Lit Lunch
10_17_14

Damian:

1) NITRIC OXIDE PLAYS A ROLE IN STEM CELL NICHE HOMEOSTASIS THROUGH ITS INTERACTION WITH AUXIN

Luis Sanz, María Fernández-Marcos, Abelardo Modrego, Daniel R. Lewis[2], Gloria K.
Muday[2], Stephan Pollmann[3], Montserrat Dueñas[4], Celestino Santos-Buelga[4], and Oscar Lorenzo[1]
PLANT PHYSIOLOGY PREVIEW

2) Intergenic Sequence between Arabidopsis ClpB-C/ 1 Hsp100 and Choline Kinase Genes Functions as a Heat Inducible Bidirectional Promoter

Ratnesh Chandra Mishra, Anil Grover*
PLANT PHYSIOLOGY PREVIEW

Stephanie:

1)A highly charged region in the middle domain of plant endoplasmic reticulum (ER)-localized heat-shock protein 90 is required for resistance to tunicamycin or high calcium-induced ER stresses

Lisa P. Chong*, Yao Wang*, Nanette Gad, Nathaniel Anderson, Bhavank Shah and Rongmin Zhao†

Journal of Experimental Botany

Keith:

1) Non-chaperone Proteins Can Inhibit Aggregation and Cytotoxicity of Alzheimer Amyloid Peptide

THE JOURNAL OF BIOLOGICAL CHEMISTRY VOL. 289, NO.40, pp. 27766–27775, October 3, 2014

Jinghui Luo‡, Sebastian K. T. S. Wärmländer§, Astrid Gräslund§, and Jan Pieter Abrahams‡1

‡*Gorlaeus Laboratory, Leiden Institute of Chemistry, Leiden University, 2300RA Leiden, The Netherlands and* §*Department of Biochemistry and Biophysics, Stockholm University SE-10691 Stockholm, Sweden*

Many factors are known to influence the oligomerization, fibrillation, and amyloid formation of the Aβ peptide that is associated with Alzheimer disease. Other proteins that are pres- ent when Aβ peptides deposit *in vivo* are likely to have an

effect on these aggregation processes. To separate specific *versus* broad-spectrum effects of proteins on Aβ□aggregation, we tested a series of proteins not reported to have chaperone activity: cat- alase, pyruvate kinase, albumin, lysozyme, □lactalbumin, and □lactoglobulin. All tested proteins suppressed the fibrillation of Alzheimer A□(1–40) peptide at substoichiometric ratios, albeit some more effectively than others. All proteins bound non-specifically to Aβ, stabilized its random coils, and reduced its cytotoxicity. Surprisingly, pyruvate kinase and catalase were at least as effective as known chaperones in inhibiting Aβ□ aggregation. We propose general mechanisms for the broad-spectrum inhibition Aβ□ fibrillation by proteins. The mechanisms we discuss are significant for prognostics and perhaps even for prevention and treatment of Alzheimer disease.

2) Chaperones Rescue Luciferase Folding by Separating Its Domains

THE JOURNAL OF BIOLOGICAL CHEMISTRY VOL. 289, NO. 41, pp. 28607–28618, October 10, 2014

Zackary N. Scholl[‡], Weitao Yang[‡§], and Piotr E. Marszalek[¶1]

Program in Computational Biology and Bioinformatics, §Department of Chemistry, and ¶Department of Mechanical Engineering and Materials Science, Center for Biologically Inspired Materials and Material Systems, Duke University, Durham, North Carolina 27705

Over the last 50 years, significant progress has been made toward understanding how small single-domain proteins fold. However, very little is known about folding mechanisms of medium and large multidomain proteins that predominate the proteomes of all forms of life. Large proteins frequently fold cotranslationally and/or require chaperones. Firefly (*Photinus pyralis*) luciferase (Luciferase, 550 residues) has been a model of a cotranslationally folding protein whose extremely slow refold- ing (approximately days) is catalyzed by chaperones. However, the mechanism by which Luciferase misfolds and how chaperones assist Luciferase refolding remains unknown. Here we combine single-molecule force spectroscopy (atomic force microscopy (AFM)/single-molecule force spectroscopy) with steered molecular dynamic computer simulations to unravel the mechanism of chaperone-assisted Luciferase refolding. Our AFM and steered molecular dynamic results show that partially unfolded Luciferase, with the N-terminal domain remaining folded, can refold robustly without chaperones. Complete unfolding causes Luciferase to get trapped in very stable non- native configurations involving interactions between N- and C-terminal residues. However, chaperones allow the completely unfolded Luciferase to refold quickly in AFM experiments, strongly suggesting that chaperones are able to sequester non-natively contacting residues. More generally, we suggest that many chaperones, rather than actively promoting the folding, mimic

the ribosomal exit tunnel and physically separate protein domains, allowing them to fold in a cotranslational-like sequential process.

3) Mechanochemical basis of protein degradation by a double-ring AAA+ machine

Nature Structural & Molecular Biology **21**, 871–875 (2014)

Adrian O Olivares[1], Andrew R Nager[1,3], Ohad Iosefson[1], Robert T Sauer[1] & Tania A Baker[1,2]

Affiliations: Stanford University and MIT

Molecular machines containing double or single AAA+ rings power energy-dependent protein degradation and other critical cellular processes, including disaggregation and remodeling of macromolecular complexes. How the mechanical activities of double-ring and single-ring AAA+ enzymes differ is unknown. Using single-molecule optical trapping, we determine how the double-ring ClpA enzyme from *Escherichia coli*, in complex with the ClpP peptidase, mechanically degrades proteins. We demonstrate that ClpA unfolds some protein substrates substantially faster than does the single-ring ClpX enzyme, which also degrades substrates in collaboration with ClpP. We find that ClpA is a slower polypeptide translocase and that it moves in physical steps that are smaller and more regular than steps taken by ClpX. These direct measurements of protein unfolding and translocation define the core mechanochemical behavior of a double-ring AAA+ machine and provide insight into the degradation of proteins that unfold via metastable intermediates.

Indu:

1. Science. 2014 Sep 19;345(6203):1479-84. doi: 10.1126/science.1256996. Epub 2014 Aug 14.

   Structural biology. Crystal structure of a CRISPR RNA-guided surveillance complex bound to a ssDNA target.

   Mulepati S(1), Héroux A(2), Bailey S(3).

   Author information:
   (1)Department of Biochemistry and Molecular Biology, Bloomberg School of Public Health, Johns Hopkins University, Baltimore, MD 21205, USA.
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   Comment in
   Science. 2014 Sep 19;345(6203):1452-3.

   In prokaryotes, RNA derived from type I and type III CRISPR loci direct large ribonucleoprotein complexes to destroy invading bacteriophage and plasmids. In

Escherichia coli, this 405-kilodalton complex is called Cascade. We report the crystal structure of Cascade bound to a single-stranded DNA (ssDNA) target at a resolution of 3.03 angstroms. The structure reveals that the CRISPR RNA and target strands do not form a double helix but instead adopt an underwound ribbon-like structure. This noncanonical structure is facilitated by rotation of every sixth nucleotide out of the RNA-DNA hybrid and is stabilized by the highly interlocked organization of protein subunits. These studies provide insight into both the assembly and the activity of this complex and suggest a mechanism to enforce fidelity of target binding.

PMID: 25123481 [PubMed - in process]

2. Science. 2014 Sep 19;345(6203):1473-9. doi: 10.1126/science.1256328. Epub 2014 Aug 7.

Structural biology. Crystal structure of the CRISPR RNA-guided surveillance complex from Escherichia coli.

Jackson RN(1), Golden SM(1), van Erp PB(1), Carter J(1), Westra ER(2), Brouns SJ(2), van der Oost J(2), Terwilliger TC(3), Read RJ(4), Wiedenheft B(5).

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(4)Department of Haematology, University of Cambridge, Cambridge Institute for Medical Research, Cambridge CB2 0XY, UK.
(5)Department of Microbiology and Immunology, Montana State University, Bozeman, MT 59717, USA. bwiedenheft@gmail.com.

Comment in
Science. 2014 Sep 19;345(6203):1452-3.

Clustered regularly interspaced short palindromic repeats (CRISPRs) are essential components of RNA-guided adaptive immune systems that protect bacteria and archaea from viruses and plasmids. In Escherichia coli, short CRISPR-derived RNAs (crRNAs) assemble into a 405-kilodalton multisubunit surveillance complex called Cascade (CRISPR-associated complex for antiviral defense). Here we present the 3.24 angstrom resolution x-ray crystal structure of Cascade. Eleven proteins and a 61-nucleotide crRNA assemble into a seahorse-shaped architecture that binds double-stranded DNA targets complementary to the crRNA-guide sequence. Conserved sequences on the 3' and 5' ends of the crRNA are anchored by proteins at opposite ends of the complex, whereas the guide sequence is displayed along a helical assembly of six interwoven subunits that present five-nucleotide segments of the crRNA in pseudo-A-form configuration. The structure of Cascade suggests a mechanism for assembly and provides insights into the mechanisms of target recognition.

PMCID: PMC4188430 [Available on 2015/3/19]
PMID: 25103409 [PubMed - in process]

4. Science. 2014 Aug 8;345(6197):1255215. doi: 10.1126/science.1255215.

Plant development. Integration of growth and patterning during vascular tissue formation in Arabidopsis.

De Rybel B(1), Adibi M(2), Breda AS(1), Wendrich JR(1), Smit ME(1), Novák O(3), Yamaguchi N(4), Yoshida S(1), Van Isterdael G(5), Palovaara J(1), Nijsse B(6), Boekschoten MV(7), Hooiveld G(8), Beeckman T(5), Wagner D(4), Ljung K(9), Fleck C(10), Weijers D(11).

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(11)Laboratory of Biochemistry, Wageningen University, Dreijenlaan 3, 6703HA Wageningen, the Netherlands. dolf.weijers@wur.nl christian.fleck@wur.nl.

Comment in
Science. 2014 Aug 8;345(6197):622-3.

Coordination of cell division and pattern formation is central to tissue and organ development, particularly in plants where walls prevent cell migration. Auxin and cytokinin are both critical for division and patterning, but it is unknown how these hormones converge upon tissue development. We identify a genetic network that reinforces an early embryonic bias in auxin distribution to create a local, nonresponding cytokinin source within the root vascular tissue. Experimental and theoretical evidence shows that these cells act as a tissue organizer by positioning the domain of oriented cell divisions. We further demonstrate that the auxin-cytokinin interaction acts as a spatial incoherent feed-forward loop, which is essential to generate distinct hormonal response zones, thus establishing a stable pattern within a growing vascular tissue.

PMID: 25104393 [PubMed - indexed for MEDLINE]

6. Science. 2014 Oct 3;346(6205):75-8. doi: 10.1126/science.1258137. Epub 2014 Oct 2.

Biofuels. Altered sterol composition renders yeast thermotolerant.

Caspeta L(1), Chen Y(1), Ghiaci P(2), Feizi A(1), Buskov S(3), Hallström BM(4), Petranovic D(5), Nielsen J(6).

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(1)Novo Nordisk Foundation Center for Biosustainability, Chalmers University of Technology, SE-41296 Gothenburg, Sweden.
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(6)Novo Nordisk Foundation Center for Biosustainability, Chalmers University of Technology, SE-41296 Gothenburg, Sweden. Department of Chemical and Biological Engineering, Chalmers Unversity of Technology, SE-41296 Gothenburg, Sweden. Novo Nordisk Foundation Center for Biosustainability, DK-2970 Hørsholm, Denmark. nielsenj@chalmers.se.

Comment in
Science. 2014 Oct 3;346(6205):35-6.

Ethanol production for use as a biofuel is mainly achieved through simultaneous saccharification and fermentation by yeast. Operating at ?40°C would be beneficial in terms of increasing efficiency of the process and reducing costs, but yeast does not grow efficiently at those temperatures. We used adaptive laboratory evolution to select yeast strains with improved growth and ethanol production at ?40°C. Sequencing of the whole genome, genome-wide gene expression, and metabolic-flux analyses revealed a change in sterol composition, from ergosterol to fecosterol, caused by mutations in the C-5 sterol desaturase gene, and increased expression of genes involved in sterol biosynthesis. Additionally, large chromosome III rearrangements and mutations in genes associated with DNA damage and respiration were found, but contributed less to the thermotolerant phenotype.

PMID: 25278608 [PubMed - in process]

7. Science. 2014 Oct 3;346(6205):1255784. doi: 10.1126/science.1255784. Epub 2014 Oct 2.

Proteomics. Tracking cancer drugs in living cells by thermal profiling of the proteome.

Savitski MM(1), Reinhard FB(2), Franken H(2), Werner T(2), Savitski MF(2), Eberhard D(2), Martinez Molina D(3), Jafari R(3), Dovega RB(3), Klaeger S(4), Kuster B(4), Nordlund P(5), Bantscheff M(1), Drewes G(1).

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(5)Division of Biophysics, Department of Medical Biochemistry and Biophysics, Karolinska Institutet, Stockholm, Sweden. Centre for Biomedical Structural Biology, Nanyang Technological University, Singapore.

The thermal stability of proteins can be used to assess ligand binding in living cells. We have generalized this concept by determining the thermal profiles of more than 7000 proteins in human cells by means of mass spectrometry. Monitoring the effects of small-molecule ligands on the profiles delineated more than 50 targets for the kinase inhibitor staurosporine. We identified the heme biosynthesis enzyme ferrochelatase as a target of kinase inhibitors and suggest that its inhibition causes the phototoxicity observed with vemurafenib and alectinib. Thermal shifts were also observed for downstream effectors of drug treatment. In live cells, dasatinib induced shifts in BCR-ABL pathway proteins, including CRK/CRKL. Thermal proteome profiling provides an unbiased measure of drug-target engagement and facilitates identification of markers for drug efficacy and toxicity.

PMID: 25278616 [PubMed - in process]

Angela:

The Plant Cell:

ROP3 GTPase Contributes to Polar Auxin Transport and Auxin Responses and Is Important for Embryogenesis and Seedling Growth in *Arabidopsis*[C][W]

Jia-bao Huang, Huili Liu, Min Chen, Xiaojuan Li, Mingyan Wang, Yali Yang, Chunling Wang, Jiaqing Huang, Guolan Liu, Yuting Liu, Jian Xu, Alice Y. Cheung, and Li-zhen Tao

ROP GTPases are crucial for the establishment of cell polarity and for controlling responses to hormones and environmental signals in plants. In this work, we show that ROP3 plays important roles in embryo development and auxin-dependent plant growth. Loss-of-function and dominant-negative (DN) mutations in ROP3 induced a spectrum of similar defects starting with altered cell division patterning during early embryogenesis to postembryonic auxin-

regulated growth and developmental responses. These resulted in distorted embryo development, defective organ formation, retarded root gravitropism, and reduced auxin-dependent hypocotyl elongation. Our results showed that the expression of AUXIN RESPONSE FACTOR5/MONOPTEROS and root master regulators PLETHORA1 (PLT1) and PLT2 was reduced in DN-rop3 mutant embryos, accounting for some of the observed patterning defects. ROP3 mutations also altered polar localization of auxin efflux proteins (PINs) at the plasma membrane (PM), thus disrupting auxin maxima in the root. Notably, ROP3 is induced by auxin and prominently detected in root stele cells, an expression pattern similar to those of several stele-enriched PINs. Our results demonstrate that ROP3 is important for maintaining the polarity of PIN proteins at the PM, which in turn ensures polar auxin transport and distribution, thereby controlling plant patterning and auxin-regulated

The Ubiquitous Distribution of Late Embryogenesis Abundant Proteins across Cell Compartments in *Arabidopsis* Offers Tailored Protection against Abiotic Stress[C][W][OPEN]

Adrien Candat, Gaël Paszkiewicz, Martine Neveu, Romain Gautier, David C. Logan, Marie-Hélène Avelange-Macherel, and David Macherel

Late embryogenesis abundant (LEA) proteins are hydrophilic, mostly intrinsically disordered proteins, which play major roles in desiccation tolerance. In Arabidopsis thaliana, 51 genes encoding LEA proteins clustered into nine families have been inventoried. To increase our understanding of the yet enigmatic functions of these gene families, we report the subcellular location of each protein. Experimental data highlight the limits of in silico predictions for analysis of subcellular localization. Thirty-six LEA proteins localized to the cytosol, with most being able to diffuse into the nucleus. Three proteins were exclusively localized in plastids or mitochondria, while two others were found dually targeted to these organelles. Targeting cleavage sites could be determined for five of these proteins. Three proteins were found to be endoplasmic reticulum (ER) residents, two were vacuolar, and two were secreted. A single protein was identified in pexophagosomes. While most LEA protein families have a unique subcellular localization, members of the LEA_4 family are widely distributed (cytosol, mitochondria, plastid, ER, and pexophagosome) but share the presence of the class A α-helix

motif. They are thus expected to establish interactions with various cellular membranes under stress conditions. The broad subcellular distribution of LEA proteins highlights the requirement for each cellular compartment to be provided with protective mechanisms to cope with desiccation or cold stress.

REPRESSOR OF SILENCING5 Encodes a Member of the Small Heat Shock Protein Family and Is Required for DNA Demethylation in *Arabidopsis*[C][W]

Yusheng Zhao, Shaojun Xie, Xiaojie Li, Chunlei Wang, Zhongzhou Chen, Jinsheng Lai, and Zhizhong Gong

In Arabidopsis thaliana, active DNA demethylation is initiated by the DNA glycosylase REPRESSOR OF SILENCING1 (ROS1) and its paralogs DEMETER, DEMETER-LIKE2 (DML2), and DML3. How these demethylation enzymes are regulated, however, is poorly understood. Here, using a transgenic Arabidopsis line harboring the stress-inducible RESPONSIVE TO DEHYDRATION29A (RD29A) promoter-LUCIFERASE (LUC) reporter gene and the cauliflower mosaic virus 35S promoter (35S)-NEOMYCIN PHOSPHOTRANSFERASE II (NPTII) antibiotic resistance marker gene, we characterize a ROS locus, ROS5, that encodes a protein in the small heat shock protein family. ROS5 mutations lead to the silencing of the 35S-NPTII transgene due to DNA hypermethylation but do not affect the expression of the RD29A-LUC transgene. ROS5 physically interacts with the histone acetyltransferase ROS4/INCREASED DNA METHYLATION1 (IDM1) and is required to prevent the DNA hypermethylation of some genes that are also regulated by ROS1 and IDM1. We propose that ROS5 regulates DNA demethylation by interacting with IDM1, thereby creating a chromatin environment that facilitates the binding of ROS1 to erase DNA methylation.

Loss of Ceramide Kinase in *Arabidopsis* Impairs Defenses and Promotes Ceramide Accumulation and Mitochondrial H_2O_2 Bursts[C][W]

Fang-Cheng Bi[a,1], Zhe Liu[a,1], Jian-Xin Wu[a], Hua Liang[b], Xue-Li Xi[a], Ce Fang[a], Tie-Jun Sun[a], Jian Yin[a], Guang-Yi Dai[a], Chan Rong[a], Jean T. Greenberg[b], Wei-Wei Su[a] and Nan Yao[a,2]

Arabidopsis thaliana plants that lack ceramide kinase, encoded by ACCELERATED CELL DEATH5 (ACD5), display spontaneous programmed cell death late in development and accumulate substrates of ACD5. Here, we compared ceramide accumulation kinetics, defense responses, ultrastructural

features, and sites of reactive oxygen species (ROS) production in wild-type and acd5 plants during development and/or Botrytis cinerea infection. Quantitative sphingolipid profiling indicated that ceramide accumulation in acd5 paralleled the appearance of spontaneous cell death, and it was accompanied by autophagy and mitochondrial ROS accumulation. Plants lacking ACD5 differed significantly from the wild type in their responses to B. cinerea, showing earlier and higher increases in ceramides, greater disease, smaller cell wall appositions (papillae), reduced callose deposition and apoplastic ROS, and increased mitochondrial ROS. Together, these data show that ceramide kinase greatly affects sphingolipid metabolism and the site of ROS accumulation during development and infection, which likely explains the developmental and infection-related cell death phenotypes. The acd5 plants also showed an early defect in restricting B. cinerea germination and growth, which occurred prior to the onset of cell death. This early defect in B. cinerea restriction in acd5 points to a role for ceramide phosphate and/or the balance of ceramides in mediating early antifungal

Combined Increases in Mitochondrial Cooperation and Oxygen Photoreduction Compensate for Deficiency in Cyclic Electron Flow in *Chlamydomonas reinhardtii*[W][OPEN]

Kieu-Van Dang[a,b,c,1], Julie Plet[a,b,c,1], Dimitri Tolleter[a,b,c,2], Martina Jokel[d], Stéphan Cuiné[a,b,c], Patrick Carrier[a,b,c], Pascaline Auroy[a,b,c], Pierre Richaud[a,b,c], Xenie Johnson[a,b,c], Jean Alric[a,b,c], Yagut Allahverdiyeva[d] and Gilles Peltier[a,b,c,3]

During oxygenic photosynthesis, metabolic reactions of CO_2 fixation require more ATP than is supplied by the linear electron flow operating from photosystem II to photosystem I (PSI). Different mechanisms, such as cyclic electron flow (CEF) around PSI, have been proposed to participate in reequilibrating the ATP/NADPH balance. To determine the contribution of CEF to microalgal biomass productivity, here, we studied photosynthesis and growth performances of a knockout Chlamydomonas reinhardtii mutant (pgrl1) deficient in PROTON GRADIENT REGULATION LIKE1 (PGRL1)-mediated CEF. Steady state biomass productivity of the pgrl1 mutant, measured in photobioreactors operated as turbidostats, was similar to its wild-type progenitor under a wide range of illumination and CO_2 concentrations. Several changes were observed in pgrl1, including higher sensitivity of photosynthesis to mitochondrial inhibitors, increased light-dependent O_2 uptake, and increased amounts of flavodiiron (FLV) proteins. We conclude that a combination of

mitochondrial cooperation and oxygen photoreduction downstream of PSI (Mehler reactions) supplies extra ATP for photosynthesis in the pgrl1 mutant, resulting in normal biomass productivity under steady state conditions. The lower biomass productivity observed in the pgrl1 mutant in fluctuating light is attributed to an inability of compensation mechanisms to respond to a rapid increase in ATP demand.

Molecular Cell:

Oxidative Stress Diverts tRNA Synthetase to Nucleus for Protection against DNA Damage

Na Wei, Yi Shi, Lan N. Truong, Kathleen M. Fisch, Tao Xu, Elisabeth Gardiner, Guangsen Fu, Yun-Shiuan Olivia Hsu, and others
Molecular Cell
Published online: October 2, 2014
Aminoacyl-tRNA synthetases are well known as an essential component of the protein synthesis machinery in the cytosol. Wei et al. found that a family member—tyrosyl-tRNA synthetase—undergoes cytosol-to-nucleus translocation during oxidative stress to protect cells against DNA damage by activating transcription factor E2F1 to promote expression of DNA repair genes.

Structural Model of a CRISPR RNA-Silencing Complex Reveals the RNA-Target Cleavage Activity in Cmr4

Christian Benda, Judith Ebert, Richard A. Scheltema, Herbert B. Schiller, Marc Baumgärtner, Fabien Bonneau, Matthias Mann, Elena Conti
Molecular Cell, Vol. 56, Issue 1, p43–54
Published in issue: October 02, 2014
The Cmr complex is the only known CRISPR system that targets foreign RNA rather than DNA. Benda et al. have used a hybrid structural and mass spectrometry approach to obtain a pseudoatomic model of the *P. furiosus* Cmr complex that allows identifying the endoribonuclease cleavage site.

The Protein Targeting Factor Get3 Functions as ATP-Independent Chaperone under Oxidative Stress Conditions

Wilhelm Voth, Markus Schick, Stephanie Gates, Sheng Li, Fabio Vilardi, Irina Gostimskaya, Daniel R. Southworth, Blanche Schwappach, and others
Molecular Cell, Vol. 56, Issue 1, p116–127
Published online: September 18, 2014
Oxidative stress threatens proteins, the workhorses in cells. It is poorly understood how eukaryotic cells deal with this challenge. Voth et al. demonstrate that Get3, a protein involved in tail-anchored membrane protein biogenesis, undergoes major structural changes and serves as effective ATP-independent chaperone when oxidized, increasing chaperoning capacity of cells.

A Global Regulatory Mechanism for Activating an Exon Network Required for Neurogenesis

Bushra Raj, Manuel Irimia, Ulrich Braunschweig, Timothy Sterne-Weiler, Dave O'Hanlon, Zhen-Yuan Lin, Ginny I. Chen, Laura E. Easton, and others
Molecular Cell, Vol. 56, Issue 1, p90–103
Published online: September 11, 2014
Alternative splicing generates extensive isoform diversity in the nervous system. Raj et al. identify and characterize *cis*-elements and *trans*-factors needed to activate a network of alternative exons with critical roles in neurogenesis.

Selective Protein Denitrosylation Activity of Thioredoxin-*h*5 Modulates Plant Immunity

Sophie Kneeshaw, Silvère Gelineau, Yasuomi Tada, Gary J. Loake, Steven H. Spoel
Molecular Cell, Vol. 56, Issue 1, p153–162
Published online: September 4, 2014
Protein S-nitrosothiols (SNOs) play important roles in pathogenesis and immunity, but how SNOs are employed as signaling cues remains poorly understood. Kneeshaw et al. demonstrate in plant immunity that Thioredoxin-h5 acts as a selective SNO reductase that discriminates between protein-SNO substrates to provide specificity and reversibility to protein-SNO signaling.

Bak Core and Latch Domains Separate during Activation, and Freed Core Domains Form Symmetric Homodimers

Jason M. Brouwer, Dana Westphal, Grant Dewson, Adeline Y. Robin, Rachel T. Uren, Ray Bartolo, Geoff V. Thompson, Peter M. Colman, and others
Molecular Cell, Vol. 55, Issue 6, p938–946
Published online: August 28, 2014
BH3-only proteins activate the proapoptotic protein Bak, resulting in its oligomerization and disruption of the mitochondrial outer membrane. Here, Brouwer et al. show that Bak separates into core and latch domains upon

activation. Released core domains form BH3:groove dimers, the likely building block for the larger Bak oligomer.

An Inducible Chaperone Adapts Proteasome Assembly to Stress

Ariane Hanssum, Zhen Zhong, Adrien Rousseau, Agnieszka Krzyzosiak, Anna Sigurdardottir, Anne Bertolotti
Molecular Cell, Vol. 55, Issue 4, p566–577
Published online: July 17, 2014
Cells increase proteasome abundance in order to survive during environmental stress. Hanssum et al. reveal a mechanism for controlling proteasome abundance, showing that Adc17 is an inducible chaperone needed for proteasome assembly during stress.

Selective Protein Denitrosylation Activity of Thioredoxin-*h*5 Modulates Plant Immunity

Sophie Kneeshaw, Silvère Gelineau, Yasuomi Tada, Gary J. Loake, Steven H. Spoel
Molecular Cell, Vol. 56, Issue 1, p153–162
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Protein S-nitrosothiols (SNOs) play important roles in pathogenesis and immunity, but how SNOs are employed as signaling cues remains poorly understood. Kneeshaw et al. demonstrate in plant immunity that Thioredoxin-h5 acts as a selective SNO reductase that discriminates between protein-SNO substrates to provide specificity and reversibility to protein-SNO signaling.

Noncoding Transcription by Alternative RNA Polymerases Dynamically Regulates an Auxin-Driven Chromatin Loop

Federico Ariel, Teddy Jegu, David Latrasse, Natali Romero-Barrios, Aurélie Christ, Moussa Benhamed, Martin Crespi
Molecular Cell, Vol. 55, Issue 3, p383–396
Published online: July 10, 2014
Dynamic changes in genome topology regulate gene expression. Ariel et al. show that the dual transcription of a long intergenic noncoding RNA, APOLO, by polymerases II and V dynamically regulates chromatin conformation and the local epigenetic landscape. This mechanism directs promoter activity of PID and modulates polar auxin transport.

BMC Biology:

Shared functions of plant and mammalian StAR-related lipid transfer (START) domains in modulating transcription factor

activity

Kathrin Schrick[12*], **Michael Bruno**[3], **Aashima Khosla**[1], **Paige N Cox**[1], **Sara A Marlatt**[2], **Remigio A Roque**[2], **Henry C Nguyen**[2], **Cuiwen He**[2], **Michael P Snyder**[3], **Daljit Singh**[4] and **Gitanjali Yadav**[4]

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Published: 27 August 2014Steroidogenic acute regulatory protein (StAR)-related lipid transfer (START) domains were first identified from mammalian proteins that bind lipid/sterol ligands via a hydrophobic pocket. In plants, predicted START domains are predominantly found in homeodomain leucine zipper (HD-Zip) transcription factors that are master regulators of cell-type differentiation in development. Here we utilized studies of *Arabidopsis* in parallel with heterologous expression of START domains in yeast to investigate the hypothesis that START domains are versatile ligand-binding motifs that can modulate transcription factor activity.

Q&A: What are strigolactones and why are they important to plants and soil microbes?

Steven M Smith

BMC Biology 2014, **12**:19 doi:10.1186/1741-7007-12-19

Published: 31 March 2014Strigolactones are signaling compounds made by plants. They have two main functions: first, as endogenous hormones to control plant development, and second as components of root exudates to promote symbiotic interactions between plants and soil microbes. Some plants that are parasitic on other plants have established a third function, which is to stimulate germination of their seeds when in close proximity to the roots of a suitable host plant. It is this third function that led to the original discovery and naming of strigolactones.

Mitochondria as signaling organelles

Navdeep S Chandel

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Published: 27 May 2014Almost 20 years ago, the discovery that mitochondrial release of cytochrome c initiates a cascade that leads to cell death brought about a wholesale change in how cell biologists think of mitochondria. Formerly viewed as sites of biosynthesis and bioenergy production, these double membrane organelles could now be thought of as regulators of signal transduction. Within a few years, multiple other mitochondria-centric signaling mechanisms have been

proposed, including release of reactive oxygen species and the scaffolding of signaling complexes on the outer mitochondrial membrane. It has also been shown that mitochondrial dysfunction causes induction of stress responses, bolstering the idea that mitochondria communicate their fitness to the rest of the cell. In the past decade, multiple new modes of mitochondrial signaling have been discovered. These include the release of metabolites, mitochondrial motility and dynamics, and interaction with other organelles such as endoplasmic reticulum in regulating signaling. Collectively these studies have established that mitochondria-dependent signaling has diverse physiological and pathophysiological outcomes. This review is a brief account of recent work in mitochondria-dependent signaling in the historical framework of the early studies.

Dan:

"Transcriptome profiling of Vitis amurensis, an extremely cold-tolerant Chinese wild Vitis species, reveals candidate genes and events that potentially connected to cold stress"

Abstract:

"*Vitis amurensis* Rupr. is an exceptional wild-growing *Vitis* (grape) species that can safely survive a wide range of cold conditions, but the underlying cold-adaptive mechanism associated with gene regulation is poorly investigated. We have analyzed the physiochemical and transcriptomic changes caused by cold stress in a cold-tolerant accession, 'Heilongjiang seedling', of Chinese wild *V. amurensis*. We statistically determined that a total of 6,850 cold-regulated transcripts were involved in cold regulation, including 3,676 up-regulated and 3,174 down-regulated transcripts. A global survey of messenger RNA revealed that skipped exon is the most prevalent form of alternative spicing event. Importantly, we found that the total splicing events increased with the prolonged cold stress. We also identified thirty-eight major *TF* families that were involved in cold regulation, some of which were previously unknown. Moreover, a large number of candidate pathways for the metabolism or biosynthesis of secondary metabolites were found to be regulated by cold, which is of potential importance in coordinating cold tolerance with growth and development. Several heat shock proteins and heat shock factors were also detected to be intensively cold-regulated. Furthermore, we validated the expression profiles of 16 candidates using qRT-PCR to further confirm the accuracy of the RNA-seq data. Our results provide a genome-wide view of the dynamic changes in the transcriptome of *V. amurensis*, in which it is evident that various structural and regulatory genes are crucial for cold tolerance/adaptation. Moreover, our robust dataset advances our knowledge of the genes involved in the complex regulatory networks of cold stress and leads to a better understanding of cold tolerance mechanisms in this extremely cold-tolerant *Vitis* species."