

Jarrett

Front. Plant Sci., 08 April 2016 | <http://dx.doi.org/10.3389/fpls.2016.00472>

Cross-Regulation between N Metabolism and Nitric Oxide (NO) Signaling during Plant Immunity

Elise Thalineau¹, Hoai-Nam Truong¹, Antoine Berger², Carine Fournier¹, Alexandre Boscari², David Wendehenne¹ and Sylvain Jeandroz^{1*}

Damian

Laureano-Marín, A. M., Moreno, I., Romero, L. C., and Gotor, C. (2016) Negative regulation of autophagy by sulfide in *Arabidopsis thaliana* is independent of reactive oxygen species, *Plant Physiol.*

Gupta, K. J., and Igamberdiev, A. U. (2016) Reactive nitrogen species in mitochondria and their implications in plant energy status and hypoxic stress tolerance, *Frontiers in Plant Science* 7.

Rogers, H. J., and Munné-Bosch, S. (2016) Production and Scavenging of Reactive Oxygen Species and Redox Signaling during Leaf and Flower Senescence: Similar but Different, *Plant Physiol.*

Minsoo

1. Mol Cell. 2016 Apr 7;62(1):63-78. doi: 10.1016/j.molcel.2016.02.025. Epub 2016 Mar 24.

Mammalian Heat Shock Response and Mechanisms Underlying Its Genome-wide Transcriptional Regulation.

Mahat DB(1), Salamanca HH(1), Duarte FM(1), Danko CG(2), Lis JT(3).

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The heat shock response (HSR) is critical for survival of all organisms. However, its scope, extent, and the molecular mechanism of regulation are poorly understood. Here we show that the genome-wide transcriptional response to heat shock in mammals is rapid and dynamic and results in induction of several hundred and repression of several thousand genes. Heat shock factor 1 (HSF1), the "master regulator" of the HSR, controls only a fraction of heat shock-induced genes and

does so by increasing RNA polymerase II release from promoter-proximal pause. Notably, HSF2 does not compensate for the lack of HSF1. However, serum response factor appears to transiently induce cytoskeletal genes independently of HSF1. The pervasive repression of transcription is predominantly HSF1-independent and is mediated through reduction of RNA polymerase II pause release. Overall, mammalian cells orchestrate rapid, dynamic, and extensive changes in transcription upon heat shock that are largely modulated at pause release, and HSF1 plays a limited and specialized role.

Keith

The α -Crystallin Domain Containing Genes: Identification, Phylogeny and Expression Profiling in Abiotic Stress, Phytohormone Response and Development in Tomato (*Solanum lycopersicum*).

Front Plant Sci. 2016; 7: 426.

Paul A1, Rao S1, Mathur S1.

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The α -crystallin domain (ACD) is an ancient domain conserved among all kingdoms. Plant ACD proteins have roles in abiotic stresses, transcriptional regulation, inhibiting virus movement, and DNA demethylation. An exhaustive in-silico analysis using Hidden Markov Model-based conserved motif search of the tomato proteome yielded a total of 50 ACD proteins that belonged to four groups, sub-divided further into 18 classes. One of these groups belongs to the small heat shock protein (sHSP) class of proteins, molecular chaperones implicated in heat tolerance. Both tandem and segmental duplication events appear to have shaped the expansion of this gene family with purifying selection being the primary driving force for evolution. The expression profiling of the Acd genes in two different heat stress regimes suggested that their transcripts are differentially regulated with roles in acclimation and adaptive response during recovery. The co-expression of various genes in response to different abiotic stresses (heat, low temperature, dehydration, salinity, and oxidative stress) and phytohormones (abscisic acid and salicylic acid) suggested possible cross-talk between various members to combat a myriad of stresses. Further, several genes were highly expressed in fruit, root, and flower tissues as compared to leaf signifying their importance in plant development too. Evaluation of the expression of this gene family in field grown tissues highlighted the prominent role they have in providing thermo-tolerance during daily temperature variations. The function of three putative sHSPs was established as holdase chaperones as evidenced by protection to malate-dehydrogenase against heat induced protein-aggregation. This study provides insights into the characterization of the Acd genes in tomato and forms the basis for further functional validation in-planta.

Effect of methylglyoxal modification on the structure and properties of human small heat shock protein HspB6 (Hsp20).

Cell Stress Chaperones. 2016 Apr 9.

Muranova LK1, Perfilov MM1, Serebryakova MV2, Gusev NB3.

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Human small heat shock protein HspB6 (Hsp20) was modified by metabolic α -dicarbonyl compound methylglyoxal (MGO). At low MGO/HspB6 molar ratio, Arg13, Arg14, Arg27, and Arg102 were the primary sites of MGO modification. At high MGO/HspB6 ratio, practically, all Arg and Lys residues of HspB6 were modified. Both mild and extensive MGO modification decreased susceptibility of HspB6 to trypsinolysis and prevented its heat-induced aggregation. Modification by MGO was accompanied by formation of small quantities of chemically crosslinked dimers and did not dramatically affect quaternary structure of HspB6. Mild modification by MGO did not affect whereas extensive modification decreased interaction of HspB6 with HspB1. Phosphorylation of HspB6 by cyclic adenosine monophosphate (cAMP)-dependent protein kinase was inhibited after mild modification and completely prevented after extensive modification by MGO. Chaperone-like activity of HspB6 measured with subfragment 1 of skeletal myosin was enhanced after MGO modifications. It is concluded that Arg residues located in the N-terminal domain of HspB6 are easily accessible to MGO modification and that even mild modification by MGO affects susceptibility to trypsinolysis, phosphorylation by cAMP-dependent protein kinase, and chaperone-like activity of HspB6.

Multiple oligomeric structures of a bacterial small heat shock protein.

Sci Rep. 2016 Apr 7;6:24019.

Mani N1, Bhandari S1, Moreno R2, Hu L2, Prasad BV2, Suguna K1.

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2Verna and Marrs McLean Department of Biochemistry and Molecular Biology, Baylor College of Medicine, Houston, United States.

Small heat shock proteins are ubiquitous molecular chaperones that form the first line of defence against the detrimental effects of cellular stress. Under conditions of stress they undergo drastic conformational rearrangements in order to bind to misfolded substrate proteins and prevent cellular protein aggregation. Owing to the

dynamic nature of small heat shock protein oligomers, elucidating the structural basis of chaperone action and oligomerization still remains a challenge. In order to understand the organization of sHSP oligomers, we have determined crystal structures of a small heat shock protein from *Salmonella typhimurium* in a dimeric form and two higher oligomeric forms: an 18-mer and a 24-mer. Though the core dimer structure is conserved in all the forms, structural heterogeneity arises due to variation in the terminal regions.

Phosphorylated Heat Shock Protein 20 (HSPB6) Regulates Transforming Growth Factor- α -Induced Migration and Invasion of Hepatocellular Carcinoma Cells.

PLoS One. 2016 Apr 5;11(4):e0151907.

Matsushima-Nishiwaki R1, Toyoda H2, Nagasawa T1, Yasuda E3, Chiba N1, Okuda S4, Maeda A5, Kaneoka Y5, Kumada T2, Kozawa O1.

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3Department of Radiological Technology, Suzuka University of Medical Science, Suzuka, Mie, Japan.

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5Department of Surgery, Ogaki Municipal Hospital, Ogaki, Gifu, Japan.

Human hepatocellular carcinoma (HCC) is one of the major malignancies in the world. Small heat shock proteins (HSPs) are reported to play an important role in the regulation of a variety of cancer cell functions, and the functions of small HSPs are regulated by post-translational modifications such as phosphorylation. We previously reported that protein levels of a small HSP, HSP20 (HSPB6), decrease in vascular invasion positive HCC compared with those in the negative vascular invasion. Therefore, in the present study, we investigated whether HSP20 is implicated in HCC cell migration and the invasion using human HCC-derived HuH7 cells. The transforming growth factor (TGF)- α -induced migration and invasion were suppressed in the wild-type-HSP20 overexpressed cells in which phosphorylated HSP20 was detected. Phospho-mimic-HSP20 overexpression reduced the migration and invasion compared with unphosphorylated HSP20 overexpression. Dibutyl cAMP, which enhanced the phosphorylation of wild-type-HSP20, significantly reduced the TGF- α -induced cell migration of wild-type HSP20 overexpressed cells. The TGF- α -induced cell migration was inhibited by SP600125, a c-Jun N-terminal kinases (JNK) inhibitor. In phospho-mimic-HSP20 overexpressed HuH7 cells, TGF- α -stimulated JNK phosphorylation was suppressed compared with the unphosphorylated HSP20 overexpressed cells. Moreover, the level of phospho-HSP20 protein in human HCC tissues was significantly correlated with tumor invasion. Taken together, our findings strongly suggest that phosphorylated HSP20

inhibits TGF- α -induced HCC cell migration and invasion via suppression of the JNK signaling pathway.

Kinetic analysis reveals the diversity of microscopic mechanisms through which molecular chaperones suppress amyloid formation

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It is increasingly recognized that molecular chaperones play a key role in modulating the formation of amyloid fibrils, a process associated with a wide range of human disorders. Understanding the detailed mechanisms by which they perform this function, however, has been challenging because of the great complexity of the protein aggregation process itself. In this work, we build on a previous kinetic approach and develop a model that considers pairwise interactions between molecular chaperones and different protein species to identify the protein components targeted by the chaperones and the corresponding microscopic reaction steps that are inhibited. We show that these interactions conserve the topology of the unperturbed reaction network but modify the connectivity weights between the different microscopic steps. Moreover, by analysing several protein-molecular chaperone systems, we reveal the striking diversity in the microscopic mechanisms by which molecular chaperones act to suppress amyloid formation.

Targeting Allosteric Control Mechanisms in Heat Shock Protein 70 (Hsp70).

Curr Top Med Chem. 2016 Apr 13.

Li X, Shao H, Taylor IR, Gestwicki JE1.

¹University of California at San Francisco Department of Pharmaceutical Chemistry 675 Nelson Rising Lane Room 311 San Francisco, CA 94038.

Heat shock protein 70 (Hsp70) is a molecular chaperone that plays critical roles in protein homeostasis. Hsp70's chaperone activity is coordinated by intermolecular interactions between its two domains, as well as inter-molecular interactions

between Hsp70 and its co-chaperones. Each of these contacts represents a potential opportunity for the development of chemical inhibitors. To illustrate this concept, we review three classes of recently identified molecules that bind distinct pockets on Hsp70. Although all three compounds share the ability to interrupt core biochemical functions of Hsp70, they stabilize different conformers. Accordingly, each compound appears to interrupt a specific subset of inter- and intra-molecular interactions. Thus, an accurate definition of an Hsp70 inhibitor may require a particularly detailed understanding of the molecule's binding site and its effects on protein-protein interactions.

Elizabeth

April 4, 2016

Yang J, Hao X, Cao X, Liu B, Nyström T.

Spatial sequestration and detoxification of Huntingtin by the ribosome quality control complex.

Elife. 2016 Apr 1;5. PMID: 27033550 [PubMed - as supplied by publisher]

Pinti M, Gibellini L, Nasi M, De Biasi S, Bortolotti CA, Iannone A, Cossarizza A.

Emerging role of Lon protease as a master regulator of mitochondrial functions.

Biochim Biophys Acta. 2016 Mar 28; PMID: 27033304 [PubMed - as supplied by publisher]

Saarikangas J, Barral Y.

Protein aggregation as a mechanism of adaptive cellular responses.

Curr Genet. 2016 Mar 31; PMID: 27032776 [PubMed - as supplied by publisher]

Xu G, Pattamatta A, Hildago R, Pace MC, Brown H, Borchelt DR.

Vulnerability of newly synthesized proteins to proteostasis stress.

J Cell Sci. 2016 Mar 29, PMID: 27026526 [PubMed - as supplied by publisher]

Fragkostefanakis S, Mesihovic A, Hu Y, Schleiff E.

Unfolded protein response in pollen development and heat stress tolerance.

Plant Reprod. 2016 Mar 29, PMID: 27022919 [PubMed - as supplied by publisher]

Li J, Zhang J, Jia H, Li Y, Xu X, Wang L, Lu M.

The *Populus trichocarpa* PtHSP17.8 involved in heat and salt stress tolerances.

Plant Cell Rep. 2016 Mar 28, PMID: 27021382 [PubMed - as supplied by publisher]

A Proposal Regarding Best Practices for Validating the Identity of Genetic Stocks and the Effects of Genetic Variants

Joy Bergelson, Edward S. Buckler, Joseph R. Ecker, Magnus Nordborg, and Detlef Weigel

Plant Cell 2016 28: 606-609. First Published on March 8, 2016;

doi:10.1105/tpc.15.00502 **OPEN**

<http://www.plantcell.org/content/28/3/606>

An Ancient Bacterial Signaling Pathway Regulates Chloroplast Function to Influence Growth and Development in Arabidopsis

Matteo Sugliani, Hela Abdelkefi, Hang Ke, Emmanuelle Bouveret, Christophe Robaglia, Stefano Caffarri, and Ben Field

Plant Cell 2016 28: 661-679. First Published on February 23, 2016;

doi:10.1105/tpc.16.00045 **OPEN**

<http://www.plantcell.org/content/28/3/661.abstract>

The signaling nucleotide guanosine tetraphosphate, a potent inhibitor of chloroplast gene expression, mediates chloroplast and nucleocytoplasmic cooperation during plant growth and development

The RNA Polymerase II C-Terminal Domain Phosphatase-Like Protein FIERY2/CPL1 Interacts with eIF4AIII and Is Essential for Nonsense-Mediated mRNA Decay in Arabidopsis

Peng Cui, Tao Chen, Tao Qin, Feng Ding, Zhenyu Wang, Hao Chen, and Liming Xiong

Plant Cell 2016 28: 770-785. First Published on February 17, 2016;

doi:10.1105/tpc.15.00771 **OPEN**

<http://www.plantcell.org/content/28/3/770.abstract>

FRY2/CLP1 interacts with two nonsense-mediated mRNA decay factors, eIF4AIII and UPF3, and is necessary for NMD.

Nature

Mitochondrial ROS regulate thermogenic energy expenditure and sulfenylation of UCP1

Edward T. Chouchani, Lawrence Kazak, Mark P. Jedrychowski, Gina Z. Lu, Brian K. Erickson [+ et al.](#)

Uncoupling protein 1 (UCP1)-dependent thermogenesis in brown adipose tissue is supported by a burst of mitochondrial reactive oxygen species upon cold exposure.

Plant, Cell & Environment Content Alert (New Articles)

The influence of drought and heat stress on long term carbon fluxes of bioenergy crops grown in the Midwestern US

Eva Joo, Mir Zaman Hussain, Marcelo Zeri, Michael D. Masters, Jesse N. Miller, Nuria Gomez-Casanovas, Evan H. DeLucia and Carl J. Bernacchi

Accepted manuscript online: 4 APR 2016 10:51AM EST | DOI: 10.1111/pce.12751

Summary

Perennial grasses have been identified as being, in many ways, ideal feedstocks for bioenergy production. Yet side-by-side comparisons of key carbon fluxes and pools, particularly in response to climate extremes, for perennial grasses compared with the traditional row crops that they replace are needed. This research represents a long-term eddy covariance experiment, encompassing a severe drought, where three perennial ecosystem are compared with traditional row crops. The results show that perennial

ecosystems are more resilient to drought than row crops both in terms of carbon uptake and storage and that a post-drought effect may be more likely in a perennial relative to annual ecosystem.

Organelle redox autonomy during environmental stress

Avishay Bratt, Shilo Rosenwasser, Andreas Meyer and Robert Fluhr

Accepted manuscript online: 2 APR 2016 12:25AM EST | DOI: 10.1111/pce.12746



Potential pitfalls of CRISPR/Cas9-mediated genome editing (pages 1218–1231)

Rongxue Peng, Guigao Lin and Jinming Li

Article first published online: 27 NOV 2015 | DOI: 10.1111/febs.13586

Recently, a novel genome editing technique named CRISPR/Cas9 which can be applied in many fields has been rapidly developed. Albeit widely used, this technique has many potential pitfalls, including Cas9 activity, target sites selection and sgRNAs design, delivery methods, off-target effects, and the incidence of HDR. Solving these problems helps with the utilization of CRISPR/Cas9 system.

Mani N, Bhandari S, Moreno R, Hu L, Prasad BV, Suguna K.

Multiple oligomeric structures of a bacterial small heat shock protein.

Sci Rep. 2016 Apr 7;6:24019.

PMID: 27053150 [PubMed - in process]

Finka A, Mattoo RU, Goloubinoff P.

Experimental Milestones in the Discovery of Molecular Chaperones as Polypeptide Unfolding Enzymes.

Annu Rev Biochem. 2016 Mar 31;. [Epub ahead of print]

PMID: 27050154 [PubMed - as supplied by publisher]

Matsushima-Nishiwaki R, Toyoda H, Nagasawa T, Yasuda E, Chiba N, Okuda S, Maeda A, Kaneoka Y, Kumada T, Kozawa O.

Phosphorylated Heat Shock Protein 20 (HSPB6) Regulates Transforming Growth Factor- β -Induced Migration and Invasion of Hepatocellular Carcinoma Cells.

PLoS One. 2016;11(4):e0151907.

PMID: 27046040 [PubMed - in process]

Li H, Wang Y, Wang Z, Guo X, Wang F, Xia XJ, Zhou J, Shi K, Yu JQ, Zhou YH.

Microarray and genetic analysis reveals that csa-miR159b plays a critical role in abscisic acid-mediated heat tolerance in grafted cucumber plants.

Plant Cell Environ. 2016 Apr 2;. [Epub ahead of print]

PMID: 27037862 [PubMed - as supplied by publisher]

Choe YJ, Park SH, Hassemer T, KÄ¶rner R, Vincenz-Donnelly L, Hayer-Hartl M, Hartl FU.

Failure of RQC machinery causes protein aggregation and proteotoxic stress.

Nature. 2016 Mar 10;531(7593):191-5.

PMID: 26934223 [PubMed - indexed for MEDLINE]

Gupta KJ, Igamberdiev AU.

Reactive Nitrogen Species in Mitochondria and Their Implications in Plant Energy Status and Hypoxic Stress Tolerance.

Front Plant Sci. 2016;7:369.

PMID: 27047533 [PubMed]

Conrad T, Albrecht AS, de Melo Costa VR, Sauer S, Meierhofer D, Årom UA.

Serial interactome capture of the human cell nucleus.

Nat Commun. 2016 Apr 4;7:11212.

PMID: 27040163 [PubMed - in process]

Rodnina MV, Wintermeyer W.

Protein elongation, co-translational folding and targeting.

J Mol Biol. 2016 Mar 30;. [Epub ahead of print]

PMID: 27038507 [PubMed - as supplied by publisher]

Plant, Cell & Environment Content Alert: 39, 5 (May 2016)

Stress-triggered redox signalling: what's in pROSPect? (pages 951–964) Review

Christine H Foyer and Graham Noctor

Article first published online: 11 DEC 2015 | DOI: 10.1111/pce.12621

The multifaceted roles of reactive oxygen species (ROS) in plants and animals continue to fascinate biologists, not least because of the dynamic relationships between reduction/oxidation (redox) signalling leading to growth and defence responses and oxidative stress leading to cell suicide programmes. We propose that ROS production is a hallmark of viable cells within a changing and challenging environment. We discuss compartment-specific differences in redox buffering capacity, the transition from hypoxia to oxidative metabolism and ROS sensing and signalling mechanisms as central future research directions.

The mechanism of Rubisco-catalysed oxygenation (pages 983–997)

Guillaume Tcherkez

Article first published online: 19 OCT 2015 | DOI: 10.1111/pce.12629

Ribulose-1,5-bisphosphate carboxylase/oxygenase is the key enzyme of photosynthetic CO₂ fixation and thus a considerable number of studies examined its kinetics and molecular properties. However, the chemical mechanism associated with O₂ fixation is not well known. This paper reviews hypotheses and describes the most plausible mechanism for oxygenation.

Auxin response factors (pages 1014–1028)

John William Chandler

Article first published online: 23 JAN 2016 | DOI: 10.1111/pce.12662

The importance of auxin in a myriad of plant developmental processes, and the recent

elucidation of many aspects of auxin signalling biology has focused attention on auxin response factors (ARFs) as central transcriptional mediators of the auxin response pathway. Recent novel facets and mechanisms of ARF function have been identified, in terms of cooperativity, binding site specificity, chromatin remodelling, translational and post-translational ARF regulation and their function independent of auxin, which have warranted review. The increasing perception that ARFs are components of higher-order protein complexes and are subject to complex regulation to integrate environmental, developmental and other hormone pathways is broadening existing paradigms of ARF function and contributing to the debate of whether auxin acts as facilitator of cell fate rather than as a determiner.

[Lipid signalling in plant responses to abiotic stress \(pages 1029–1048\)](#)

Quancau Hou, Guido Ufer and Dorothea Bartels

Article first published online: 12 FEB 2016 | DOI: 10.1111/pce.12666

[Interaction between hormonal and mitochondrial signalling during growth, development and in plant defence responses \(pages 1127–1139\)](#)

Oliver Berkowitz, Inge De Clercq, Frank Van Breusegem and James Whelan

Article first published online: 20 MAR 2016 | DOI: 10.1111/pce.12712

This review summarizes the current knowledge on the intricate interaction networks between mitochondrial and hormonal signalling. Mitochondria play a central role in plant energy metabolism, and their biogenesis and function are dependent on the regulation of nuclear encoded genes. Only recently the influence of plant hormones on the communication between mitochondria and the nucleus as well as the impact of mitochondria on hormone homeostasis has been revealed. Cross-talks and their importance for plant growth, development and stress responses are also discussed

Oxidative stress and antioxidative systems: recipes for successful data collection and interpretation (pages 1140–1160)

Graham Noctor, Amna Mhamdi and Christine H. Foyer

Article first published online: 6 APR 2016 | DOI: 10.1111/pce.12726

Summary Statement

Oxidative stress and related redox processes have become integrated into many parts of plant biology research. Here, we provide a critical methodological evaluation of some of the approaches that are used to monitor, gauge and dissect oxidative stress and related redox signalling in plants. Our Forward Look review discusses current obstacles to progress and foreseeable technological developments that are likely to promote ever faster advances within this intensely studied area.

Current Opinion in Structural Biology: Alert 7 April-13 April

[Translation regulation via nascent polypeptide-mediated ribosome stalling](#) Review Article

Pages 123-133

Daniel N Wilson, Stefan Arenz, Roland Beckmann.

SCIENCE

Belowground carbon trade among tall trees in a temperate forest

Competition between individual plants for resources is well known, but sharing of resources may also occur. Klein *et al.* observed tree-to-tree carbon shuttling between roots of tall trees in a mixed temperate forest in Switzerland (see the Perspective by van der Heijden). By applying stable carbon isotope labeling to individual tree canopies, they show that up to 40% of the carbon in the fine roots of one individual may be derived from photosynthetic products of a neighbor. Carbon transfer of this kind, mediated by plant-associated fungi, or mycorrhizae, in the soil, has been reported on a smaller scale in seedlings, but not before in trees. *Science*, this issue p. [342](#); see also p. [290](#)

‘Starshot’ probes aim for stars

Russian internet billionaire Yuri Milner, teaming up with physicist Stephen Hawking and Facebook co-founder Mark Zuckerberg, announced this week the start of a project to send miniaturized spacecraft to the nearest nearby stars. The Breakthrough Starshot initiative will use cellphone technology to make a postage stamp-sized spacecraft-on-a-chip, with camera, thrusters, and communications. Thousands of these will be launched into space, each equipped with a solar sail a few meters across. Rather than rely on the weak power of the sun for propulsion, an array of powerful ground-based lasers will fire a 100-gigawatt beam to boost the tiny craft on their way. At 20% of the speed of light, the craft will reach the nearest star, Alpha Centauri, in 20 years. They will flash by in about an hour, sending back pictures and other data about any planets. “For the first time in human history, we can do more than just stare at the stars,” Milner said 12 April at a press conference in New York.

[Architecture of the symmetric core of the nuclear pore](#)

By Daniel H. Lin, Tobias Stuwe, Sandra Schilbach, Emily J. Rundlet, Thibaud Perriches, George Mobbs, Yanbin Fan, Karsten Thierbach, Ferdinand M. Huber, Leslie N. Collins, Andrew M. Davenport, Young E. Jeon, André Hoelz

Science 15 Apr 2016

Reconstitution, spectroscopy, and crystallography allow the construction of a model of the human nuclear pore.

Nuclear pore complexes (NPCs) are 110-megadalton assemblies that mediate nucleocytoplasmic transport. NPCs are built from multiple copies of ~30 different nucleoporins, and understanding how these nucleoporins assemble into the NPC scaffold imposes a formidable challenge. Recently, it has been shown how the Y complex, a prominent NPC module, forms the outer rings of the nuclear pore. However, the organization of the inner ring has remained unknown until now. We used molecular modeling combined with cross-linking mass spectrometry and cryo-electron tomography to obtain a composite structure of the inner ring. This architectural map explains the vast majority of the electron density of the scaffold. We conclude that despite obvious differences in morphology and composition, the higher-order structure of the inner and outer rings is unexpectedly similar.

Proc. Natl. Acad. Sci. U.S.A. 10.1073/pnas.1516546113 (2016).

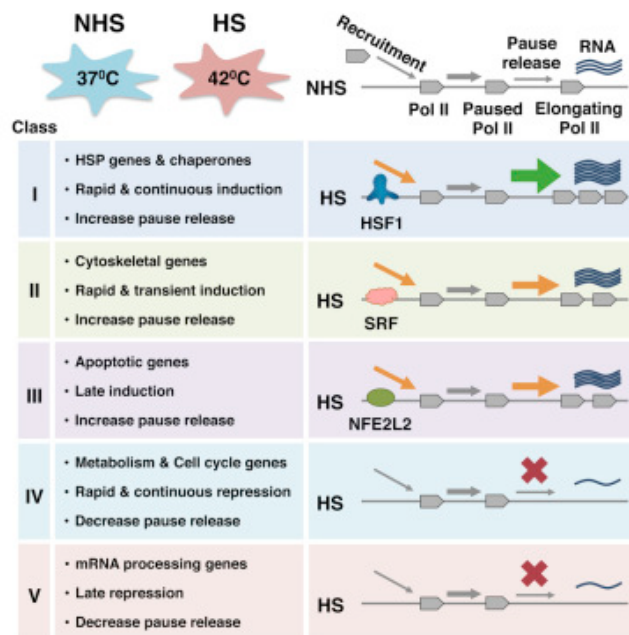
The pathological deposition of aberrant protein aggregates and fibrils is associated with a variety of neurodegenerative disorders. The protein α -synuclein is implicated in Parkinson's disease. Pinotsi *et al.* used super-resolution imaging to visualize α -synuclein as it formed aggregates in neuronal cells in culture. First they introduced pre-formed fibrils of α -synuclein and saw the endogenous soluble protein adding onto the fibrils. This process did not seem to harm the cells; however, when they added exogenous monomeric α -synuclein, it formed aggregates within the cells, which killed them. Thus, α -synuclein fibrils seem to be protective rather than harmful to neurons—at least in culture.

Molecular Cell: Alert 2 April-8 April

[Mammalian Heat Shock Response and Mechanisms Underlying Its Genome-wide Transcriptional Regulation](#) Original Research Article

Pages 63-78

Dig B. Mahat, H. Hans Salamanca, Fabiana M. Duarte, Charles G. Danko, John T. Lis



[Archives of Biochemistry and Biophysics](#)

Volume 595 , Pages 1-184, 1 April 2016

Special Issue: Tribute Issue: Helmut Sies and Oxidative Stress: venit, vidit, vicit

Edited by Henry Jay Forman and Shinya Toyokuni

Lots of articles

[Role of NAD⁺/NADH redox ratio in cell metabolism: A tribute to Helmut Sies and Theodor Bücher and Hans A. Krebs](#) Original Research Article

Pages 176-180

Jose Viña, Guillermo T. Saez, Juan Gambini, Mari Carmen Gomez-Cabrera, Consuelo Borrás

[Peroxynitrite: From interception to signaling](#) Original Research Article

Pages 153-160

Bodo Speckmann, Holger Steinbrenner, Tilman Grune, Lars-Oliver Klotz

Current Opinion in Biotechnology: Alert 2 April-8 April

[Soil memory as a potential mechanism for encouraging sustainable plant health and productivity](#) Review Article

Pages 137-142

Erin R Lapsansky, Arwen M Milroy, Marie J Andales, Jorge M Vivanco

The unspecified components of plant–microbe and plant–microbiome associations in the rhizosphere are complex, but recent research is simplifying our understanding of these relationships. We propose that the strong association between hosts, symbionts, and pathogens could be simplified by the concept of soil memory, which explains how a plant could promote their fecundity and protect their offspring through tightly associated relationships with the soil. Although there are many questions surrounding the mechanisms of this phenomenon, recent research has exposed evidence of its existence. Along with evidence from observations and mechanisms related to soil memory, we report means to utilize our understanding as sustainable protection for agricultural crops and propose future research questions.

Cell, Volume 165, Issue 2, 7 April 2016, Pages 464-474

[Root Endophyte *Colletotrichum tofieldiae* Confers Plant Fitness Benefits that Are Phosphate Status Dependent](#) Kei Hiruma, Nina Gerlach, Soledad Sacristán, Ryohei Thomas Nakano,

Stéphane Hacquard, Barbara Kracher, Ulla Neumann, Diana Ramírez, Marcel Bucher, Richard J. O’Connell, Paul Schulze-Lefert

Endophytic fungi are found within the roots of healthy plants, but their function is poorly understood. In this issue, Hiruma et al. demonstrate that, under phosphate-limiting conditions, the endophytic fungus, *Colletotrichum tofieldiae*, provides growth-promoting and fitness benefits to *Arabidopsis*, but the plant must restrict fungal growth or risk pathogenesis.

Nature Biotechnology

Transcriptome-scale RNase-footprinting of RNA-protein complexes - pp410 - 413

Zhe Ji, Ruisheng Song, Hailiang Huang, Aviv Regev & Kevin Struhl

doi:10.1038/nbt.3441

Transcriptome-scale detection of RNA regions protected by nonribosomal RNA-protein complexes.

[First Paragraph - | Full Text - Transcriptome-scale RNase-footprinting of RNA-protein complexes | PDF \(881 KB\) - Transcriptome-scale RNase-footprinting of RNA-protein complexes | Supplementary information](#)