechococcus* sp. PCC 7002 and *Synechocystis* sp PCC 6803. Hyperspectral confocal fluorescence microscopy (HCFM) and three-dimensional structured illumination microscopy (3D-SIM) of *Synechocystis* sp PCC 6803 cells visualise PSI domains within the context of the complete thylakoid system.

Crystallographic and AFM data were used to build a structural model of a membrane landscape comprising 96 PSI trimers and 27,648 chlorophyll a molecules. Rather than facilitating inter-trimer energy transfer the close associations between PSI primarily maximise packing efficiency; short-range interactions with Complex I and cytochrome b6f are excluded from these regions of the membrane, so PSI turnover is sustained by long-distance diffusion of the electron donors at the membrane surface. Elsewhere, PSI-photosystem II (PSII) contact zones provide sites for docking phycobilisomes and the formation of megacomplexes. PSI-enriched domains in

cyanobacteria might foreshadow the partitioning of PSI into stromal lamellae in plants, similarly sustained by long-distance diffusion of electron carriers.

#### Protein Degradation Rate in *Arabidopsis thaliana* Leaf Growth and Development

Lei Li, Clark J Nelson, Josua Trösch, Ian Castleden, Shaobai Huang, and A. Harvey Millar

Plant Cell 2017 tpc.16.00768; Advance Publication January 30, 2017; doi:10.1105/tpc.16.00768

**OPEN**

<http://www.plantcell.org/content/early/2017/01/30/tpc.16.00768.abstract>

We have applied  $^{15}\text{N}$  labeling approaches to leaves of the *Arabidopsis thaliana* rosette to characterize their protein degradation rate and understand its determinants. The progressive labeling of new peptides with  $^{15}\text{N}$  and measuring the decrease in the abundance of >60,000 existing peptides over time allowed us to define the degradation rate of 1228 proteins in vivo. We show that *Arabidopsis* protein half-lives vary from several hours to several months based on the exponential constant of the decay rate for each protein. This rate was calculated from the relative isotope abundance of each peptide and the fold change in protein abundance during growth. Protein complex membership and specific protein domains were found to be strong predictors of degradation rate, while N-end amino acid, hydrophobicity or aggregation propensity of proteins were not. We discovered rapidly degrading subunits in a variety of protein complexes in plastids and identified the set of plant proteins whose degradation rate changed in different leaves of the rosette and correlated with leaf growth rate. From this information, we have calculated the protein turnover energy costs in different leaves and their key determinants within the proteome.

#### More than Window Dressing: Revealing 5-Methylcytosine Patterns that Decorate *Arabidopsis* RNA

Jennifer A Lockhart

Plant Cell 2017 tpc.17.00026; Advance Publication January 12, 2017; doi:10.1105/tpc.17.00026

**OPEN**

<http://www.plantcell.org/content/early/2017/01/12/tpc.17.00026>

Transcriptome-wide Mapping of RNA 5-Methylcytosine in *Arabidopsis* mRNAs and non-coding RNAs

Rakesh David, Alice Burgess, Brian Parker, Jun Li, Kalinya Pulsford, Tennille Sibbritt, Thomas Preiss, and Iain R Searle

Plant Cell 2017 tpc.16.00751; Advance Publication January 6, 2017; doi:10.1105/tpc.16.00751

<http://www.plantcell.org/content/early/2017/01/06/tpc.16.00751.abstract>

*Arabidopsis* seed mitochondria are bioenergetically active immediately upon imbibition and specialize via biogenesis in preparation for autotrophic growth

Gael Paszkiewicz, Jose Manuel Gualberto, Abdelilah Benamar, David Macherel, and David C. Logan

Plant Cell 2017 tpc.16.00700; Advance Publication January 6, 2017; doi:10.1105/tpc.16.00700

**OPEN**

<http://www.plantcell.org/content/early/2017/01/06/tpc.16.00700.abstract>

Seed germination is a vital developmental transition for production of progeny by sexual reproduction in spermatophytes. Quiescent cells in non-dormant dry embryos are reawakened first by imbibition and then by perception of germination triggers. Reanimated tissues enter into a germination program requiring energy for expansion growth. However, germination requires

that embryonic tissues develop to support the more energy-demanding processes of cell division and organogenesis of the new seedling. Reactivation of mitochondria to supply the required energy is thus a key process underpinning germination and seedling survival. Using live imaging, we investigated reactivation of mitochondrial bioenergetics and dynamics using *Arabidopsis thaliana* L. Heynth, as a model. Bioenergetic reactivation, visualized by presence of a membrane potential, is immediate upon rehydration. However, reactivation of mitochondrial dynamics only occurs after transfer to germination conditions. Reactivation of mitochondrial bioenergetics is followed by dramatic reorganization of the chondriome (all mitochondrial in a cell, collectively) involving massive fusion and membrane biogenesis to form a perinuclear tubuloreticular structure enabling mixing of previously discrete mtDNA nucleoids. The end of germination coincides with fragmentation of the chondriome, doubling of mitochondrial number and heterogeneous redistribution of nucleoids amongst the mitochondria, generating a population of mitochondria tailored to seedling growth.

### **Plant Journal**

[Leghemoglobin is nitrated in functional legume nodules in a tyrosine residue within the heme cavity by a nitrite/ peroxide-dependent mechanism](#)

Martha Sainz, Laura Calvo-Begueria, Carmen Pérez-Rontomé, Stefanie Wienkoop, Joaquín Abián, Christiana Staudinger, Silvina Bartesaghi, Rafael Radi and Manuel Becana  
Accepted manuscript online: 20 JAN 2015 08:31AM EST | DOI: 10.1111/tpj.12762

[he RNA helicase, eIF4A-1, is required for ovule development and cell size homeostasis in](#)

### [Arabidopsis](#)

Maxwell S. Bush, Natalie Crowe, Tao Zheng and John H. Doonan

Accepted manuscript online: 23 OCT 2015 01:06AM EST | DOI: 10.1111/tpj.13062

[Changes in specific protein degradation rates in \*Arabidopsis thaliana\* reveal multiple roles of Lon1 in mitochondrial protein homeostasis](#)

Lei Li, Clark Nelson, Ricarda Fenske, Josua Trösch, Adriana Pružinská, A. Harvey Millar and Shaobai Huang

Accepted manuscript online: 11 OCT 2016 06:45AM EST | DOI: 10.1111/tpj.13392

[What can we do with 1000 plastid genomes?](#)

Julian Tonti-Filippini, Paul G. Nevill, Kingsley Dixon and Ian Small

Accepted manuscript online: 23 JAN 2017 07:20AM EST | DOI: 10.1111/tpj.13491

[Orchestrating Rapid Long-Distance Signaling in Plants with Ca<sup>2+</sup>, ROS, and Electrical Signals](#)

Won-Gyu Choi, Gad Miller, Ian Wallace, Jeffrey Harper, Ron Mittler and Simon Gilroy

Accepted manuscript online: 23 JAN 2017 07:20AM EST | DOI: 10.1111/tpj.13492

[Integrated omics analysis of specialized metabolism in medicinal plants](#)

Amit Rai, Kazuki Saito and Mami Yamazaki

Accepted manuscript online: 21 JAN 2017 08:55AM EST | DOI: 10.1111/tpj.13485

[The SUFBC<sub>2</sub>D Complex is Required for the Biogenesis of All Major Classes of Plastid Fe-S Proteins](#)

Xueyun Hu, Yukako Kato, Akihiro Sumida, Ayumi Tanaka and Ryouichi Tanaka

Accepted manuscript online: 19 JAN 2017 02:15PM EST | DOI: 10.1111/tpj.13483

[Engineering central metabolism - a grand challenge for plant biologists](#)

Lee J Sweetlove, Jens Nielsen and Alisdair R Fernie

Accepted manuscript online: 22 DEC 2016 02:24AM EST | DOI: 10.1111/tpj.13464

Maintaining the Factory: The Roles of the Unfolded Protein Response in Cellular Homeostasis in Plants

Evan Angelos, Cristina Ruberti, Sang-Jin Kim and Federica Brandizzi

Accepted manuscript online: 10 DEC 2016 04:15PM EST | DOI: 10.1111/tpj.13449

Identification of Core Subunits of Photosystem II as Action Sites of HSP21 That Is Activated by the GUN5-Mediated Retrograde Pathway in *Arabidopsis*

Si-Ting Chen, Ning-Yu He, Juan-Hua Chen and Fang-Qing Guo

Accepted manuscript online: 10 DEC 2016 04:05PM EST | DOI: 10.1111/tpj.13447

The mitochondrial complexome of *Arabidopsis thaliana*

Jennifer Senkler, Michael Senkler, Holger Eubel, Tatjana Hildebrandt, Christian Lengwenus, Peter Schertl, Markus Schwarzländer, Stephan Wagner, Ilka Wittig and Hans-Peter Braun

Accepted manuscript online: 10 DEC 2016 04:05PM EST | DOI: 10.1111/tpj.13448

Integrated omics analyses of retrograde signaling mutant delineate interrelated stress response strata

Marta Bjornson, Gerd Ulrich Balcke, Yanmei Xiao, Amancio de Souza, Jin-Zheng Wang, Dina Zhabinskaya, Ilias Tagkopoulos, Alain Tissier and KatTo maintain homeostasis in the face of intrinsic and extrinsic insults, cells have evolved elaborate quality control networks to resolve damage at multiple levels. Interorganellar communication is a key requirement for this maintenance, however the underlying mechanisms of this communication have remained an enigma. Here we integrate the outcome of transcriptomic, proteomic, and metabolomics analyses of genotypes including *ceh1*, a mutant with constitutively elevated levels of both the stress-specific plastidial retrograde signaling metabolite methyl-erythritol cyclodiphosphate (MEcPP) and the defense hormone salicylic acid (SA), as well as the high MEcPP but SA deficient genotype *ceh1/eds16*, along with corresponding controls. Integration of multi-omic analyses enabled us to delineate the function of MEcPP from SA, and expose the compartmentalized role of this retrograde signaling metabolite in induction of distinct but interdependent signaling cascades instrumental in adaptive responses. Specifically, here we identify strata of MEcPP-sensitive stress-response cascades, among which we focus on selected pathways including organelle-specific regulation of jasmonate biosynthesis; simultaneous induction of synthesis and breakdown of SA; and MEcPP-mediated alteration of cellular redox status in particular glutathione redox balance. Collectively, these integrated multi-omic analyses provided a vehicle to gain an in-depth knowledge of genome-metabolism interactions, and to further probe the extent of these interactions and delineate their functional contributions. Through this approach we were able to pinpoint stress-mediated transcriptional and metabolic signatures and identify the downstream processes modulated by the independent or overlapping functions of MEcPP and SA in adaptive responses. ayoon Dehesh

Accepted manuscript online: 28 MAR 2017 03:04AM EST | DOI: 10.1111/tpj.13547

*Emp10* encodes a mitochondrial PPR protein that affects the *cis*-splicing of *nad2* intron 1 and seed development in maize

Manjun Cai, L Shuzhen, Feng Sun, Qin Sun, Hailiang Zhao, Xuemei Ren, Yanxin Zhao, Baocai Tan, Zuxin Zhang and Fazhan Qiu



Accepted manuscript online: 27 MAR 2017 10:30AM EST | DOI: 10.1111/tpj.13551

The chloroplast RNA helicase ISE2 is required for multiple chloroplast RNA processing steps in *Arabidopsis thaliana*

Krzysztof Bobik, Tyra N. McCray, Ben Ernest, Jessica C. Fernandez, Katharine A. Howell, Thomas Lane, Margaret Staton and Tessa M. Burch-Smith  
Accepted manuscript

Differences and commonalities of plant responses to single and combined stresses

Haina Zhang and Uwe Sonnewald

Accepted manuscript online: 2 APR 2017 06:15AM EST | DOI: 10.1111/tpj.13557

Laser Ablation Electrospray Ionization Mass Spectrometry with Ion Mobility Separation Reveals Metabolites in the Symbiotic Interactions of Soybean Roots and Rhizobia

Sylwia A. Stopka, Beverly J. Agtuca, David W. Koppelaar, Ljiljana Paša-Tolić, Gary Stacey, Akos Vertes and Christopher R. Anderton

Accepted manuscript online: 10 APR 2017 09:20AM EST | DOI: 10.1111/tpj.13569

Chloroplastic ATP synthase builds up *proton motive force* for preventing reactive oxygen species production in photosystem I

Daisuke Takagi, Katsumi Amako, Masaki Hashiguchi, Hidehiro Fukaki, Kimitsune Ishizaki, Goh Tatsuaki, Yoichiro Fukao, Ryosuke Sano, Tetsuya Kurata, Taku Demura, Shinichiro Sawa and Chikahiro Miyake

Accepted manuscript online: 5 APR 2017 01:17PM EST | DOI: 10.1111/tpj.13566

Reactive oxygen species-provoked mitochondria-dependent cell death during ageing of elm (*Ulmus pumila* L.) seeds (pages 438–452)

Yu Wang, Ying Li, Hua Xue, Hugh W. Pritchard and Xiaofeng Wang

Article first published online: 14 JAN 2015 | DOI: 10.1111/tpj.12737

HB1, a truncated hemoglobin, modulates nitric oxide levels and nitrate reductase activity (pages 467–479)

Emanuel Sanz-Luque, Francisco Ocaña-Calahorra, Amaury de Montaigu, Alejandro Chamizo-Ampudia, Ángel Llamas, Aurora Galván and Emilio Fernández

Article first published online: 23 JAN 2015 | DOI: 10.1111/tpj.12744

Hemoglobins are ubiquitous proteins that sense, store and transport oxygen, but the physiological processes in which they are implicated is currently expanding. Recent examples of previously unknown hemoglobin functions, which include scavenging of the signaling molecule nitric oxide (NO), illustrate how the implication of hemoglobins in different cell signaling processes is only starting to be unraveled. The extent and diversity of the hemoglobin protein family suggest that hemoglobins have diverged and have potentially evolved specialized functions in certain organisms. A unique model organism to study this functional diversity at the cellular level is the green alga *Chlamydomonas reinhardtii* because, among other reasons, it contains an unusually high number of a particular type of hemoglobins known as truncated hemoglobins (THB1–THB12). Here, we reveal a cell signaling function for a truncated hemoglobin of *Chlamydomonas* that affects the nitrogen assimilation pathway by simultaneously

modulating NO levels and nitrate reductase (NR) activity. First, we found that *THB1* and *THB2* expression is modulated by the nitrogen source and depends on NIT2, a transcription factor required for nitrate assimilation genes expression. Furthermore, *THB1* is highly expressed in the presence of NO and is able to convert NO into nitrate *in vitro*. Finally, THB1 is maintained on its active and reduced form by NR, and *in vivo* lower expression of THB1 results in increased NR activity. Thus, THB1 plays a dual role in NO detoxification and in the modulation of NR activity. This mechanism can partly explain how NO inhibits NR post-translationally.

[Leghemoglobin is nitrated in functional legume nodules in a tyrosine residue within the heme cavity by a nitrite/peroxide-dependent mechanism \(pages 723–735\)](#)

Martha Sainz, Laura Calvo-Begueria, Carmen Pérez-Rontomé, Stefanie Wienkoop, Joaquín Abián, Christiana Staudinger, Silvina Bartesaghi, Rafael Radi and Manuel Becana  
Article first published online: 24 FEB 2015 | DOI: 10.1111/tpj.12762

[Retrograde signalling caused by heritable mitochondrial dysfunction is partially mediated by ANAC017 and improves plant performance \(pages 542–558\)](#)

Olivier Van Aken, Ethan Ford, Ryan Lister, Shaobai Huang and A. Harvey Millar  
Version of Record online: 17 OCT 2016 | DOI: 10.1111/tpj.13276

#### Significance Statement

Mitochondria communicate information on their functional status to the nucleus via retrograde signalling, but it was unclear if retrograde signalling in response to constitutive mitochondrial biogenesis defects is mediated by the same pathways as those triggered during acute mitochondrial dysfunction. Here we show that the transcription factor ANAC017 plays a key role in both biogenic and operational mitochondrial retrograde signalling, improving plant growth and productivity.

[Araport11: a complete reannotation of the \*Arabidopsis thaliana\* reference genome \(pages 789–804\)](#)

Chia-Yi Cheng, Vivek Krishnakumar, Agnes P. Chan, Françoise Thibaud-Nissen, Seth Schobel and Christopher D. Town  
Version of Record online: 10 FEB 2017 | DOI: 10.1111/tpj.13415

#### Significance Statement

The most recent annotation of the *Arabidopsis thaliana* genome (TAIR10), released more than 5 years ago, had a profound impact on *Arabidopsis* research. Here we present Araport11, a re-annotation of the Col-0 reference genome. We used extensive RNA-seq data to update and extend structural gene models, thus identifying over 700 novel protein-coding genes, 500 novel transcribed regions, 5000 non-coding genes, and 35 000 small RNA loci that formerly eluded annotation.

[Translation regulation in plants: an interesting past, an exciting present and a promising future \(pages 628–653\)](#)

Catharina Merchante, Anna N. Stepanova and Jose M. Alonso  
Version of Record online: 30 MAR 2017 | DOI: 10.1111/tpj.13520

#### Significance Statement

Regulation at the translational level is an important point in the control of gene expression. Here we review examples of translation regulation studies in plants. We highlight new technologies such as Ribo-Seq and Structure-Seq that can be used to mechanistically understand how plants regulate translation under different conditions as well as the consequences of perturbing such mechanisms.

Engineering central metabolism – a grand challenge for plant biologists (pages 749–763)

Lee J. Sweetlove, Jens Nielsen and Alisdair R. Fernie

Version of Record online: 11 MAR 2017 | DOI: 10.1111/tpj.13464

Significance Statement

Increasing the biochemical efficiency and productivity of crops will require substantial changes in fluxes of central metabolism. Here we review the difficulties in achieving such changes and discuss new developments that, when combined, could lead to a new era of rational intervention in plant metabolic networks.

Integrated omics analysis of specialized metabolism in medicinal plants (pages 764–787)

Amit Rai, Kazuki Saito and Mami Yamazaki

Version of Record online: 30 MAR 2017 | DOI: 10.1111/tpj.13485

Significance Statement

Medicinal plants produce highly diverse pharmacologically important specialized metabolites, but the absence of genomics resources has limited their exploitation. Here, we review the recent developments of multi-omics approach that facilitate analysis of specialized metabolism in medicinal plants.

Small molecules below-ground: the role of specialized metabolites in the rhizosphere (pages 788–807)

Hassan Massalha, Elisa Korenblum, Dorothea Tholl and Asaph Aharoni

Version of Record online: 22 APR 2017 | DOI: 10.1111/tpj.13543

Significance Statement

The below-ground environment of plants is a dynamic setting involving complex interactions. Specialized metabolites exuded from roots to the rhizosphere play a key role in the crosstalk between roots and other neighboring soil organisms. Here, we provide an overview of the role of non-volatile as well as emitted compounds in below-ground interactions. Consequently, this review will likely inspire future research to develop solutions for combating soil pathogens and bio-stimulate growth and productivity of crops.

Current Opinion in Plant Biology: Alert 25 September-1 October

[Unravelling chemical priming machinery in plants: the role of reactive oxygen–nitrogen–sulfur species in abiotic stress tolerance enhancement](#) Review Article

Pages 101-107

Chrystalla Antoniou, Andreas Savvides, Anastasis Christou, Vasileios Fotopoulos

**NATURE PLANTS**

[MORF9 increases the RNA-binding activity of PLS-type pentatricopeptide repeat protein in plastid RNA editing](#)

Junjie Yan, Qunxia Zhang, Zeyuan Guan, Qiang Wang, Li Li *et al.*

*Nature Plants* 3, Article number: 17037 | doi:10.1038/nplants.2017.37

*Genome Res.* 2017. 27: 885-896

An improved assembly and annotation of the allohexaploid wheat genome identifies complete families of agronomic genes and provides genomic evidence for chromosomal translocations

Bread wheat (*Triticum aestivum*) is a staple crop in much of the world, but its large, complex genome has slowed efforts to produce a comprehensive map of the plant's DNA. Wheat has three similar versions of its genome and more than 80% of it consists of repetitive sequences, making it difficult to piece sequenced fragments together into a full genome. Matt Clark at the Earlham Institute in Norwich, UK, and his colleagues combined next-generation sequencing technology with computer algorithms to produce the most accurate map of the wheat genome so far. The authors identified more than 100,000 genes, including nearly 23,000 that were absent or fragmented in previous wheat genome assemblies.