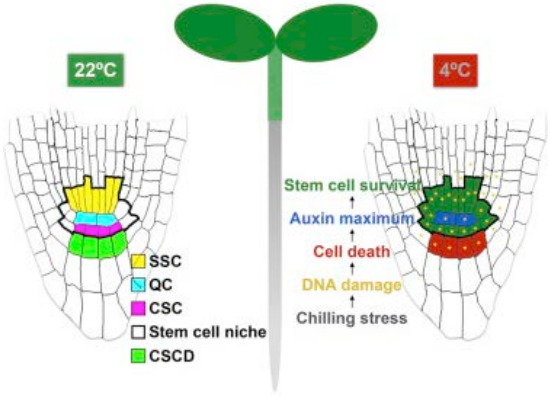
Elizabeth

The redox-sensitive module of cyclophilin 20-3, 2-cysteine peroxiredoxin and cysteine synthase integrates sulfur metabolism and oxylipin signaling in the high light acclimation response

Sara M. Müller, Shanshan Wang, Wilena Telman, Michael Liebthal, Helena Schnitzer, Andrea Viehhauser, Carsten Sticht, Carolina Delatorre, Markus Wirtz, Rüdiger Hell and Karl-Josef Dietz
Accepted manuscript online: 23 JUN 2017 10:50AM EST | DOI: 10.1111/tpj.13622

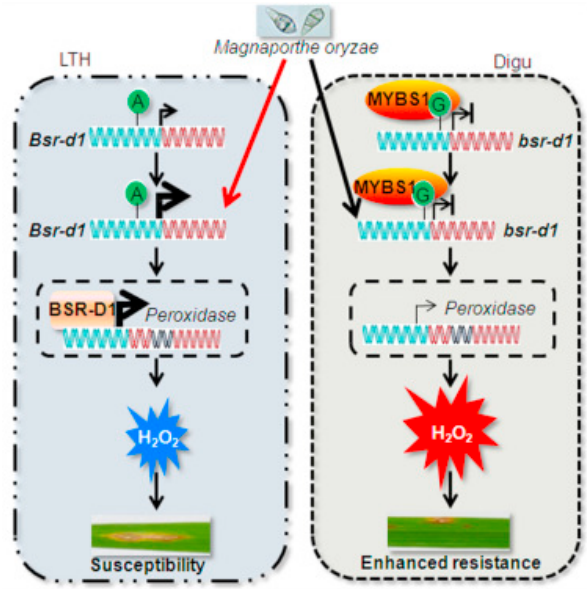
A Sacrifice-for-Survival Mechanism Protects Root Stem Cell Niche from Chilling Stress Original Research Article
Pages 102-113.e14
Jing Han Hong, Maria Savina, Jing Du, Ajay Devendran, Karthikbabu Kannivadi Ramakanth, Xin Tian, Wei Shi Sim, Victoria V. Mironova, Jian Xu

Graphical abstract



A Natural Allele of a Transcription Factor in Rice Confers Broad-Spectrum Blast Resistance Original Research Article
Pages 114-126.e15
Weitao Li, Ziwei Zhu, Mawsheng Chern, Junjie Yin, Chao Yang, Li Ran, Mengping Cheng, Min He, Kang Wang, Jing Wang, Xiaogang Zhou, Xiaobo Zhu, Zhixiong Chen, Jichun Wang, Wen Zhao, Bingtian Ma, Peng Qin, Weilan Chen, Yuping Wang, Jiali Liu, et al.

Graphical abstract



Keefer KM, True HL.
A toxic imbalance of Hsp70s in Saccharomyces cerevisiae is caused by competition for cofactors.
Mol Microbiol. 2017 Jun 30;. PMID: 28665048 [PubMed - as supplied by publisher]
Ye Y, Tang WK, Zhang T, Xia D.
A Mighty "Protein Extractor" of the Cell: Structure and Function of the p97/CDC48 ATPase.
Front Mol Biosci. 2017;4:39.PMID: 28660197 [PubMed - in process]

Bhasin H, HÃ¼lskamp M.
ANGUSTIFOLIA, a Plant Homolog of CtBP/BARS Localizes to Stress Granules and Regulates Their Formation.
Front Plant Sci. 2017;8:1004. PMID: 28659951 [PubMed - in process]

Cuevas-Velazquez CL, Reyes JL, Covarrubias AA.
Group 4 Late Embryogenesis Abundant Proteins as a Model to Study Intrinsically Disordered Proteins in Plants.
Plant Signal Behav. 2017 Jun 26;:0. PMID: 28650260 [PubMed - as supplied by publisher]

Usman MG, Rafii MY, Martini MY, Yusuff OA, Ismail MR, Miah G.
Molecular analysis of Hsp70 mechanisms in plants and their function in response to stress.
Biotechnol Genet Eng Rev. 2017 Jun 25;:1-14. PMID: 28649918
Hartings S, Paradies S, Karnuth B, Eisfeld S, Mehsing J, Wolff C, Levey T, Westhoff P, Meierhoff K.
The DnaJ-like zinc-finger protein HCF222 is required for thylakoid membrane biogenesis.
Plant Physiol. 2017 Jun 1;. PMID: 28572458 [PubMed - as supplied by publisher]

Dikic I.
Proteasomal and Autophagy Degradation Systems.
Annu Rev Biochem. 2017 May 1;. PMID: 28460188 [PubMed - as supplied by publisher]

Huang C, Alapa M, Shu P, Nagarajan N, Wu C, Sadoshima J, Kholodovych V, Li H, Beuve A.

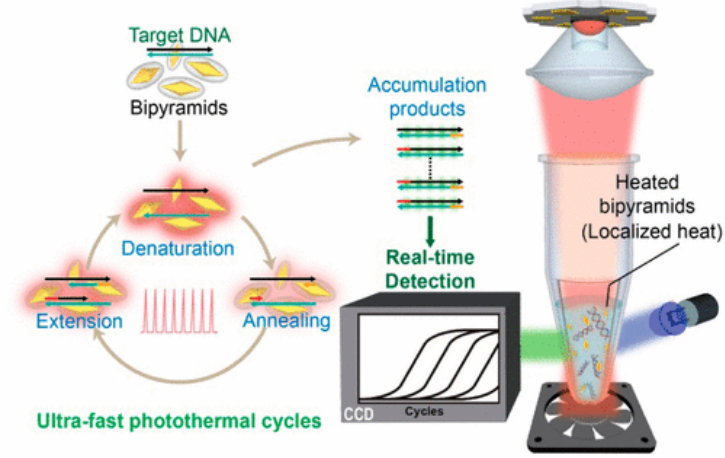
Guanylyl Cyclase Sensitivity to Nitric Oxide is Protected by a Thiol Oxidation-Driven Interaction with Thioredoxin1.
J Biol Chem. 2017 Jun 28;. PMID: 28659344 [PubMed - as supplied by publisher

Lintner NG, McClure KF, Petersen D, Londregan AT, Piotrowski DW, Wei L, Xiao J, Bolt M, Loria PM, Maguire B, Geoghegan KF, Huang A, Rolph T, Liras S, Doudna JA, Dullea RG, Cate JH.
Selective stalling of human translation through small-molecule engagement of the ribosome nascent chain.
PLoS Biol. 2017 Mar 21;15(3):e2001882.PMID: 28323820 [PubMed - in process]

Nature Protocols Contents: Volume 12 Number 7, pp 1289-1512
Quantitative proteomics: challenges and opportunities in basic and applied research **pp1289 - 1294**
In their Perspective, Schubert *et al*. discuss developments and challenges in mass-spectrometry-based proteomics technology in the past decade and explore its role in molecular systems biology, clinical research and personalized medicine.
Olga T Schubert *et al.* Published online: 01 June 2017 | doi:10.1038/nprot.2017.040 Abstract | Full Text | PDF (776K)

Plasmonic Photothermal Gold Bipyramid Nanoreactors for Ultrafast Real-Time Bioassays

Jung-Hoon Lee†, *J. Am. Chem. Soc.*, 2017, 139 (24), pp 8054–8057



Nature Methods Contents: July 2017 Volume 14 pp 637 - 752
Illuminating redox biology using NADH- and NADPH-specific sensors **pp671 - 672**
Andreas Wiederkehr and Nicolas Demaurex doi:10.1038/nmeth.4336
Genetically encoded NAD and NADP sensors will revolutionize the study of redox biology.
Genetically encoded fluorescent sensors reveal dynamic regulation of NADPH metabolism **pp720 - 728**
Rongkun Tao, Yuzheng Zhao, Huanyu Chu, Aoxue Wang, Jiahuan Zhu *et al.*
doi:10.1038/nmeth.4306
Genetically encoded iNap sensors allow imaging of NADPH with high spatiotemporal resolution in living systems. The iNaps cover physiologically relevant NADPH concentrations and are demonstrated in mammalian cells and live zebrafish.

Dasgupta MG, Dharanishanthi V.
Identification of PEG-induced water stress responsive transcripts using co-expression network in Eucalyptus grandis.
Gene. 2017 Jul 4;. [Epub ahead of print]
PMID: 28687330 [PubMed - as supplied by publisher]

Bascos NAD, Mayer MP, Bukau B, Landry SJ.
The Hsp40 J-domain modulates Hsp70 conformation and ATPase activity with a semi-elliptical spring.
Protein Sci. 2017 Jul 7;. [Epub ahead of print]
PMID: 28685898 [PubMed - as supplied by publisher]

Eickhoff P, Costa A.
Escorting Client Proteins to the Hsp90 Molecular Chaperone.
Structure. 2017 Jul 5;25(7):964-965.
PMID: 28683276 [PubMed - in process]

Mitchell JA, O'Mara ML.
Capturing the Dynamics of a Spring-Loaded Protein.
Structure. 2017 Jul 5;25(7):963-964.
PMID: 28683275 [PubMed - in process]

Wen F, Wu X, Li T, Jia M, Liu X, Li P, Zhou X, Ji X, Yue X.
Genome-wide survey of heat shock factors and heat shock protein 70s and their regulatory network under abiotic stresses in Brachypodium distachyon.
PLoS One. 2017;12(7):e0180352.
PMID: 28683139 [PubMed - in process]

Rusmini P, Cristofani R, Galbiati M, Cicardi ME, Meroni M, Ferrari V, Vezzoli G, Tedesco B, Messi E, Piccolella M, Carra S, Crippa V, Poletti A.
The Role of the Heat Shock Protein B8 (HSPB8) in Motoneuron Diseases.
Front Mol Neurosci. 2017;10:176.
PMID: 28680390 [PubMed - in process]

Kishor A, White EJF, Matsangos AE, Yan Z, Tandukar B, Wilson GM.
Hsp70's RNA-binding and mRNA-stabilizing activities are independent of its protein chaperone functions.
J Biol Chem. 2017 Jul 5;. [Epub ahead of print]
PMID: 28679534 [PubMed - as supplied by publisher]

Lu Y, Li R, Wang R, Wang X, Zheng W, Sun Q, Tong S, Dai S, Xu S.
Comparative Proteomic Analysis of Flag Leaves Reveals New Insight into Wheat Heat Adaptation.
Front Plant Sci. 2017;8:1086.
PMID: 28676819 [PubMed - in process]

McCormick C, Khaperskyy DA.
Translation inhibition and stress granules in the antiviral immune response.
Nat Rev Immunol. 2017 Jun 26;. [Epub ahead of print]
PMID: 28669985 [PubMed - as supplied by publisher

Ge H, Fang L, Huang X, Wang J, Chen W, Liu Y, Zhang Y, Wang X, Xu W, He Q, Wang Y.
Translating Divergent Environmental Stresses into a Common Proteome Response through the Histidine Kinase 33 (Hik33) in a Model Cyanobacterium.
Mol Cell Proteomics. 2017 Jul;16(7):1258-1274.
PMID: 28668777 [PubMed - in process]

Venkatesh S, Suzuki CK.
HSP60 Takes a Hit: Inhibition of Mitochondrial Protein Folding.
Cell Chem Biol. 2017 May 18;24(5):543-545.
PMID: 28525768 [PubMed - in process]

Chiti F, Dobson CM.
Protein Misfolding, Amyloid Formation, and Human Disease: A Summary of Progress Over the Last Decade.
Annu Rev Biochem. 2017 May 12;. [Epub ahead of print]
PMID: 28498720 [PubMed - as supplied by publisher]

Gayatri G, Agurla S, Kuchitsu K, Anil K, Podile AR, Raghavendra AS.
Stomatal Closure and Rise in ROS/NO of Arabidopsis Guard Cells by Tobacco Microbial Elicitors: Cryptogein and Harpin.
Front Plant Sci. 2017;8:1096.
PMID: 28680439 [PubMed - in process]

Elphinstone RE, Besla R, Shikatani EA, Lu Z, Hausladen A, Davies M, Robbins CS, Husain M, Stamler JS, Kain KC.
S-Nitrosoglutathione Reductase (GSNOR) Deficiency Confers Improved Survival and Neurological Outcome in Experimental Cerebral Malaria.
Infect Immun. 2017 Jul 3;. [Epub ahead of print]
PMID: 28674030 [PubMed - as supplied by publisher]

Mateyak MK, Kinzy TG.
Breaking the Silos of Protein Synthesis.
Trends Biochem Sci. 2017 Jun 29;. [Epub ahead of print]
PMID: 28669455 [PubMed - as supplied by publisher]

DÃƒÂ¶ring K, Ahmed N, Riemer T, Suresh HG, Vainshtein Y, Habich M, Riemer J, Mayer MP, O'Brien EP, Kramer G, Bukau B.
Profiling Ssb-Nascent Chain Interactions Reveals Principles of Hsp70-Assisted Folding.
Cell. 2017 Jul 13;170(2):298-311.e20.
PMID: 28708998 [PubMed - in process]

Rosenzweig R, Sekhar A, Nagesh J, Kay LE.
Promiscuous binding by Hsp70 results in conformational heterogeneity and fuzzy chaperone-substrate ensembles.
Elife. 2017 Jul 14;6.
PMID: 28708484 [PubMed - in process]

Zander G, Krebber H.
Quick or Quality? How mRNA escapes nuclear quality control during stress.
RNA Biol. 2017 Jul 14;:0. PMID: 28708448 [PubMed - as supplied by publisher]

Parmar N, Singh KH, Sharma D, Singh L, Kumar P, Nanjundan J, Khan YJ, Chauhan DK, Thakur AK.
Genetic engineering strategies for biotic and abiotic stress tolerance and quality enhancement in horticultural crops: a comprehensive review.
3 Biotech. 2017 Aug;7(4):239.
PMID: 28702937 [PubMed]

FernÃƒÂ¡ndez-FernÃƒÂ¡ndez MR, Gragera M, Ochoa-Ibarrola L, Quintana-Gallardo L, Valpuesta JM.
Hsp70: a master regulator in protein degradation.
FEBS Lett. 2017 Jul 11;. [Epub ahead of print]
PMID: 28696498 [PubMed - as supplied by publisher]

Editorial: Nitric oxide in plants.
Nitric Oxide. 2017 Aug 1;68:1-4.
PMID: 28693805 [PubMed - in process]

Wu S, Hu C, Tan Q, Xu S, Sun X.
Nitric Oxide Mediates Molybdenum-Induced Antioxidant Defense in Wheat under Drought Stress.
Front Plant Sci. 2017;8:1085.
PMID: 28690625 [PubMed - in process]

Bose D, Chakrabarti A.
Substrate specificity in the context of molecular chaperones.
IUBMB Life. 2017 Jul 27;. [Epub ahead of print]
PMID: 28748601 [PubMed - as supplied by publisher]

Elsholz AKW, Birk MS, Charpentier E, Turgay K.
Functional Diversity of AAA+ Protease Complexes in <i>Bacillus subtilis</i>.
Front Mol Biosci. 2017;4:44.
PMID: 28748186 [PubMed]

Sheinberger J, Shav-Tal Y.
mRNPs meet stress granules.

FEBS Lett. 2017 Jul 26;. [Epub ahead of print]
PMID: 28746974 [PubMed - as supplied by publisher]

Nguyen B, Hartich D, Seifert U, Rios PL.
Thermodynamic Bounds on the Ultra- and Infra-affinity of Hsp70 for Its Substrates.
Biophys J. 2017 Jul 25;113(2):362-370.
PMID: 28746847 [PubMed - in process]

Elnatan D, Betegon M, Liu Y, Ramelot T, Kennedy MA, Agard DA.
Symmetry broken and rebroken during the ATP hydrolysis cycle of the mitochondrial Hsp90 TRAP1.
Elife. 2017 Jul 25;6. [Epub ahead of print]
PMID: 28742020 [PubMed - as supplied by publisher]

Horowitz S, Koldewey P, Stull F, Bardwell JC.
Folding while bound to chaperones.
Curr Opin Struct Biol. 2017 Jul 19;48:1-5. [Epub ahead of print]
PMID: 28734135 [PubMed - as supplied by publisher]

Zhang TY, Li FC, Fan CM, Li X, Zhang FF, He JM.
Role and interrelationship of MEK1-MPK6 cascade, hydrogen peroxide and nitric oxide in darkness-induced stomatal closure.
Plant Sci. 2017 Sep;262:190-199.
PMID: 28716416 [PubMed - in process]

PÃ©rez-PÃ©rez ME, MauriÃ¨s A, Maes A, Tourasse NJ, Hamon M, Lemaire SD, Marchand CH.
The deep thioredoxome in Chlamydomonas reinhardtii: new insights into redox regulation.
Mol Plant. 2017 Jul 21;. [Epub ahead of print]
PMID: 28739495 [PubMed - as supplied by publisher]

McDonagh B.
Detection of ROS Induced Proteomic Signatures by Mass Spectrometry.
Front Physiol. 2017;8:470.
PMID: 28736529 [PubMed]

Chouchani ET, James AM, Methner C, Pell VR, Prime TA, Erikson BK, Forkink M, Lau GY, Bright TP, Menger KE, Fearnley IM, Krieg T, Murphy MP.
Identification and Quantification of Protein S-nitrosation by Nitrite in the Mouse Heart during Ischemia.
J Biol Chem. 2017 Jul 14;. [Epub ahead of print]
PMID: 28710281 [PubMed - as supplied by publisher]

Olivares AO, Kotamarthi HC, Stein BJ, Sauer RT, Baker TA.

Effect of directional pulling on mechanical protein degradation by ATP-dependent proteolytic machines.
Proc Natl Acad Sci U S A. 2017 Jul 19;. [Epub ahead of print]
PMID: 28724722 [PubMed - as supplied by publisher]

Kizawa A, Kawahara A, Takashima K, Takimura Y, Nishiyama Y, Hihara Y.
The LexA transcription factor regulates fatty acid biosynthetic genes in the cyanobacterium Synechocystis sp. PCC 6803.
Plant J. 2017 Jul 26;. [Epub ahead of print]
PMID: 28744961 [PubMed - as supplied by publisher]

Li YF, Mahalingam R, Sunkar R.
Isolation of Polysomal RNA for Analyzing Stress-Responsive Genes Regulated at the Translational Level in Plants.
Methods Mol Biol. 2017;1631:151-161.
PMID: 28735396 [PubMed - in process]

Prezioso SM, Brown NE, Goldberg JB.
Elfamycins: Inhibitors of Elongation Factor-Tu.
Mol Microbiol. 2017 Jul 15;. [Epub ahead of print]
PMID: 28710887 [PubMed - as supplied by publisher]

Science 14 Jul 2017:
Vol. 357, Issue 6347, pp. 168-175
DOI: 10.1126/science.aan0693

Global analysis of protein folding using massively parallel design, synthesis, and testing

Gabriel J. Rocklin, …..David Baker[1,6,*]

Abstract: Proteins fold into unique native structures stabilized by thousands of weak interactions that collectively overcome the entropic cost of folding. Although these forces are "encoded" in the thousands of known protein structures, "decoding" them is challenging because of the complexity of natural proteins that have evolved for function, not stability. We combined computational protein design, next-generation gene synthesis, and a high-throughput protease susceptibility assay to measure folding and stability for more than 15,000 de novo designed miniproteins, 1000 natural proteins, 10,000 point mutants, and 30,000 negative control sequences. This analysis identified more than 2500 stable designed proteins in four basic folds—a number sufficient to enable us to systematically examine how sequence determines folding and stability in uncharted protein space. Iteration between design and experiment increased the design success rate from 6% to 47%, produced stable proteins unlike those found in nature for topologies where design was initially unsuccessful, and revealed subtle contributions to stability as designs became increasingly optimized. Our approach

achieves the long-standing goal of a tight feedback cycle between computation and experiment and has the potential to transform computational protein design into a data-driven science.

In *Science Advances*

Production, use, and fate of all plastics ever made

Abstract: Plastics have outgrown most man-made materials and have long been under environmental scrutiny. However, robust global information, particularly about their end-of-life fate, is lacking. By identifying and synthesizing dispersed data on production, use, and end-of-life management of polymer resins, synthetic fibers, and additives, we present the first global analysis of all mass-produced plastics ever manufactured. We estimate that 8300 million metric tons (Mt) as of virgin plastics have been produced to date. As of 2015, approximately 6300 Mt of plastic waste had been generated, around 9% of which had been recycled, 12% was incinerated, and 79% was accumulated in landfills or the natural environment. If current production and waste management trends continue, roughly 12,000 Mt of plastic waste will be in landfills or in the natural environment by 2050.

Plant Journal

Stable megadalton TOC-TIC supercomplexes as major mediators of protein import into chloroplasts

Lih-Jen Chen and Hsou-min Li

Accepted manuscript online: 26 JUL 2017 03:40AM EST | DOI: 10.1111/tpj.13643

Current Opinion in Cell Biology: Alert 21 July-28 July

Cell adaptation upon stress: the emerging role of membrane-less compartments Review Article

Pages 34-42

Catherine Rabouille, Simon Alberti

The mitochondria–endoplasmic reticulum contact sites: a signalling platform for cell death Review Article

Pages 52-63

Julien Prudent, Heidi M McBride

Nature Methods Contents: August 2017 Volume 14 pp 753 - 825

CrY2H-seq: a massively multiplexed assay for deep-coverage interactome mapping pp819 - 825

Shelly A Trigg, Renee M Garza, Andrew MacWilliams, Joseph R Nery, Anna Bartlett *et al. Joe Ecker.*

doi:10.1038/nmeth.4343

CrY2H-seq, a Cre recombinase reporter-mediated yeast two-hybrid method coupled with next-generation sequencing, enables ultra-high-throughput screening of transcription factor interactions in *Arabidopsis thaliana*.

Broad-scale protein–protein interaction mapping is a major challenge given the cost, time, and sensitivity constraints of existing technologies. Here, we present a massively multiplexed yeast two-hybrid method, CrY2H-seq, which uses a Cre recombinase interaction reporter to intracellularly fuse the coding sequences of two interacting proteins and next-generation DNA sequencing to identify these interactions *en masse*. We applied CrY2H-seq to investigate sparsely annotated *Arabidopsis thaliana* transcription factors interactions. By performing ten independent screens testing a total of 36 million binary interaction combinations, and

uncovering a network of 8,577 interactions among 1,453 transcription factors, we demonstrate CrY2H-seq's improved screening capacity, efficiency, and sensitivity over those of existing technologies. The deep-coverage network resource we call AtTFIN-1 recapitulates one-third of previously reported interactions derived from diverse methods, expands the number of known plant transcription factor interactions by three-fold, and reveals previously unknown family-specific interaction module associations with plant reproductive development, root architecture, and circadian coordination.

Plant, Cell & Environment Content Alert (New Articles)

Temperature heterogeneity over leaf surfaces: the contribution of the lamina microtopography

Marc Saudreau, Amélie Ezanic, Boris Adam, Robin Caillon, Pascal Walser and Sylvain Pincebourde

Accepted manuscript online: 14 JUL 2017 08:25PM EST | DOI: 10.1111/pce.13026

Redox regulation at the site of primary growth: Auxin, cytokinin and ROS crosstalk

Vanesa B. Tognetti, Agnieszka Bielach and Mónika Hrtyan

Accepted manuscript online: 14 JUL 2017 07:30AM EST | DOI: 10.1111/pce.13021

Changing climate affects agriculture and plant biodiversity around the globe. Given that the recovery of the plants after abiotic stress periods requires apical meristems survival, a more thorough understanding of plant meristem functioning and maintenance is crucial. Therefore, in this review we provide an overview of how ROS and the main developmental hormones auxin and cytokinin are interconnected through redox systems to balance maintenance of meristematic zones upon stress. We also emphasize the need to interpret hormonal and ROS networks as interconnected mechanisms rather than as independent pathways.

Corey

Arabidopsis Nonsymbiotic Hemoglobin AHb1 Modulates Nitric Oxide Bioactivity

Abstract:

Nitric oxide (NO) is a widespread signaling molecule, and numerous targets of its action exist in plants. Whereas the activity of NO in erythrocytes, microorganisms, and invertebrates has been shown to be regulated by several hemoglobins, the function of plant hemoglobins in NO detoxification has not yet been elucidated. Here, we show that *Arabidopsis thaliana* nonsymbiotic hemoglobin AHb1 scavenges NO through production of *S*-nitrosohemoglobin and reduces NO emission under hypoxic stress, indicating its role in NO detoxification. However, AHb1 does not affect NO-mediated hypersensitive cell death in response to avirulent *Pseudomonas syringae*, suggesting that it is not involved in the removal of NO bursts originated from acute responses when NO mediates crucial defense signaling functions.

Patrick

Scientific Reports | 7: *5020* | DOI:10.1038/s41598-017-05206-2

The glyceraldehyde-3-phosphate dehydrogenase GapDH of *Corynebacterium diphtheriae* is redox-controlled by protein *S*mycothiolation under oxidative stress

Melanie Hillion 1, Marcel Imber1, Brandán Pedre2,3,4, Jörg Bernhardt5, Malek Saleh1, Vu Van Loi1, Sandra Maaß5, Dörte Becher5, Leonardo Astolfi Rosado2,3,4, Lorenz Adrian6, Christoph Weise7, Rüdiger Hell8, Markus Wirtz 8, Joris Messens2,3,4 & Haike Antelmann1

ABSTRACT

Mycothiol (MSH) is the major low molecular weight (LMW) thiol in Actinomycetes and functions in post-translational thiol-modification by protein *S*-mycothiolation as emerging thiol-protection and redox-regulatory mechanism. Here, we have used shotgun-proteomics to identify 26 *S*-mycothiolated proteins in the pathogen *Corynebacterium diphtheriae* DSM43989 under hypochlorite stress that are involved in energy metabolism, amino acid and nucleotide biosynthesis, antioxidant functions and translation. The glyceraldehyde-3-phosphate dehydrogenase (GapDH) represents the most abundant *S*-mycothiolated protein that was modified at its active site Cys153 *in vivo*. Exposure of purified GapDH to H2O2 and NaOCl resulted in irreversible inactivation due to overoxidation of the active site*in vitro*. Treatment of GapDH with H2O2 or NaOCl in the presence of MSH resulted in *S*-mycothiolation and reversible GapDH inactivation *in vitro* which was faster compared to the overoxidation pathway. Reactivation of *S*-mycothiolated GapDH could be catalyzed by both, the Trx and the Mrx1 pathways *in vitro*, but demycothiolation by Mrx1 was faster compared to Trx. In summary, we show here that *S*-mycothiolation can function in redox-regulation and protection of the GapDH active site against overoxidation in *C. diphtheriae* which can be reversed by both, the Mrx1 and Trx pathways.

Plant, Cell and Environment (2017) doi: 10.1111/pce.12989

Nitric oxide induces monosaccharide accumulation through enzyme S-nitrosylation

Zhong-Wei Zhang1†, Sha Luo2†, Gong-Chang Zhang1†, Ling-Yang Feng1†, Chong Zheng3†, Yang-Hong Zhou1, Jun-BoDu4, Ming Yuan5,
Yang-Er Chen5, Chang-QuanWang1, Wen-Juan Liu6, Xiao-Chao Xu7, Yong Hu3, Su-Lan Bai3, Dong-Dong Kong8, ShuYuan1 &
Yi-Kun He3
1College of Resources, Sichuan Agricultural University, Chengdu 611130, China, 2The High School Attached to Tsinghua University,
Beijing 100084, China, 3College of Life Science, Capital Normal University, Beijing 100048, China, 4College of Agronomy, Sichuan
Agricultural University, Chengdu 611130, China, 5College of Life Science, Sichuan Agricultural University, Ya'an 625014, China,

6Center ofAnalysis and Testing, SichuanAcademy ofAgricultural Sciences, Chengdu 610066, China, 7College ofBioindustry, Chengdu
University, Chengdu 610106, China and 8Department of Chemistry, Capital Normal University, Beijing 100048, China
ABSTRACT
Nitric oxide (NO) is extensively involved in various growth processes and stress responses in plants; however, the regulatory mechanism of NO-modulated cellular sugar metabolism is still largely unknown. Here, we report that NO significantly inhibited monosaccharide catabolism by modulating sugar metabolic enzymes through S-nitrosylation (mainly by oxidizing dihydrolipoamide, a cofactor of pyruvate dehydrogenase). These S-nitrosylation modifications led to a decrease in cellular glycolysis enzymes and ATP synthase activities as well as declines in the content of acetyl coenzyme A, ATP, ADP-glucose and UDP-glucose, which eventually caused polysaccharide-biosynthesis inhibition and monosaccharide accumulation. Plant developmental defects that were caused by high levels of NO included delayed flowering time, retarded root growth and reduced starch granule formation. These phenotypic defects could be mediated by sucrose supplementation, suggesting an essential role of NO-sugar cross-talks in plant growth and development. Our findings suggest that molecular manipulations could be used to improve fruit and vegetable sweetness.

Minsoo

1. Elife. 2017 Jul 18;6. pii: e26770. doi: 10.7554/eLife.26770.

ATP sensing in living plant cells reveals tissue gradients and stress dynamics of energy physiology.

De Col V(1)(2), Fuchs P(1), Nietzel T(1), Elsässer M(1), Voon CP(3), Candeo A(4), Seeliger I(1), Fricker MD(5), Grefen C(6), Møller IM(7), Bassi A(4), Lim BL(3)(8), Zancani M(2), Meyer AJ(1)(9), Costa A(10), Wagner S(1), Schwarzländer M(1)(9).

Author information:
(1)Institute of Crop Science and Resource Conservation, University of Bonn, Bonn, Germany.
(2)Department of Agricultural, Food, Environmental and Animal Sciences, University of Udine, Udine, Italy.

(3)School of Biological Sciences, University of Hong Kong, Hong Kong, China.
(4)Dipartimento di Fisica, Politecnico di Milano, Milano, Italy.
(5)Department of Plant Sciences, University of Oxford, Oxford, United Kingdom.
(6)Centre for Plant Molecular Biology, Developmental Genetics, University of Tübingen, Tübingen, Germany.
(7)Department of Molecular Biology and Genetics, Aarhus University, Aarhus, Denmark.
(8)State Key Laboratory of Agrobiotechnology, Chinese University of Hong Kong, Hong Kong, China.
(9)Bioeconomy Science Center, Forschungszentrum Jülich, Jülich, Germany.
(10)Dipartimento di Bioscienze, Università degli Studi di Milano, Milano, Italy.

Growth and development of plants is ultimately driven by light energy captured through photosynthesis. ATP acts as universal cellular energy cofactor fuelling all life processes, including gene expression, metabolism, and transport. Despite a mechanistic understanding of ATP biochemistry, ATP dynamics in the living plant have been largely elusive. Here, we establish MgATP(2-) measurement in living plants using the fluorescent protein biosensor ATeam1.03-nD/nA. We generate Arabidopsis sensor lines and investigate the sensor in vitro under conditions appropriate for the plant cytosol. We establish an assay for ATP fluxes in isolated mitochondria, and demonstrate that the sensor responds rapidly and reliably to MgATP(2-) changes in planta. A MgATP(2-) map of the Arabidopsis seedling highlights different MgATP(2-) concentrations between tissues and within individual cell types, such as root hairs. Progression of hypoxia reveals substantial plasticity of ATP homeostasis in seedlings, demonstrating that ATP dynamics can be monitored in the living plant.

2. Cell. 2017 Jul 13;170(2):298-311.e20. doi: 10.1016/j.cell.2017.06.038.

Profiling Ssb-Nascent Chain Interactions Reveals Principles of Hsp70-Assisted Folding.

Döring K(1), Ahmed N(2), Riemer T(1), Suresh HG(3), Vainshtein Y(4), Habich M(5), Riemer J(5), Mayer MP(4), O'Brien EP(6), Kramer G(7), Bukau B(8).

Author information:
(1)Center for Molecular Biology of Heidelberg University (ZMBH), DKFZ-ZMBH Alliance, Im Neuenheimer Feld 282, Heidelberg, Germany; German Cancer Research Center (DKFZ), Im Neuenheimer Feld 280, Heidelberg, Germany.
(2)Bioinformatics and Genomics Graduate Program, The Huck Institutes of the Life Sciences, Pennsylvania State University, University Park, PA, USA.
(3)Center for Molecular Biology of Heidelberg University (ZMBH), DKFZ-ZMBH Alliance, Im Neuenheimer Feld 282, Heidelberg, Germany; German Cancer Research

Center (DKFZ), Im Neuenheimer Feld 280, Heidelberg, Germany; The Donnelly Centre, University of Toronto, 160 College Street, Toronto ON, Canada.
(4)Center for Molecular Biology of Heidelberg University (ZMBH), DKFZ-ZMBH Alliance, Im Neuenheimer Feld 282, Heidelberg, Germany.
(5)Institute of Biochemistry, University of Cologne, Zuelpicher Str. 47, Cologne, Germany.
(6)Bioinformatics and Genomics Graduate Program, The Huck Institutes of the Life Sciences, Pennsylvania State University, University Park, PA, USA; Department of Chemistry, Pennsylvania State University, University Park, PA, USA.
(7)Center for Molecular Biology of Heidelberg University (ZMBH), DKFZ-ZMBH Alliance, Im Neuenheimer Feld 282, Heidelberg, Germany; German Cancer Research Center (DKFZ), Im Neuenheimer Feld 280, Heidelberg, Germany. Electronic address: g.kramer@zmbh.uni-heidelberg.de.
(8)Center for Molecular Biology of Heidelberg University (ZMBH), DKFZ-ZMBH Alliance, Im Neuenheimer Feld 282, Heidelberg, Germany; German Cancer Research Center (DKFZ), Im Neuenheimer Feld 280, Heidelberg, Germany. Electronic address: bukau@zmbh.uni-heidelberg.de.

The yeast Hsp70 chaperone Ssb interacts with ribosomes and nascent polypeptides to assist protein folding. To reveal its working principle, we determined the nascent chain-binding pattern of Ssb at near-residue resolution by in vivo selective ribosome profiling. Ssb associates broadly with cytosolic, nuclear, and hitherto unknown substrate classes of mitochondrial and endoplasmic reticulum (ER) nascent proteins, supporting its general chaperone function. Ssb engages most substrates by multiple binding-release cycles to a degenerate sequence enriched in positively charged and aromatic amino acids. Timely association with this motif upon emergence at the ribosomal tunnel exit requires ribosome-associated complex (RAC) but not nascent polypeptide-associated complex (NAC). Ribosome footprint densities along orfs reveal faster translation at times of Ssb binding, mainly imposed by biases in mRNA secondary structure, codon usage, and Ssb action. Ssb thus employs substrate-tailored dynamic nascent chain associations to coordinate co-translational protein folding, facilitate accelerated translation, and support membrane targeting of organellar proteins.

Ian

McDonagh B.

Detection of ROS Induced Proteomic Signatures by Mass Spectrometry.

Front Physiol. 2017;8:470.
PMID: 28736529 [PubMed]

A 2-aza-Cope reactivity-based platform for ratiometric fluorescence imaging of formaldehyde in living cells

Thomas F. Brewer,a Guillermo Burgos-Barragan,b Niek Wit,b Ketan J. Patelbc and Christopher J. Chang*ade

Keith

CRISPR-Cas encoding of a digital movie into the genomes of a population of living bacteria

Nature. 2017 Jul 20;547(7663):345-349.

Shipman SL[1,2,3], Nivala J[1,3], Macklis JD[2], Church GM[1,3].

1 Department of Genetics, Harvard Medical School, 77 Avenue Louis Pasteur, Boston, Massachusetts 02115, USA.
2 Department of Stem Cell and Regenerative Biology, Center for Brain Science, and Harvard Stem Cell Institute, Harvard University, Bauer Laboratory 103, Cambridge, Massachusetts 02138, USA.
3 Wyss Institute for Biologically Inspired Engineering, Harvard University, Cambridge, Massachusetts 02138, USA.

DNA is an excellent medium for archiving data. Recent efforts have illustrated the potential for information storage in DNA using synthesized oligonucleotides assembled in vitro. A relatively unexplored avenue of information storage in DNA is the ability to write information into the genome of a living cell by the addition of nucleotides over time. Using the Cas1-Cas2 integrase, the CRISPR-Cas microbial immune system stores the nucleotide content of invading viruses to confer adaptive immunity. When harnessed, this system has the potential to write arbitrary information into the genome. Here we use the CRISPR-Cas system to encode the pixel values of black and white images and a short movie into the genomes of a population of living bacteria. In doing so, we push the technical limits of this information storage system and optimize strategies to minimize those limitations. We also uncover underlying principles of the CRISPR-Cas adaptation system, including sequence determinants of spacer acquisition that are relevant for understanding both the basic biology of bacterial adaptation and its technological applications. This work demonstrates that this system can capture and stably store practical amounts of real data within the genomes of populations of living cells.

Cryo-EM structures of tau filaments from Alzheimer's disease.

Nature. 2017 Jul 13;547(7662):185-190.

Fitzpatrick AWP[1], Falcon B[1], He S[1], Murzin AG[1], Murshudov G[1], Garringer HJ[2], Crowther RA[1], Ghetti B[2], Goedert M[1], Scheres SHW[1].

1 MRC Laboratory of Molecular Biology, Francis Crick Avenue, Cambridge, CB2 0QH, UK.
2 Department of Pathology and Laboratory Medicine, Indiana University School of Medicine, Indianapolis, Indiana 46202, USA.

Alzheimer's disease is the most common neurodegenerative disease, and there are no mechanism-based therapies. The disease is defined by the presence of abundant neurofibrillary lesions and neuritic plaques in the cerebral cortex. Neurofibrillary lesions comprise paired helical and straight tau filaments, whereas tau filaments with different morphologies characterize other neurodegenerative diseases. No high-resolution structures of tau filaments are available. Here we present cryo-electron microscopy (cryo-EM) maps at 3.4-3.5 Å resolution and corresponding atomic models of paired helical and straight filaments from the brain of an individual with Alzheimer'sdisease. Filament cores are made of two identical protofilaments comprising residues 306-378 of tau protein, which adopt a combined cross-β/β-helix structure and define the seed for tau aggregation. Paired helical and straight filaments differ in their inter-protofilament packing, showing that they are ultrastructural polymorphs. These findings demonstrate that cryo-EM allows atomic characterization of amyloid filaments from patient-derived material, and pave the way for investigation of a range of neurodegenerative diseases.

An immunogenic personal neoantigen vaccine for patients with melanoma.

Nature. 2017 Jul 13;547(7662):217-221.

Ott PA[1,2,3], Hu Z[1], Keskin DB[1,3,4], Shukla SA[1,4], Sun J[1], Bozym DJ[1], Zhang W[1], Luoma A[5], Giobbie-Hurder A[6], Peter L[7,8], Chen C[1], Olive O[1], Carter TA[4], Li S[4], Lieb DJ[4], Eisenhaure T[4], Gjini E[9], Stevens J[10], Lane WJ[10], Javeri I[11], Nellaiappan K[11], Salazar AM[12], Daley H[1], Seaman M[7], Buchbinder EI[1,2,3], Yoon CH[3,13], Harden M[4], Lennon N[4], Gabriel S[4], Rodig SJ[9,10], Barouch DH[3,7,8], Aster JC[3,10], Getz G[3,4,1], Wucherpfennig K[3,5], Neuberg D[6], Ritz J[1,2,3], Lander ES[3,4], Fritsch EF[1,4], Hacohen N[3,4,1], Wu CJ[1,2,3,4].

1 Department of Medical Oncology, Dana-Farber Cancer Institute, Boston, Massachusetts 02215, USA.
2 Department of Medicine, Brigham and Women's Hospital, Boston, Massachusetts 02215, USA.
3 Harvard Medical School, Boston, Massachusetts 02215, USA.
4 Broad Institute of MIT and Harvard, Cambridge, Massachusetts 02142, USA.
5 Department of Cancer Immunology and Virology, Dana-Farber Cancer Institute, Boston, Massachusetts 02215, USA.

6 Department of Biostatistics and Computational Biology, Dana-Farber Cancer Institute, Boston, Massachusetts 02215, USA.
7 Center for Virology and Vaccine Research, Beth Israel Deaconess Medical Center, Boston, Massachusetts 02215, USA.
8 Ragon Institute of MGH, MIT, and Harvard, Cambridge, Massachusetts 02139, USA.
9 Center for Immuno-Oncology (CIO), Dana-Farber Cancer Institute, Boston, Massachusetts 02215, USA.
10 Department of Pathology, Brigham and Women's Hospital, Boston, Massachusetts 02215, USA.
11 CuriRx, Inc., Wilmington, Massachusetts 01887, USA.
12 Oncovir, Inc., 3203 Cleveland Avenue, NW, Washington DC 20008, USA.
13 Department of Surgery, Brigham and Women's Hospital, Boston, Massachusetts 02215, USA.

Effective anti-tumour immunity in humans has been associated with the presence of T cells directed at cancer neoantigens, a class of HLA-bound peptides that arise from tumour-specific mutations. They are highly immunogenic because they are not present in normal tissues and hence bypass central thymic tolerance. Although neoantigens were long-envisioned as optimal targets for an anti-tumour immune response, their systematic discovery and evaluation only became feasible with the recent availability of massively parallel sequencing for detection of all coding mutations within tumours, and of machine learning approaches to reliably predict those mutated peptides with high-affinity binding of autologous human leukocyte antigen (HLA) molecules. We hypothesized that vaccination with neoantigens can both expand pre-existing neoantigen-specific T-cell populations and induce a broader repertoire of new T-cell specificities in cancer patients, tipping the intra-tumoural balance in favour of enhanced tumour control. Here we demonstrate the feasibility, safety, and immunogenicity of a vaccine that targets up to 20 predicted personal tumour neoantigens. Vaccine-induced polyfunctional $CD4^+$ and $CD8^+$ T cells targeted 58 (60%) and 15 (16%) of the 97 unique neoantigens used across patients, respectively. These T cells discriminated mutated from wild-type antigens, and in some cases directly recognized autologous tumour. Of six vaccinated patients, four had no recurrence at 25 months after vaccination, while two with recurrent disease were subsequently treated with anti-PD-1 (anti-programmed cell death-1) therapy and experienced complete tumour regression, with expansion of the repertoire of neoantigen-specific T cells. These data provide a strong rationale for further development of this approach, alone and in combination with checkpoint blockade or other immunotherapies.

Personalized RNA mutanome vaccines mobilize poly-specific therapeutic immunity against cancer

Nature. 2017 Jul 13;547(7662):222-226

Sahin U[1,2,3], Derhovanessian E[1], Miller M[1], Kloke BP[1], Simon P[1], Löwer M[2], Bukur V[1,2], Tadmor AD[2], Luxemburger U[1], Schrörs B[2], Omokoko T[1], Vormehr M[1,3], Albrecht C[2], Paruzynski A[1], Kuhn AN[1], Buck J[1], Heesch S[1], Schreeb KH[1], Müller F[1], Ortseifer I[1], Vogler I[1], Godehardt E[1], Attig

S[2,3], Rae R[2], Breitkreuz A[1], Tolliver C[1], Suchan M[2], Martic G[2], Hohberger A[3], Sorn P[2], Diekmann J[1], Ciesla J[4], Waksmann O[4], Brück AK[1], Witt M[1], Zillgen M[1], Rothermel A[2], Kasemann B[2], Langer D[1], Bolte S[1], Diken M[1,2], Kreiter S[1,2], Nemecek R[5], Gebhardt C[6,7], Grabbe S[3], Höller C[5], Utikal J[6,7], Huber C[1,2,3], Loquai C[3], Türeci

1 Biopharmaceutical New Technologies (BioNTech) Corporation, An der Goldgrube 12, 55131 Mainz, Germany.
2 TRON - Translational Oncology at the University Medical Center of Johannes Gutenberg University gGmbH, Freiligrathstraße 12, 55131 Mainz, Germany.
3 University Medical Center of the Johannes Gutenberg University, Langenbeckstraße 1, 55131 Mainz, Germany.
4 EUFETS GmbH, Vollmersbachstraße 66, 55743 Idar-Oberstein, Germany.
5 Medical University of Vienna, Spitalgasse 23, 1090 Vienna, Austria.
6 German Cancer Research Center (DKFZ), Im Neuenheimer Feld 280, 69120 Heidelberg, Germany.
7 University Medical Center Mannheim, Heidelberg University, Theodor-Kutzer-Ufer 1-3, 68135 Mannheim, Germany.
8 CI3 - Cluster for Individualized Immunointervention e.V, Hölderlinstraße 8, 55131 Mainz, Germany.

T cells directed against mutant neo-epitopes drive cancer immunity. However, spontaneous immune recognition of mutations is inefficient. We recently introduced the concept of individualized mutanome vaccines and implemented an RNA-based poly-neo-epitope approach to mobilize immunity against a spectrum of cancer mutations. Here we report the first-in-human application of this concept in melanoma. We set up a process comprising comprehensive identification of individual mutations, computational prediction of neo-epitopes, and design and manufacturing of a vaccine unique for each patient. All patients developed T cell responses against multiple vaccine neo-epitopes at up to high single-digit percentages. Vaccine-induced T cell infiltration and neo-epitope-specific killing of autologous tumour cells were shown in post-vaccination resected metastases from two patients. The cumulative rate of metastatic events was highly significantly reduced after the start of vaccination, resulting in a sustained progression-free survival. Two of the five patients with metastatic disease experienced vaccine-related objective responses. One of these patients had a late relapse owing to outgrowth of β2-microglobulin-deficient melanoma cells as an acquired resistance mechanism. A third patient developed a complete response to vaccination in combination with PD-1 blockade therapy. Our study demonstrates that individual mutations can be exploited, thereby opening a path to personalized immunotherapy for patients with cancer.