Lit Lunch 6_20_14

Damian:

1) Shi H, Ye T, Zhu JK, Chan Z.
Constitutive production of nitric oxide leads to enhanced drought stress resistance and extensive transcriptional reprogramming in Arabidopsis.
J Exp Bot. 2014 May 27;. [Epub ahead of print]
PMID: 24868034 [PubMed - as supplied by publisher]

2) Corpas FJ, Barroso JB.
Peroxisomal plant nitric oxide synthase (NOS) protein is imported by peroxisomal targeting signal Type 2 (PTS2) in a process that depends on the cytosolic receptor PEX7 and calmodulin.
FEBS Lett. 2014 May 3;. [Epub ahead of print]
PMID: 24801177 [PubMed - as supplied by publisher]

Keith:

1) Crowding Activates ClpB and Enhances Its Association with DnaK for Efficient Protein Aggregate Reactivation

Journal of Structural Biology, Volume 135, Issue 2, August 2001, Pages 84–93

Ianire Martín[†], Garbiñe Celaya[†], Carlos Alfonso[‡], Fernando Moro[†], Germán Rivas[‡], Arturo Muga[†]

[†] Unidad de Biofísica (Consejo Superior de Investigaciones Científicas/Universidad del País Vasco-Euskal Herriko Unibertsitatea) and Departamento de Bioquímica y Biología Molecular, Universidad del País Vasco, Apartado 644, Bilbao 48080, Spain
[‡] Centro de Investigaciones Biológicas (Consejo Superior de Investigaciones Científicas), Ramiro de Maeztu 9, Madrid 28040, Spain

Reactivation of intracellular protein aggregates after a severe stress is mandatory for cell survival. In bacteria, this activity depends on the collaboration between the DnaK system and ClpB, which in vivo occurs in a highly crowded environment. The reactivation reaction includes two steps: extraction of unfolded monomers from the aggregate and their subsequent refolding into the native conformation. Both steps might be compromised by excluded volume conditions that would favor aggregation of unstable protein folding intermediates. Here, we have investigated whether ClpB and the DnaK system are able to compensate this unproductive effect and efficiently reactivate aggregates of three different substrate proteins under crowding conditions. To this aim, we have compared the association equilibrium, biochemical properties, stability, and chaperone activity of the disaggregase ClpB in the absence and presence of an inert macromolecular crowding agent. Our data show that crowding i), increases three to four orders of magnitude the association constant of the functional hexamer; ii), shifts the conformational equilibrium of the protein monomer toward a compact state; iii), stimulates its ATPase activity; and iv), favors association of the chaperone with substrate proteins and with aggregate-bound DnaK. These effects strongly enhance protein aggregate reactivation by the DnaK-ClpB network, highlighting the importance of volume exclusion in complex processes in which several proteins have to work in a sequential manner.

2) Effect of disulfide crosslinking on thermal transitions and chaperone-like activity of human small heat shock protein HspB1

Cell Stress and Chaperones June 2014

Anna S. Chalova & Maria V. Sudnitsyna & Pavel I. Semenyuk & Victor N. Orlov & Nikolai B. Gusev

Temperature-induced conformational changes of reduced and oxidized HspB1 crosslinked by disulfide bond between single Cys137 of neighboring monomers were analyzed by means of different techniques. Heating of reduced HspB1 was accompanied by irreversible changes of Trp fluorescence, whereas oxidized HspB1 underwent completely reversible changes of fluorescence. Increase of the temperature in the range of 20–70 °C was accompanied by self-association of both reduced and oxidized protein. Further increase of the temperature led to formation of heterogeneous mixture of large self-associated complexes of reduced HspB1 and to formation of smaller and less heterogeneous complexes of oxidized HspB1. Heat-induced changes of oligomeric state of reduced HspB1 were only partially reversible, whereas the corresponding changes of oligomeric state of oxidized HspB1 were almost completely reversible. Oxidation resulted in decrease of chaperone-like activity of HspB1. It is concluded that oxidative stress, inducing formation of disulfide bond, can affect stability and conformational mobility of human HspB1.

Elizabeth:

** Stephanie** The Plant Journal Content Alert (New Articles)

HSP90s are required for NLR immune receptor accumulation in Arabidopsis

Shuai Huang, Jacqueline Monaghan, Xionghui Zhong, Ling Lin, Tongjun Sun, Oliver Xiaoou Dong and Xin Li
Accepted manuscript online: 2 JUN 2014 06:11AM EST | DOI: 10.1111/tpj.12573

Large scale gene expression profiling data of the model moss *Physcomitrella patens* help to understand developmental progression, culture and stress conditions

M Hiss, O Laule, RM Meskauskiene, MA Arif, EL Decker, A Erxleben, W Frank, ST Hanke, D Lang, A Martin, C Neu, R Reski, S Richardt, M Schallenberg-Rüdinger, P Szövényi, T Tiko, G Wiedemann, L Wolf, P Zimmermann and SA Rensing
Accepted manuscript online: 2 JUN 2014 06:10AM EST | DOI: 10.1111/tpj.12572

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Conditional Depletion of the Chlamydomonas Chloroplast ClpP1 Protease

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Plastid casein kinase 2 knockout reduces abscisic acid (ABA) sensitivity, thermotolerance, and expression of ABA- and heat-stress-responsive nuclear genes.
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Nature Structural & Molecular Biology Contents: 2014 Volume #21 pp 501-571

Plant ubiquitin ligases as signaling hubs - pp293 - 296

Nitzan Shabek & Ning Zheng
doi:10.1038/nsmb.2804

The past decade has witnessed an explosion in the identification of ubiquitin-ligase complexes as the missing receptors for important small-molecule hormones regulating plant growth and development. These breakthroughs were initiated by genetic approaches, with structural analysis providing mechanistic insights into how hormone perception and signaling are coupled to protein ubiquitination. Although there are still many unknowns, plants have imparted valuable lessons about the pharmacology of ubiquitin modification.

Nature 510,172–175(05 June 2014) doi:10.1038/nature13419

Membrane proteins bind lipids selectively to modulate their structure and function

Arthur Laganowsky, Eamonn Reading, Timothy M. Allison, Martin B. Ulmschneider, Matteo T. egiacomi, Andrew J. Baldwin & Carol V. Robinson

Previous studies have established that the folding, structure and function of membrane proteins are influenced by their lipid environments[1, 2, 3, 4, 5, 6, 7] and that lipids can bind to specific sites, for example, in potassium channels[8]. Fundamental questions remain however regarding the extent of membrane protein selectivity towards lipids. Here we report a mass spectrometry approach designed to determine the selectivity of lipid binding to membrane protein complexes. We investigate the mechanosensitive channel of large conductance (MscL) from *Mycobacterium tuberculosis* and aquaporin Z (AqpZ) and the ammonia channel (AmtB) from *Escherichia coli*, using ion mobility mass spectrometry (IM-MS), which reports gas-phase collision cross-sections. We demonstrate that folded conformations of membrane protein complexes can exist in the gas phase. By resolving lipid-bound states, we then rank bound lipids on the basis of their ability to resist gas phase unfolding and thereby stabilize membrane protein structure. Lipids bind non-selectively and with high avidity to MscL, all imparting comparable stability; however, the highest-ranking lipid is phosphatidylinositol phosphate, in line with its proposed functional role in mechanosensation[9].

AqpZ is also stabilized by many lipids, with cardiolipin imparting the most significant resistance to unfolding. Subsequently, through functional assays we show that cardiolipin modulates AqpZ function. Similar experiments identify AmtB as being highly selective for phosphatidylglycerol, prompting us to obtain an X-ray structure in this lipid membrane-like environment. The 2.3 Å resolution structure, when compared with others obtained without lipid bound, reveals distinct conformational changes that re-position AmtB residues to interact with the lipid bilayer. Our results demonstrate that resistance to unfolding correlates with specific lipid-binding events, enabling a distinction to be made between lipids that merely bind from those that modulate membrane protein structure and/or function. We anticipate that these findings will be important not only for defining the selectivity of membrane proteins towards lipids, but also for understanding the role of lipids in modulating protein function or drug binding.

Chalova AS, Sudnitsyna MV, Semenyuk PI, Orlov VN, Gusev NB.
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The Plant Journal Content Alert: 78, 6 (June 2014)

The Arabidopsis mitochondrial membrane-bound ubiquitin protease UBP27 contributes to mitochondrial morphogenesis (pages 1047–1059)
Ronghui Pan, Navneet Kaur and Jianping Hu
Article first published online: 23 MAY 2014 | DOI: 10.1111/tpj.12532

Plett, J. M. *et al*. Effector MiSSP7 of the mutualistic fungus *Laccaria bicolor* stabilizes the *Populus* JAZ6 proteins and represses jasmonic acid (JA) responsive genes. Proc. Natl Acad. Sci. USA http://dx.doi.org/10.1073/pnas.1322671111 (2014)

Structural basis of the non-coding RNA RsmZ acting as a protein sponge

Olivier Duss, Erich Michel, Maxim Yulikov, Mario Schubert, Gunnar Jeschke & Frédéric H.-T. Allain
Nature 509, 588–592 (29 May 2014) doi:10.1038/nature13271

MicroRNA and protein sequestration by non-coding RNAs (ncRNAs) has recently generated much interest. In the bacterial Csr/Rsm system, which is considered to be the most general global post-transcriptional regulatory system responsible for bacterial virulence, ncRNAs such as CsrB or RsmZ activate translation initiation by sequestering homodimeric CsrA-type proteins from the ribosome-binding site of a subset of messenger RNAs. However, the mechanism of ncRNA-mediated protein sequestration is not understood at the molecular level. Here we show for *Pseudomonas fluorescens* that RsmE protein dimers assemble sequentially, specifically and cooperatively onto the ncRNA RsmZ within a narrow affinity range. This assembly yields two different native ribonucleoprotein structures. Using a powerful combination of nuclear magnetic resonance and electron paramagnetic resonance spectroscopy we elucidate these 70-kilodalton solution structures, thereby revealing the molecular mechanism of the sequestration process and how RsmE binding protects the ncRNA from RNase E degradation. Overall, our findings suggest that RsmZ is well-tuned to sequester, store and release RsmE and therefore can be viewed as an ideal protein ‘sponge’.

de la Fuente-Núñez, C. *et al*. Broad-spectrum anti-biofilm peptide that targets a cellular stress response. PLoS Pathog. 10, e1004152 (2014)

Biofilms are a major health concern worldwide, and no drugs are licensed to target them. Now, de la Fuente-Núñez *et al*. describe the identification of a new peptide that prevents the formation, and promotes the disruption, of biofilms that are formed by several pathogens, including *Pseudomonas aeruginosa*, methicillin-resistant *Staphylococcus aureus* and multiple Enterobacteriaceae. Peptide 1018 functions by directly interacting with guanosine tetra- or pentaphosphate, (p)ppGpp — a second messenger that is known to regulate the stringent response — and marking it for degradation. These data establish (p)ppGpp as a new drug target in the fight against biofilms.

Analytical Biochemistry: Alert 10 June-16 June

Simplified 2,4-dinitrophenylhydrazine spectrophotometric assay for quantification of carbonyls in oxidized proteins

Pages 69-71

Cristina S. Mesquita, Raquel Oliveira, Fátima Bento, Dulce Geraldo, João V. Rodrigues, João C. Marcos

Zhang Z, Shrestha J, Tateda C, Greenberg JT.
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Science 13 June 2014: Vol. 344 no. 6189 pp. 1211-1212 DOI: 10.1126/science.344.6189.1211

Carbon-mapping satellite will monitor plants' faint glow

With the launch of NASA's Orbiting Carbon Observatory-2 on 1 July, scientists are not just going to get their best tool for mapping carbon sources and sinks. They are also going to get the most precise maps yet of chlorophyll fluorescence—a faint glow of light re-emitted by the plant during photosynthesis. The fluorescence—a much more direct measure for carbon uptake than proxies such as greenness or leaf area—promises to transform scientists' understanding of how ecosystems will behave under the stresses of climate change.

Nature Volume 510 Number 7504 pp187-306

A growing problem

Without careful stewardship, genetically engineered crops will do little to stop the spread of herbicide-resistant weeds.

Intake and transformation to a glycoside of (*Z*)-3-hexenol from infested neighbors reveals a mode of plant odor reception and defense *PNAS 2014 111 (19) 7144-7149; published ahead of print April 28, 2014,*
Plants receive volatile compounds emitted by neighboring plants that are infested by herbivores, and consequently the receiver plants begin to defend against forthcoming herbivory. To date, how plants receive volatiles and, consequently, how they fortify their defenses, is largely unknown. We found that tomato plants absorbed the airborne green leaf alcohol (*Z*)-3-hexenol emitted by neighboring conspecific plants under attack by herbivores and subsequently converted the alcohol to a glycoside. The glycoside suppressed growth and survival rates of cutworms. The accumulation of glycoside in the receiver plants explained the defense acquired via “smelling” their neighbors. This study showed that the processing of a volatile compound is a mechanism of volatile reception in tomato plants.

Nature 510,298–302(12 June 2014)doi:10.1038/nature13236

Quantitative flux analysis reveals folate-dependent NADPH production

A metabolomics quantification of NADPH production and consumption fluxes in proliferating mammalian cells reveals that, in addition to canonical pathways such as the oxidative pentose phosphate pathway, NADPH can also be produced by a folate metabolism pathway, a discovery providing new insights into the metabolism of cell growth.

Plant, Cell & Environment Content Alert (New Articles)

Heme-heme oxygenase1 system is involved in ammonium tolerance by regulating antioxidant defence in *Oryza sativa*

YANJIE XIE, YU MAO, SHENG XU, HENG ZHOU, XINGLIANG DUAN, WEITI CUI, JING ZHANG and GUOHUA XU

Accepted manuscript online: 6 JUN 2014 06:35AM EST | DOI: 10.1111/pce.12380

Nature Chemical Biology10,477–482(2014)doi:10.1038/nchembio.1524

The plant stress hormone abscisic acid (ABA) is critical for several abiotic stress responses. ABA signaling is normally repressed by group-A protein phosphatases 2C (PP2Cs), but stress-induced ABA binds *Arabidopsis* PYR/PYL/RCAR (PYL) receptors, which then bind and inhibit PP2Cs. X-ray structures of several receptor–ABA complexes revealed a tunnel above ABA's 3′ ring CH that opens at the PP2C binding interface. Here, ABA analogs with sufficiently long 3′ alkyl chains were predicted to traverse this tunnel and block PYL-PP2C interactions. To test this, a series of 3′-alkylsulfanyl ABAs were synthesized with different alkyl chain lengths. Physiological, biochemical and structural analyses revealed that a six-carbon alkyl substitution produced a potent ABA antagonist that was sufficiently active to block multiple stress-induced ABA responses *in vivo*. This study provides a new approach for the design of ABA analogs, and the results validated structure-based design for this target class.

Gut microbiota-generated metabolites in animal health and disease pp416 - 424

Won-Jae Lee and Koji Hase

doi:10.1038/nchembio.1535

Understanding the mechanisms by which gut metabolites impact host physiology should help understand a variety of disease associated with gut-microbiota dysbiosis. A review of this microbial impact in both invertebrate and vertebrate highlights roles in energy harvest, pathogen resistance and the development of allergic and neurological disorders.

eIF5B employs a novel domain release mechanism to catalyze ribosomal subunit joining

Bernhard Kuhle and Ralf Ficner

Published online 31.03.2014
http://EMBOJ.embopress.org/content/33/10/1177?etoc

A panel of crystal structures allows the first visualization of the entire GTP hydrolysis cycle on translation initiation factor eIF5B and reveals a novel release mechanism for eIF5B/IF2 activation on the ribosome.

The Plant Journal Content Alert (New Articles)

ABA Signaling is Necessary but not Sufficient for *RD29B* Transcriptional Memory during Successive Dehydration Stresses in *Arabidopsis thaliana*

Laetitia Virlouvet, Yong Ding, Hiroaki Fujii, Zoya Avramova and Michael Fromm

Accepted manuscript online: 7 MAY 2014 01:07PM EST | DOI: 10.1111/tpj.12548

A universal protocol for the combined isolation of metabolites, DNA, long RNAs, small RNAs, and proteins from plants and microorganisms

Luis Valledor, Mónica Escandón, Mónica Meijón, Ella Nukarinen, María Jesús Cañal and Wolfram Weckwerth

Accepted manuscript online: 7 MAY 2014 01:07PM EST | DOI: 10.1111/tpj.12546

Physiologia Plantarum Content Alert (New Articles)

Leaf architectural, vascular, and photosynthetic acclimation to temperature in two biennials

Onno Muller, Jared J. Stewart, Christopher M. Cohu, Stephanie K. Polutchko, Barbara Demmig-Adams and William W. Adams III

Accepted manuscript online: 12 MAY 2014 06:51AM EST | DOI: 10.1111/ppl.12226

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Regulation of G6PD acetylation by SIRT2 and KAT9 modulates NADPH
  homeostasis and cell survival during oxidative stress
  Yi-Ping Wang, Li-Sha Zhou, Yu-Zheng Zhao, Shi-Wen Wang, Lei-Lei Chen,
  Li-Xia Liu, Zhi-Qiang Ling, Fu-Jun Hu, Yi-Ping Sun, Jing-Ye Zhang, Chen
  Yang, Yi Yang, Yue Xiong, Kun-Liang Guan, and Dan Ye
   Published online 25.04.2014
  http://EMBOJ.embopress.org/content/33/12/1304?etoc
Following oxidative stress, production of the reductant NADPH via the
pntose phosphate pathway is stimulated by SIRT2-mediated deacetylatio
and
activation of G6PD.
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Journal of Agronomy and Crop Sci... Content Alert (New Articles)
Reviews

An Overview of Cold Resistance in Plants
L.-J. Chen, H.-Z. Xiang, Y. Miao, L. Zhang, Z.-F. Guo, X.-H. Zhao, J.-W. Lin and T.-L. Li
Article first published online: 10 JUN 2014 | DOI: 10.1111/jac.12082

Nathen:

1) **The predictability of molecular evolution during functional innovation**
Diana Blanka,1, Luise Wolfa,1, Martin Ackermannb,c, and Olin K. Silandera,2
PNAS

2) **Proteomics to study adaptations in marine organisms to environmental stress**

- Lars Tomanek
-
  - Journal of Proteomics

3) **Coffee and chocolate in danger**
Michael Gross
Current Biology

Umaru:

Sci Transl Med. 2014 Jun 11;6(240):240ra73. doi: 10.1126/scitranslmed.3008659.

Macrophage models of Gaucher disease for evaluating disease pathogenesis and candidate drugs.

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Abstract

Gaucher disease is caused by an inherited deficiency of glucocerebrosidase that manifests with storage of glycolipids in lysosomes, particularly in macrophages. Available cell lines modeling Gaucher disease do not demonstrate lysosomal storage of glycolipids; therefore, we set out to develop two macrophage models of Gaucher disease that exhibit appropriate substrate accumulation. We used these cellular models both to investigate altered macrophage biology in Gaucher disease and to evaluate candidate drugs for its treatment. We generated and characterized monocyte-derived macrophages from 20 patients carrying different Gaucher disease mutations. In addition, we created induced pluripotent stem cell (iPSC)-derived macrophages from five fibroblast lines taken from patients with type 1 or type 2 Gaucher disease. Macrophages derived from patient monocytes or iPSCs showed reduced glucocerebrosidase activity and increased storage of glucocerebroside and glucosylsphingosine in lysosomes. These macrophages showed efficient phagocytosis of bacteria but reduced production of intracellular reactive oxygen species and impaired chemotaxis. The disease phenotype was reversed with a noninhibitory small-molecule chaperone drug that enhanced glucocerebrosidase activity in the macrophages, reduced glycolipid storage, and normalized chemotaxis and production of reactive oxygen species. Macrophages differentiated from patient monocytes or patient-derived iPSCs provide cellular models that can be used to investigate disease pathogenesis and facilitate drug development.

Indu:

1. Science. 2014 Apr 25;344(6182):427-30. doi: 10.1126/science.1250322. Epub 2014 Apr 10.

   A chloroplast retrograde signal regulates nuclear alternative splicing.

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Light is a source of energy and also a regulator of plant physiological adaptations. We show here that light/dark conditions affect alternative splicing of a subset of Arabidopsis genes preferentially encoding proteins involved in RNA processing. The effect requires functional chloroplasts and is also observed in roots when the communication with the photosynthetic tissues is not interrupted, suggesting that a signaling molecule travels through the plant. Using photosynthetic electron transfer inhibitors with different mechanisms of action, we deduce that the reduced pool of plastoquinones initiates a chloroplast retrograde signaling that regulates nuclear alternative splicing and is necessary for proper plant responses to varying light conditions.

PMID: 24763593 [PubMed - indexed for MEDLINE]

2. Science. 2014 May 23;344(6186):909-13. doi: 10.1126/science.1250691.

Stop codon reassignments in the wild.

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The canonical genetic code is assumed to be deeply conserved across all domains of life with very few exceptions. By scanning 5.6 trillion base pairs of metagenomic data for stop codon reassignment events, we detected recoding in a substantial fraction of the >1700 environmental samples examined. We observed extensive opal and amber stop codon reassignments in bacteriophages and of opal in bacteria. Our data indicate that bacteriophages can infect hosts with a different genetic code and demonstrate phage-host antagonism based on code differences. The abundance and diversity of genetic codes present in environmental organisms should be considered in the design of engineered organisms with altered genetic codes in order to preclude the exchange of genetic information with naturally occurring species.

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3. Plant Cell Environ. 2014 May 8. doi: 10.1111/pce.12366. [Epub ahead of print]

Potato plants ectopically expressing Arabidopsis thaliana?CBF3 exhibit enhanced tolerance to high-temperature stress.

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CBF3, a known cold-inducible gene that encodes a transcription factor, was isolated from Arabidopsis thaliana and introduced into the potato (Solanum tuberosum cv. 'luyin NO.1') under the control of the CaMV35S promoter or the rd29A promoter. Our results revealed that temperature of 40?°C or higher can significantly induce AtCBF3 expression. After heat stress, the net photosynthetic rate (Pn), the maximal photochemical efficiency of photosystem II (PSII) (Fv /Fm) and the accumulation of the D1 protein were higher in the transgenic lines than in the wild-type (WT) line. Moreover, compared with the WT line, O2 (?-) and H2 O2 accumulation in the transgenic lines were reduced. A Q-PCR assay of a subset of the genes involved in photosynthesis and antioxidant defence further verified the above results. Interestingly, under heat stress conditions, the accumulation of heat-shock protein 70 (HSP70) increased in the WT line but decreased in the transgenic lines. These results suggest that potato plants ectopically expressing AtCBF3 exhibited enhanced tolerance to high temperature, which is associated with improved photosynthesis and antioxidant defence via induction of the expression of many stress-inducible genes. However, this mechanism may not depend upon the regulatory pathways in which HSP70 is involved.

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