Lit Lunch 3/7/14

ELIZABETH:

Molecular Cell: Alert 17 February-23 February
Polyphosphate Is a Primordial Chaperone Original Research Article
Michael J. Gray, Wei-Yun Wholey, Nico O. Wagner, Claudia M. Cremers, Antje Mueller-Schickert, Nathaniel T. Hock, Adam G. Krieger, Erica M. Smith, Robert A. Bender, James C.A. Bardwell, Ursula Jakob
Ozgur R, Turkan I, Uzilday B, Sekmen AH.
Endoplasmic reticulum stress triggers ROS signalling, changes the redox state, and regulates the antioxidant defence of Arabidopsis thaliana.
J Exp Bot. 2014 Feb 20;. [Epub ahead of print]
PMID: 24558072 [PubMed - as supplied by publisher]

Lin W, Yang Z, Lu Y, Zhao X.
Refined Purification of Large Amounts of Rat cvHsp/HspB7 and Partial Biological Characterization In Vitro.
Protein Pept Lett. 2014 May;21(5):503-10.
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Singleton RS, Liu-Yi P, Formenti F, Ge W, Sekirnik R, Fischer R, Adam J, Pollard PJ, Wolf A, Thalhammer A, Loenarz C, Flashman E, Yamamoto A, Coleman ML, Kessler BM, Wappner P, Schofield CJ, Ratcliffe PJ, Cockman ME.
OGFOD1 catalyzes prolyl hydroxylation of RPS23 and is involved in translation control and stress granule formation.
Proc Natl Acad Sci U S A. 2014 Feb 18;. [Epub ahead of print]
PMID: 24550447 [PubMed - as supplied by publisher]

Noguchi A, Ikeda A, Mezaki M, Fukumori Y, Kanemori M.
DnaJ-promoted binding of DnaK to multiple sites on Ïƒ32 in the presence of ATP.
J Bacteriol. 2014 Feb 14;. [Epub ahead of print]
PMID: 24532774 [PubMed - as supplied by publisher]

Zeymer C, Barends TR, Werbeck ND, Schlichting I, Reinstein J.
Elements in nucleotide sensing and hydrolysis of the AAA+ disaggregation machine ClpB: a structure-based mechanistic dissection of a molecular motor.
Acta Crystallogr D Biol Crystallogr. 2014 Feb;70(Pt 2):582-95.
PMID: 24531492 [PubMed - in process]

Ding Y, Tang Y, Kwok CK, Zhang Y, Bevilacqua PC, Assmann SM.
In vivo genome-wide profiling of RNA secondary structure reveals novel regulatory features.
Nature. 2014 Jan 30;505(7485):696-700.
PMID: 24270811 [PubMed - indexed for MEDLINE]

Chemistry & Biology: Alert 15 February-21 February
Distinct Prion Strains Are Defined by Amyloid Core Structure and Chaperone Binding Site Dynamics Original Research Article
Kendra K. Frederick, Galia T. Debelouchina, Can Kayatekin, Tea Dorminy, Angela C. Jacavone, Robert G. Griffin, Susan Lindquist

The Plant Journal Content Alert (New Articles)

Correlation of mRNA and protein abundance in the developing maize leaf
Lalit Ponnala, Yupeng Wang, Qi Sun and Klaas J. van Wijk
Accepted manuscript online: 19 FEB 2014 03:58AM EST | DOI: 10.1111/tpj.12482

Plant, Cell & Environment Content Alert (New Articles)

Histone chaperone ASF1 is involved in gene transcription activation in response to heat stress in Arabidopsis thaliana
MINJIE WENG, YUE YANG, HAIYANG FENG, ZONGDE PAN, WEN-HUI SHEN, YAN ZHU and AIWU DONG
Accepted manuscript online: 18 FEB 2014 08:12AM EST | DOI: 10.1111/pce.12299

Boelens WC.
Cell Biological roles of Î±B-crystallin.
Prog Biophys Mol Biol. 2014 Feb 24;. [Epub ahead of print]
PMID: 24576798 [PubMed - as supplied by publisher]

Kumar R, Tamuli R.
Calcium/calmodulin-dependent kinases are involved in growth, thermotolerance, oxidative stress survival, and fertility in Neurospora crassa.
Arch Microbiol. 2014 Feb 26;. [Epub ahead of print]
PMID: 24570326 [PubMed - as supplied by publisher]

Chen X, Lin S, Zhang B, Huang J, Zhang W, Lin J, Wang Y, Ke Y, He H.
Expression and interaction of small heat shock proteins (sHsps) in rice in response to heat stress.
Biochim Biophys Acta. 2014 Feb 22;. [Epub ahead of print]
PMID: 24566471 [PubMed - as supplied by publisher]

Veyel D, Sommer F, Muranaka LS, RÃ¼tgers M, Lemaire SD, Schroda M.
In vitro characterization of bacterial and chloroplast HSP70 systems reveals an evolutionary optimization of the co-chaperones for their HSP70 partner.
Biochem J. 2014 Feb 25;. [Epub ahead of print]
PMID: 24564700 [PubMed - as supplied by publisher]

Niforou K, Cheimonidou C, Trougakos IP.
Molecular chaperones and proteostasis regulation during redox imbalance.
Redox Biol. 2014;2:323-332. Review.
PMID: 24563850 [PubMed - as supplied by publisher]

Zhu Y, Dong A, Shen WH.
Histone variants and chromatin assembly in plant abiotic stress responses.
Biochim Biophys Acta. 2013 Mar-Apr;1819(3-4):343-8.
PMID: 24459736 [PubMed - indexed for MEDLINE]

Igamberdiev AU, George Ratcliffe R, Gupta KJ.
Plant mitochondria: Source and target for nitric oxide.
Mitochondrion. 2014 Feb 19;. [Epub ahead of print]
PMID: 24561220 [PubMed - as supplied by publisher]

Atkinson GC, Kuzmenko A, Chicherin I, Soosaar A, Tenson T, Carr M, Kamenski P, Hauryliuk V.
An evolutionary ratchet leading to loss of elongation factors in eukaryotes.
BMC Evol Biol. 2014 Feb 24;14(1):35. [Epub ahead of print]
PMID: 24564225 [PubMed - as supplied by publisher]

Cell: Alert 22 February-28 February

Hsp90-Tau Complex Reveals Molecular Basis for Specificity in Chaperone Action Original Research Article

Pages 963-974

G. Elif Karagöz, Afonso M.S. Duarte, Elias Akoury, Hans Ippel, Jacek Biernat, Tania Morán Luengo, Martina Radli, Tatiana Didenko, Bryce A. Nordhues, Dmitry B. Veprintsev, Chad A. Dickey, Eckhard Mandelkow, Markus Zweckstetter, Rolf Boelens, Tobias Madl, Stefan G.D. Rüdiger

Plant, Cell & Environment Content Alert: 37, 4 (April 2014)

Ammonium tolerance in the cyanobacterium *Synechocystis* sp. strain PCC 6803 and the role of the *psbA* multigene family (pages 840–851)

Ammonium at higher concentrations can be toxic to many plants and oxygenic photosynthetic microorganisms. This study clarifies that in the model cyanobacterium Synechocystis PCC 6803, the toxic effect of ammonium is due to light-dependent photodamage of PSII as shown in vivo and in isolated thylakoid membranes. Whereas ammonium does not affect the repair of PSII photodamage, all three psbA genes contribute to ammonium tolerance in Synechocystis PCC 6803 and thus to the repair of ammonium-photodamaged PSII.

The Plant Journal Content Alert (New Articles)

Thiol-based Redox Proteins in *Brassica napus* Guard Cell Abscisic Acid and Methyl Jasmonate Signaling

Mengmeng Zhu, Ning Zhu, Wen-yuan Song, Alice C. Harmon, Sarah M. Assmann and Sixue Chen

Accepted manuscript online: 1 MAR 2014 11:46PM EST | DOI: 10.1111/tpj.12490

DAMIAN:

1) iroshi Nishimasu, F. Ann Ran, Patrick D. Hsu, Silvana Konermann, Soraya I. Shehata, Naoshi Dohmae, Ryuichiro Ishitani, Feng Zhang, Osamu Nureki

Crystal Structure of Cas9 in Complex with Guide RNA and Target DNA

Cell - 27 February 2014 (Vol. 156, Issue 5, pp. 935-949)

2) G. Elif Karagöz, Afonso M.S. Duarte, Elias Akoury, Hans Ippel, Jacek Biernat, Tania Morán Luengo, Martina Radli, Tatiana Didenko, Bryce A. Nordhues, Dmitry B. Veprintsev, Chad A. Dickey, Eckhard Mandelkow, Markus Zweckstetter, Rolf Boelens, Tobias Madl, Stefan G.D. Rüdiger,

Hsp90-Tau Complex Reveals Molecular Basis for Specificity in Chaperone Action, Cell, Volume 156, Issue 5, 27 February 2014, Pages 963-974

3) Vanesa Eleonora Tossi, Lorenzo Lamattina, Gareth Jenkins, and Raul Cassia

UV-B-Induced Stomatal Closure in Arabidopsis is Regulated by the UVR8 Photoreceptor in an NO-Dependent Mechanism

Plant Physiol. pp.113.231753; First Published on February 28, 2014; doi:10.1104/pp.113.231753

David Roy Smith and Robert W Lee

4) A plastid without a genome: evidence from the nonphotosynthetic green alga Polytomella

Plant Physiol. pp.113.233718; First Published on February 21, 2014;
doi:10.1104/pp.113.233718

KEITH:

1) Expression and interaction of small heat shock proteins (sHsps) in rice in response to heat stress

Biochimica et Biophysica Acta (BBA) – Proteins and ProteomicsAvailable online 22 February 2014

Xinhai Chen[a, b, c, 1], Shoukai Lin[a, d, 1], Baoqian Zhang[b], Jian Huang[a, b], Wenfeng Zhang[a, b], Jun Lin[a, b], Yongfei Wang[a, b], Yuqin Ke[a, b], Huaqin He[a, b]

[a] Key Laboratory of Ministry of Education for Genetic, Breeding and Multiple Utilization of Crops, Fuzhou 350002, PR China
[b] College of Life Science, Fujian Agriculture and Forestry University, Fuzhou 350002, PR China
[c] Center for Proteomics, State Key Laboratory of Biocontrol, College of Life Sciences, Sun Yat-sen University, Guangzhou 510275, PR China
[d] Putian College, Fujian 351100, PR China

The inherent immobility of rice (Oryza sativa L.) limited their abilities to avoid heat stress and required them to contend with heat stress through innate defense abilities in which heat shock proteins played important roles. In this study, Hsp26.7, Hsp23.2, Hsp17.9A, Hsp17.4 and Hsp16.9A were up-regulated in Nipponbare during seedling and anthesis stages in response to heat stress. Subsequently, the expressing levels of five sHsps in the heat-tolerant rice cultivar, Co39, were all significantly higher than that in the heat-susceptible rice cultivar, Azucena. This indicated that the expressive level of these five sHsps was positively related to the ability of rice plants to avoid heat stress. Thus, the expression level of these five sHsps can be regarded as bio-markers for screening rice cultivars with different abilities to avoid heat stress. Hsp18.1, Hsp17.9A, Hsp17.7 and Hsp16.9A, in the three rice cultivars under heat stress were found to be involved in one protein complex by Native-PAGE, and the interactions of Hsp18.1 and Hsp 17.7, Hsp18.1 and Hsp 17.9A, and Hsp17.7 and Hsp16.9A were further validated by yeast 2-hybridization. Pull down assay also confirmed the interaction between Hsp17.7 and Hsp16.9A in rice under heat stress. In conclusion, the up-regulation of the 5 sHsps is a key step for rice to tolerate heat stress, after that some sHsps assembled into a large hetero-oligomeric complex. In addition, through protein–protein interaction, Hsp101 regulated thiamine biosynthesis, and Hsp82 homology affected nitrogen metabolism, while Hsp81-1 were involved in the maintenance of sugar or starch synthesis in rice plants under heat stress. These results provide new insight into the regulatory mechanism of sHsps in rice.

2) *In vitro* characterization of bacterial and chloroplast HSP70 systems reveals an evolutionary optimization of the co-chaperones for their HSP70 partner

Published on 25 Feb 2014

Daniel Veyel, Frederik Sommer, Ligia Segatto Muranaka, Mark Rütgers, Stéphane D. Lemaire and Michael Schroda

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[†]Max-Planck-Institut für Molekulare Pflanzenphysiologie, Am Mühlenberg 1, D-14476 Potsdam-Golm, Germany

[‡]Laboratoire de Biologie Moléculaire et Cellulaire des Eucaryotes, FRE3354, Centre National de la Recherche Scientifique, Université Pierre et Marie Curie, Institut de Biologie Physico-Chimique, 75005 Paris, France

The chloroplast Hsp70 system involved in protein folding in *Chlamydomonas reinhardtii* consists of HSP70B, the DnaJ homolog CDJ1, and the GrpE-type nucleotide exchange factor CGE1. The finding that HSP70B needs to be co-expressed with the escort protein HEP2 to become functional allowed reconstituting the chloroplast Hsp70 system *in vitro* and comparing it with the homologous *E. coli* system. Both systems support luciferase refolding and display ATPase and holdase activities. Steady-state activities are low and strongly stimulated by the co-chaperones, whose concentrations need to be balanced to optimally support luciferase refolding. Although the co-chaperones of either system generally stimulate ATPase and folding assistance activities of the other, luciferase refolding is reduced ~10-fold and <2-fold if either Hsp70 is supplemented with the foreign DnaJ and GrpE protein, respectively, suggesting an evolutionary specialization of the co-chaperones for their Hsp70 partner. Distinct features are that HSP70B's steady-state ATPase exhibits ~20-fold higher values for Vmax and Km, and that the HSP70B system displays a ~6-fold higher folding assistance on denatured luciferase. While truncating up to 16 N-terminal amino acids of CGE1 does not affect HSP70B's general ATPase and folding assistance activities in the physiological temperature range, further deletions hampering dimerization of CGE1 via its N-terminal coiled-coil do.

INDU:

`1. Science. 2014 Jan 24;343(6169):419-22. doi: 10.1126/science.1242939.`

Single β-actin mRNA detection in neurons reveals a mechanism for regulating its translatability.
Buxbaum AR(1), Wu B, Singer RH.

Author information:
(1)Department of Anatomy and Structural Biology, Albert Einstein College of
Medicine, 1300 Morris Park Avenue, Bronx, NY 10461, USA.
Comment in
    Science. 2014 Jan 24;343(6169):375-6.

The physical manifestation of learning and memory formation in the brain can be expressed by strengthening or weakening of synaptic connections through morphological changes. Local actin remodeling underlies some forms of plasticity and may be facilitated by local β-actin synthesis, but dynamic information is lacking. In this work, we use single-molecule in situ hybridization to demonstrate that dendritic β-actin messenger RNA (mRNA) and ribosomes are in a masked, neuron-specific form. Chemically induced long-term potentiation prompts transient mRNA unmasking, which depends on factors active during synaptic activity. Ribosomes and single β-actin mRNA motility increase after stimulation,indicative of release from complexes. Hence, the single-molecule assays we developed allow for the quantification of activity-induced unmasking and availability for active translation. Further, our work demonstrates that β-actin mRNA and ribosomes are in a masked state that is alleviated by stimulation.

2. Science. 2014 Jan 24;343(6169):422-4. doi: 10.1126/science.1239200.

Visualization of dynamics of single endogenous mRNA labeled in live mouse.
Park HY(1), Lim H, Yoon YJ, Follenzi A, Nwokafor C, Lopez-Jones M, Meng X, Singer RH.
Author information:
(1)Department of Anatomy and Structural Biology, Albert Einstein College of
Medicine, Bronx, NY 10461, USA.
Comment in
    Science. 2014 Jan 24;343(6169):375-6.

The transcription and transport of messenger RNA (mRNA) are critical steps in regulating the spatial and temporal components of gene expression, but it has not been possible to observe the dynamics of endogenous mRNA in primary mammalian tissues. We have developed a transgenic mouse in which all β-actin mRNA is fluorescently labeled. We found that β-actin mRNA in primary fibroblasts localizes predominantly by diffusion and trapping as single mRNAs. In cultured neurons and acute brain slices, we found that multiple β-actin mRNAs can assemble together, travel by active transport, and disassemble upon depolarization by potassium chloride. Imaging of brain slices revealed immediate early induction of β-actin transcription after depolarization. Studying endogenous mRNA in live mouse tissues provides insight into its dynamic regulation within the context of the cellular and tissue microenvironment.

3. Science. 2014 Jan 24;343(6169):375-6. doi: 10.1126/science.1249623.
Molecular biology. mRNA, live and unmasked. Akbalik G(1), Schuman EM.
Author information:
(1)Max Planck Institute for Brain Research, 60438 Frankfurt, Germany.

Comment on
    Science. 2014 Jan 24;343(6169):422-4.
    Science. 2014 Jan 24;343(6169):419-22.
PMID: 24458628 [PubMed - indexed for MEDLINE]

4. Science. 2014 Feb 7;343(6171):656-61. doi: 10.1126/science.1246135.

A structurally distinct human mycoplasma protein that generically blocks antigen-antibody union.

Grover RK(1), Zhu X, Nieusma T, Jones T, Boero I, MacLeod AS, Mark A,
Niessen S, Kim HJ, Kong L, Assad-Garcia N, Kwon K, Chesi M, Smider VV,
Salomon DR, Jelinek DF, Kyle RA, Pyles RB, Glass JI, Ward AB, Wilson IA,
Lerner RA.

Author information:
(1)Department of Cell and Molecular Biology, The Scripps Research Institute, La Jolla, CA 92037, USA.

We report the discovery of a broadly reactive antibody-binding protein (ProteinM) from human mycoplasma. The crystal structure of the ectodomain of transmembrane Protein M differs from other known protein structures, as does its mechanism of antibody binding. Protein M binds with high affinity to all types of human and nonhuman immunoglobulin G, predominantly through attachment to the conserved portions of the variable region of the κ and λ light chains. Protein M blocks antibody-antigen union, likely because of its large C-terminal domain extending over the antibody-combining site, blocking entry to large antigens. Similar to the other immunoglobulin-binding proteins such as Protein A, Protein M as well as its orthologs in other Mycoplasma species could become invaluable reagents in the antibody field.

PMID: 24503852 [PubMed - indexed for MEDLINE]

5.Boycotting All-Boy Conferences

http://sciencecareers.sciencemag.org/career_magazine/previous_issues/articles/2014_03_04/caredit.a1400057

STEPHANIE:

1) NATURAL VARIATION IN EPIGENETIC GENE REGULATION AND ITS EFFECTS ON PLANT DEVELOPMENTAL TRAITS

Franziska Turck, George Coupland Article first published online: 31 OCT 2013 DOI: 10.1111/evo.12286

Summary: In plants, epigenetic variation contributes to phenotypic differences in developmental traits. At the mechanistic level, this variation is conferred by DNA methylation and histone modifications. We describe several examples in which changes in gene expression caused by variation in DNA methylation lead to alterations in plant development. In these examples, the presence of repeated sequences or transposons within the promoters of the affected genes are associated with DNA methylation and gene inactivation. Small interfering RNAs expressed from these sequences recruit DNA methylation to the gene. Some of these methylated alleles are unstable giving rise to revertant sectors during mitosis and to progeny in which the methylated state is lost. However, others are stable for many generations and persist through speciation. These examples indicate that although DNA methylation influences gene expression, this is frequently dependent on classical changes to DNA sequence such as transposon insertions. By contrast, forms of histone methylation cause repression of gene expression that is stably inherited through mitosis but that can also be erased over time or during meiosis. A striking example involves the induction of flowering by exposure to low winter temperatures in *Arabidopsis thaliana* and its relatives. Histone methylation participates in repression of expression of an inhibitor of flowering during cold. In annual, semelparous species such as *A. thaliana*, this histone methylation is stably inherited through mitosis after return from cold to warm temperatures allowing the plant to flower continuously during spring and summer until it senesces. However, in perennial, iteroparous relatives the histone modification rapidly disappears when temperatures rise, allowing expression of the floral inhibitor to increase and limiting flowering to a short interval. In this case, epigenetic histone modifications control a key adaptive trait, and their pattern changes rapidly during evolution associated with life-history strategy. We discuss these examples of epigenetic developmental traits with emphasis on the underlying mechanisms, their stability, and adaptive value.

2) Deciphering the role of natural variation in age-related protein homeostasis – BMC Biology – commentary

Understanding the genetic basis of age-related diseases is a critical step toward developing therapies that promote healthy aging. Numerous genes have been identified that modulate lifespan, but the influence of natural variation in aging has not been well studied. A new report utilizing a transgenic protein aggregation model in *Caenorhabditis elegans* has provided important tools and insights into the relationship between natural genetic variation, protein aggregation, and age-related pathology.

FIONN:

Plant Cell

Synthetic Lethality in the Tobacco Plastid Ribosome and Its Rescue at Elevated Growth Temperatures.

Ehrnthaler M1, Scharff LB, Fleischmann TT, Hasse C, Ruf S, Bock R.

Abstract
Consistent with their origin from cyanobacteria, plastids (chloroplasts) perform protein biosynthesis on bacterial-type 70S ribosomes. The plastid genomes of seed plants contain a conserved set of ribosomal protein genes. Three of these have proven to be nonessential for translation and, thus, for cellular viability: rps15, rpl33, and rpl36. To help define the minimum ribosome, here, we examined whether more than one of these nonessential plastid ribosomal proteins can be removed from the 70S ribosome. To that end, we constructed all possible double knockouts for the S15, L33, and L36 ribosomal proteins by stable transformation of the tobacco (Nicotiana tabacum) plastid genome. We find that, although S15 and L33 function in different ribosomal particles (30S and 50S, respectively), their combined deletion from the plastid genome results in synthetic lethality under autotrophic conditions. Interestingly, the lethality can be overcome by growth under elevated temperatures due to an improved efficiency of plastid ribosome biogenesis. Our results reveal functional interactions between protein and RNA components of the 70S ribosome and uncover the interdependence of the biogenesis of the two ribosomal subunits. In addition, our findings suggest that defining a minimal set of plastid genes may prove more complex than generally believed.

ATP Requirement for Chloroplast Protein Import Is Set by the Km for ATP Hydrolysis of Stromal Hsp70 in Physcomitrella patens

Li Liu, Robert T. McNeilage, Lan-xin Shi and Steven M. Theg1

Abstract

The 70-kD family of heat shock proteins (Hsp70s) is involved in a number of seemingly disparate cellular functions, including folding of nascent proteins, breakup of misfolded protein aggregates, and translocation of proteins across membranes. They act through the binding and release of substrate proteins, accompanied by hydrolysis of ATP. Chloroplast stromal Hsp70 plays a crucial role in the import of proteins into plastids. Mutations of an ATP binding domain Thr were previously reported to result in an increase in the Km for ATP and a decrease in the enzyme?s kcat. To ask which chloroplast stromal chaperone, Hsp70 or Hsp93, both of which are ATPases, dominates the energetics of the motor responsible for protein import, we made transgenic moss (Physcomitrella patens) harboring the Km-altering mutation in the essential stromal Hsp70-2 and measured the effect on the amount of ATP required for protein import into chloroplasts. Here, we report that increasing the Km for ATP hydrolysis of Hsp70 translated into an increased Km for ATP usage by chloroplasts for protein import. This thus directly demonstrates that the ATP-derived energy long known to be required for chloroplast protein import is delivered via the Hsp70 chaperones and that the chaperone?s ATPase activity dominates the energetics of the reaction.