May 30, 2018
Plant Cell
Response to Persistent ER Stress in Plants: a Multiphasic Process that Transitions Cells from Prosurvival Activities to Cell Death
Renu Srivastava, Zhaoxia Li, Giulia Russo, Jie Tang, Ran Bi, Usha Muppirala, Sivanandan Chudalayandi, Andrew Severin, Mingze He, Samuel I Vaitkevicius, Carolyn J. Lawrence-Dill, Peng Liu, Ann E. Stapleton, Diane C. Bassham, Federica Brandizzi and Stephen H. Howell
Plant Cell 2018 tpc.18.00153; Advance Publication May 25, 2018; doi:10.1105/tpc.18.00153 **OPEN**
http://www.plantcell.org/content/early/2018/05/25/tpc.18.00153.abstract

Nature Genetics
The *Rosa* genome provides new insights into the domestication of modern roses
High-quality genome assembly of diploid *Rosa chinensis* and resequencing of major genotypes highlights the origin of modern rose cultivars and provides insights into color biosynthesis and scent pathways.
Olivier Raymond,, Jérôme Gouzy,[…], & Mohammed Bendahmane

Resequencing of 243 diploid cotton accessions based on an updated A genome identifies the genetic basis of key agronomic traits
The authors report an improved genome assembly of *G. arboretum* and resequencing of 243 diploid cotton accessions. GWAS and QTL-seq identify a number of candidate loci that associate with seed oil content, disease resistance and yield traits in cotton.
Xiongming Dun, Gai Huangn[…]n & Fuguang Li

Resequencing a core collection of upland cotton identifies genomic variation and loci influencing fiber quality and yield
The authors resequence a core collection of upland cotton (*Gossypium hirsutum*) comprising 419 accessions. They analyze genomic variation and conduct a genome-wide association study for 13 fiber quality and yield traits in 12 different environments.
Zhiying Ma,, Shoupu He,,[…], & Xiongming Du

Locus-specific control of the de novo DNA methylation pathway in *Arabidopsis* by the CLASSY family
CLASSY chromatin remodeling factors (CLSY 1–4) are shown to regulate DNA methylation in *Arabidopsis*, both globally and in a locus-specific manner. CLSYs and RNA polymerase IV control the production of 24-nucleotide siRNAs, which guide DNA methylation.
Ming Zhou, , Ana Marie S. Palanca, & Julie A. Law

iScience
In Mitochondria β-Actin Regulates mtDNA Transcription and Is Required for Mitochondrial Quality Control
Xin Xie, Tomas Venit, Nizar Drou, Piergiorgio Percipalle

Cell: Alert 25 May-01 June – Cell is publishing plant papers!
The Positives and Negatives of NPR: A Unifying Model for Salicylic Acid Signaling in Plants
Pages 1314-1315 Roger Innes
Opposite Roles of Salicylic Acid Receptors NPR1 and NPR3/NPR4 in Transcriptional Regulation of Plant Immunity Yuli Ding, Tongjun Sun, Kevin Ao, Yujun Peng, Yaxi Zhang, Xin Li, Yuelin Zhang
Cell, Volume 173, Issue 6, 31 May 2018, Pages 1454-1467.e15

Bracing for Abscission *Pages 1320-1322*
Anja Geitmann
A lignin molecular brace controls precision processing of cell walls critical for surface integrity in Arabidopsis
Y. Lee, T.H. Yoon, J. Lee, S.Y. Jeon, J.H. Lee, M.K. Lee, H. Chen, J. Yun, S.Y. Oh, *et al.*
Cell, 173 (2018), pp. 1468–1480 this issue

Pervasive Protein Thermal Stability Variation during the Cell Cycle Original Research Article
Pages 1495-1507.e18
Isabelle Becher, Amparo Andrés-Pons, Natalie Romanov, Frank Stein, Maike Schramm, Florence Baudin, Dominic Helm,

Nils Kurzawa, André Mateus, Marie-Therese Mackmull, Athanasios Typas, Christoph W. Müller, Peer Bork, Martin Beck, Mikhail M. Savitski
Quantitative mass spectrometry has established proteome-wide regulation of protein abundance and post-translational modifications in various biological processes. Here, we used quantitative mass spectrometry to systematically analyze the thermal stability and solubility of proteins on a proteome-wide scale during the eukaryotic cell cycle. We demonstrate pervasive variation of these biophysical parameters with most changes occurring in mitosis and G1. Various cellular pathways and components vary in thermal stability, such as cell-cycle factors, polymerases, and chromatin remodelers. We demonstrate that protein thermal stability serves as a proxy for enzyme activity, DNA binding, and complex formation *in situ*. Strikingly, a large cohort of intrinsically disordered and mitotically phosphorylated proteins is stabilized and solubilized in mitosis, suggesting a fundamental remodeling of the biophysical environment of the mitotic cell. Our data represent a rich resource for cell, structural, and systems biologists interested in proteome regulation during biological transitions.
Modulation of Protein-Interaction States through the Cell Cycle Original Research Article
Pages 1481-1494.e13
Lingyun Dai, Tianyun Zhao, Xavier Bisteau, Wendi Sun, Nayana Prabhu, Yan Ting Lim, Radoslaw M. Sobota, Philipp Kaldis, Pär Nordlund
Global profiling of protein expression through the cell cycle has revealed subsets of periodically expressed proteins. However, expression levels alone only give a partial view of the biochemical processes determining cellular events. Using a proteome-wide implementation of the cellular thermal shift assay (CETSA) to study specific cell-cycle phases, we uncover changes of interaction states for more than 750 proteins during the cell cycle. Notably, many protein complexes are modulated in specific cell-cycle phases, reflecting their roles in processes such as DNA replication, chromatin remodeling, transcription, translation, and disintegration of the nuclear envelope. Surprisingly, only small differences in the interaction states were seen between the G1 and the G2 phase, suggesting similar hardwiring of biochemical processes in these two phases. The present work reveals novel molecular details of the cell cycle and establishes proteome-wide CETSA as a new strategy to study modulation of protein-interaction states in intact cells.
Current Opinion in Plant Biology: Alert 24 May-31 May
Unsung and understudied: plastids involved in secondary growth Review Article *Pages 30-36*
Desre Pinard, Eshchar Mizrachi

Great moments in evolution: the conquest of land by plants Review Article *Pages 49-54*
Stefan A Rensing

Science
Feedback regulation of COOLAIR expression controls seed dormancy and flowering time
By Min Chen, Steven Penfield
*Science*01 Jun 2018 : 1014-1017 Full Access
Two genes and an antisense RNA interpret seasonal temperature information to control plant seed dormancy in *Arabidopsis*.

Samelson AJ, Bolin E, Costello SM, Sharma AK, O'Brien EP, Marqusee S.
Kinetic and structural comparison of a protein's cotranslational folding and refolding pathways.
Sci Adv. 2018 May;4(5):eaas9098. PMID: 29854950 [PubMed - in process]

Danilova MN, Kudryakova NV, Andreeva AA, Doroshenko AS, Pojidaeva ES, Kusnetsov VV.
Differential impact of heat stress on the expression of chloroplast-encoded genes.
Plant Physiol Biochem. 2018 May 23;129:90-100. PMID: 29852366 [PubMed - as supplied by publisher]

Durie CL, Duran EC, Lucius AL.
Escherichia coli DnaK allosterically modulates ClpB between high and low peptide affinity states.
Biochemistry. 2018 May 29;. PMID: 29812913 [PubMed - as supplied by publisher]

Shurtleff MJ, Itzhak DN, Hussmann JA, Schirle Oakdale NT, Costa EA, Jonikas M, Weibezahn J, Popova KD, Jan CH, Sinitcyn P, Vembar SS, Hernandez H, Cox J, Burlingame AL, Brodsky J, Frost A, Borner GH, Weissman JS.
The ER membrane protein complex interacts cotranslationally to enable biogenesis of multipass membrane proteins.
Elife. 2018 May 29;7. PMID: 29809151 [PubMed - as supplied by publisher]

Zabinsky RA, Mason GA, Queitsch C, Jarosz DF.
It's not magic - Hsp90 and its effects on genetic and epigenetic variation.
Semin Cell Dev Biol. 2018 May 25;.PMID: 29807130 [PubMed - as supplied by publisher]

Hoang HD, Graber TE, Alain T.
Battling for ribosomes: Translational control at the forefront of the antiviral response.
J Mol Biol. 2018 May 7;. PMID: 29746850 [PubMed - as supplied by publisher]

Joshi S, Wang T, Araujo TLS, Sharma S, Brodsky JL, Chiosis G.
Adapting to stress - chaperome networks in cancer.
Nat Rev Cancer. 2018 May 23;.PMID: 29795326 [PubMed - as supplied by publisher]

Choudhury FK, Devireddy AR, Azad RK, Shulaev V, Mittler R.
Rapid accumulation of glutathione during light stress in Arabidopsis.
Plant Cell Physiol. 2018 May 25;.PMID: 29800382 [PubMed - as supplied by publisher]

Lu H, Yu D, Hansen AS, Ganguly S, Liu R, Heckert A, Darzacq X, Zhou Q.
Phase-separation mechanism forÂ C-terminal hyperphosphorylation of RNA polymerase II.
Nature. 2018 May 30;.PMID: 29849146 [PubMed - as supplied by publisher]

Ross JA, Thakor N.
Toeprinting Analysis of Translation Initiation Complex Formation on Mammalian mRNAs.
J Vis Exp. 2018 May 10;(135). PMID: 29806829 [PubMed - in process]

Murakami R, Singh CR, Morris J, Tang L, Harmon I, Azuma T, Miyoshi T, Ito K, Asano K, Uchiumi T.
The interaction between the ribosomal stalk proteins and translation initiation factor 5B promotes translation initiation.
Mol Cell Biol. 2018 May 29;.PMID: 29844065 [PubMed - as supplied by publisher]

Current Opinion in Cell Biology: Alert 26 May-02 June
PML nuclear bodies: from architecture to function Review Article *Pages 154-161*
Valérie Lallemand-Breitenbach, Hugues de Thé

PML nuclear bodies are nucleated by the PML protein, which polymerizes into spherical shells where it concentrates many unrelated partner proteins. Emerging data has connected PML bodies to post-translational control, notably conjugation by SUMOs. High concentrations of SUMO-bound proteins were proposed to condense into liquid-like droplets and such phase transition may occur within NBs. Many stress pathways modulate NB formation and recent findings have directly implicated PML in oxidative stress response *in vivo*. PML may also undergo SUMO-dependent ubiquitination/degradation. We highlight recent advances linking PML to partner degradation and other adaptative post-translational modifications in the context of chromatin remodeling, telomere biology, senescence or viral infections.

Relation to plants: From TIBS Volume 26, Issue 1, p18–20, 1 January 2001 :The recent discovery that the RING-finger domain is involved in mediating ubiquitin transfer from ubiquitin-conjugating enzymes to substrates have highlighted the importance of protein degradation through the ubiquitin–proteasome pathway in the regulation of different cellular processes. Two RING-finger-containing proteins, the promyelocytic leukemia protein (PML) from mammals and the constitutive photomorphogenic protein (COP1) from plants, show conspicuous similarities in their cellular distribution, dynamics and structure, indicating that they share a related function. Comparison of these two proteins suggests that they are involved in regulating the targeting of nuclear proteins to specific nuclear compartments for degradation through the ubiquitin–proteasome pathway.
Plant J.
The CRISPR/Cas revolution reaches the RNA world: Cas13, a new Swiss Army knife for plant biologists (pages 767–775)
Felix Wolter and Holger Puchta
Version of Record online: 4 MAY 2018 | DOI: 10.1111/tpj.13899
Significance Statement
Cas13 is a recently identified CRISPR effector that specifically cleaves single stranded RNA. In this review, we cover its

basics and discuss its manifold promising applications for plant biology, from the regulation of gene expression to virus interference, to diverse RNA manipulations.

Elevated temperature increases meiotic crossover frequency via the interfering (Type I) pathway in Arabidopsis thaliana

Jennifer L. Modliszewski, Hongkuan Wang, Ashley R. Albright, Scott M. Lewis, Alexander R. Bennett, Jiyue Huang, Hong Ma, Yingxiang Wang, Gregory P. Copenhaver

Auxin production in diploid microsporocytes is necessary and sufficient for early stages of pollen development

Xiaozhen Yao, Lei Tian, Jun Yang, Yan-Na Zhao, Ying-Xiu Zhu, Xinhua Dai, Yunde Zhao, Zhong-Nan Yang

Nature

Deciphering the catalytic mechanism of bacterial ubiquitination

Structural analysis reveals how a bacterial enzyme catalyses attachment of the protein tag ubiquitin to host proteins, illuminating a process that allows pathogenic bacteria to subvert host-cell function.

Synthetic yeast genome reveals its versatility

A redesigned yeast genome is being constructed to allow it to be extensively rearranged on demand. A suite of studies reveals the versatility of the genome-shuffling system, and shows how it could be used for biotechnology applications.
A global consortium of scientists is well on the way to making a synthetic genome for the yeast *Saccharomyces cerevisiae*[1] — the first synthetic genome for a member of the group of organisms known as eukaryotes, which includes plants, animals and fungi. Embedded within the extensively redesigned 'version 2.0' genome of *S. cerevisiae* (Sc2.0) are DNA sequences that form part of a system known as Synthetic Chromosome Rearrangement and Modification by LoxP-mediated Evolution (SCRaMbLE). This system allows extensive reorganization of the genome to be triggered on demand, generating Sc2.0 variants that have diverse genetic make-ups and characteristics. Sc2.0 is therefore a versatile platform that can be easily modified and evolved to produce yeasts that have desired attributes[2]. A collection of seven papers[3–9] published in *Nature Communications* demonstrates the immense potential of Sc2.0 for engineering and understanding yeast.

Mutant phenotypes for thousands of bacterial genes of unknown function

A large-scale mutagenesis screen identifies mutant phenotypes for over 11,000 protein-coding genes in bacteria that had previously not been assigned a specific function.
One-third of all protein-coding genes from bacterial genomes cannot be annotated with a function. Here, to investigate the functions of these genes, we present genome-wide mutant fitness data from 32 diverse bacteria across dozens of growth conditions. We identified mutant phenotypes for 11,779 protein-coding genes that had not been annotated with a specific function. Many genes could be associated with a specific condition because the gene affected fitness only in that condition, or with another gene in the same bacterium because they had similar mutant phenotypes. Of the poorly annotated genes, 2,316 had associations that have high confidence because they are conserved in other bacteria. By combining these conserved associations with comparative genomics, we identified putative DNA repair proteins; in addition, we propose specific functions for poorly annotated enzymes and transporters and for uncharacterized protein families. Our study demonstrates the scalability of microbial genetics and its utility for improving gene annotations.

The Plant Journal Content Alert (New Articles)

High-throughput detection and screening of plantsmodified by geneediting using quantitative real-time PCR

Cheng Peng, Hua Wang, Xiaoli Xu, Xiaofu Wang, Xiaoyun Chen, Wei Wei, Yongmin Lai, Guoquan Liu, Godwin Ian, Jieqin Li, Ling Zhang and Junfeng Xu
Accepted manuscript online: 15 MAY 2018 12:00AM EST | DOI: 10.1111/tpj.13961

Molecular Cell: Alert 11 May-18 May

A Liquid to Solid Phase Transition Underlying Pathological Huntingtin Exon1 Aggregation Original Research Article
Pages 588-601.e6
Thomas R. Peskett, Frédérique Rau, Jonathan O'Driscoll, Rickie Patani, Alan R. Lowe, Helen R. Saibil

Current Biology: Alert 29 May-05 June

Mitochondrial Biogenesis: MitoCPR Resuscitates Import-Defective Mitochondria
Pages R669-R671 Jacqueline Pires, Cole M. Haynes

Fan D, Cao S, Zhou Q, Zhang Y, Yue L, Han C, Yang B, Wang Y, Ma Z, Zhu L, Liu C.
Exploring the roles of substrate-binding surface of the chaperone site in the chaperone activity of trigger factor.
FASEB J. 2018 Jun 15;:fj201701576. [Epub ahead of print]
PMID: 29906241 [PubMed - as supplied by publisher]

Yu J, Li Y, Wang T, Zhong X.
Modification of N6-methyladenosine RNA methylation on heat shock protein expression.
PLoS One. 2018;13(6):e0198604.
PMID: 29902206 [PubMed - in process]

Sung YJ, Kao TY, Kuo CL, Fan CC, Cheng AN, Fang WC, Chou HY, Lo YK, Chen CH, Jiang SS, Chang IS, Hsu CH, Lee JC, Lee AY.
Mitochondrial Lon sequesters and stabilizes p53 in the matrix to restrain apoptosis under oxidative stress via its chaperone activity.
Cell Death Dis. 2018 Jun 13;9(6):697.
PMID: 29899330 [PubMed - in process]

Ravindran MS.
Molecular Chaperones: From Proteostasis to Pathogenesis.
FEBS J. 2018 Jun 11;. [Epub ahead of print]
PMID: 29890022 [PubMed - as supplied by publisher]

Santra M, Dill KA, de Graff AMR.
How Do Chaperones Protect a Cell's Proteins from Oxidative Damage?
Cell Syst. 2018 Jun 1;. [Epub ahead of print]
PMID: 29886110 [PubMed - as supplied by publisher]

Keller M, Simm S.
The coupling of transcriptome and proteome adaptation during development and heat stress response of tomato pollen.
BMC Genomics. 2018 Jun 8;19(1):447.
PMID: 29884134 [PubMed - in process]

Wilkening A, RÃ¼b C, Sylvester M, Voos W.
Analysis of heat-induced protein aggregation in human mitochondria.
J Biol Chem. 2018 Jun 12;. [Epub ahead of print]
PMID: 29895621 [PubMed - as supplied by publisher]

Morscher RJ, Ducker GS, Li SH, Mayer JA, Gitai Z, Sperl W, Rabinowitz JD.
Mitochondrial translation requires folate-dependent tRNA methylation.
Nature. 2018 Jan 24;. [Epub ahead of print]
PMID: 29364879 [PubMed - as supplied by publisher]

Plant Journal
Changes in mitochondrial DNA levels during early embryogenesis in *Torenia fournieri* and *Arabidopsis thaliana*
Long Gao, Xue Guo, Xue-Qiong Liu, Li Zhang, Jilei Huang, Li Tan, Zhen Lin, Shingo Nagawa and Dan-Yang Wang
Accepted manuscript online: 8 JUN 2018 12:00AM EST | DOI: 10.1111/tpj.13987

Yatsuzuka K, Sato SI, Pe KB, Katsuda Y, Takashima I, Watanabe M, Uesugi M.
Live-cell imaging of multiple endogenous mRNAs permits the direct observation of RNA granule dynamics.
Chem Commun (Camb). 2018 Jun 8;. [Epub ahead of print]
PMID: 29882951 [PubMed - as supplied by publisher]

Zamora-BriseÃ±o JA, Reyes-HernÃ¡ndez SJ, Zapata LCR.
Does water stress promote the proteome-wide adjustment of intrinsically disordered proteins in plants?
Cell Stress Chaperones. 2018 Jun 2;. [Epub ahead of print]

PMID: 29860709 [PubMed - as supplied by publisher]

Sethi R, Iyer SS, Das E, Roy I.
Discrete roles of trehalose and Hsp104 in inhibition of protein aggregation in yeast cells.
FEMS Yeast Res. 2018 May 30;. [Epub ahead of print]
PMID: 29860440 [PubMed - as supplied by publisher]

Uchihashi T, Watanabe YH, Nakazaki Y, Yamasaki T, Watanabe H, Maruno T, Ishii K, Uchiyama S, Song C, Murata K, Iino R, Ando T.
Dynamic structural states of ClpB involved in its disaggregation function.
Nat Commun. 2018 Jun 1;9(1):2147.
PMID: 29858573 [PubMed - in process]

Sun H, Feng F, Liu J, Zhao Q.
Nitric Oxide Affects Rice Root Growth by Regulating Auxin Transport Under Nitrate Supply.
Front Plant Sci. 2018;9:659.
PMID: 29875779 [PubMed]

Corpas FJ, Palma JM.
NO on/off in fruit ripening.
Plant Biol (Stuttg). 2018 Jun 5;. [Epub ahead of print]
PMID: 29869825 [PubMed - as supplied by publisher]

Li J, Zhang Y, Zhang Y, LÃ¼ S, Miao Y, Yang J, Huang S, Ma X, Han L, Deng J, Fan F, Liu B, Huo Y, Xu Q, Chen C, Wang X, Feng J.
GSNOR modulates hyperhomocysteinemia-induced T cell activation and atherosclerosis by switching Akt S-nitrosylation to phosphorylation.
Redox Biol. 2018 May 1;17:386-399. [Epub ahead of print]
PMID: 29860106 [PubMed - as supplied by publisher]

Buskirk AR.
Toxins that Trash Translation.
Mol Cell. 2018 Jun 7;70(5):759-760.
PMID: 29883601 [PubMed - in process]

Zurita RendÃ³n O, Fredrickson EK, Howard CJ, Van Vranken J, Fogarty S, Tolley ND, Kalia R, Osuna BA, Shen PS, Hill CP, Frost A, Rutter J.
Vms1p is a release factor for the ribosome-associated quality control complex.
Nat Commun. 2018 Jun 6;9(1):2197.
PMID: 29875445 [PubMed - in process]

Planchard N, Bertin P, Quadrado M, Dargel-Graffin C, Hatin I, Namy O, Mireau H.
The translational landscape of Arabidopsis mitochondria.
Nucleic Acids Res. 2018 Jun 5;. [Epub ahead of print]
PMID: 29873797 [PubMed - as supplied by publisher]

Cell Metab. 10.1016/j.cmet.2018.02.023 (2018).
Autophagy is a cellular response to nutrient starvation that allows cells to recycle existing molecules and organelles. Tang *et al.* investigated the mechanisms by which TORC1 (target of rapamycin complex 1) regulates autophagy. They discovered that regulation occurs through control of RNA processing. Using a genetic screen in fruitflies, they pinpointed the CPA (cleavage and polyadenylation) complex as the regulator of autophagy. CPA in turn regulates polyadenylation and alternative splicing of RNAs encoding the key proteins that regulate autophagy. This control appears to be conserved in mammalian cells, too: Loss of a component of the CPA complex disrupted regulation of metabolism and autophagy in cultured human cells.