

Lit Lunch: 2/21/14

KEITH:

Programmed Cell Death Protein 5 Interacts with the Cytosolic Chaperonin Containing Tailless Complex Polypeptide 1 (CCT) to Regulate β -Tubulin Folding

February 14, 2014 The Journal of Biological Chemistry, 289, 4490-4502.

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Programmed cell death protein 5 (PDCD5) has been proposed to act as a pro-apoptotic factor and tumor suppressor. However, the mechanisms underlying its apoptotic function are largely unknown. A proteomics search for binding partners of phospho-tyrosine kinase, a co-chaperone for the cytosolic chaperonin containing tailless complex polypeptide 1 (CCT), revealed a robust interaction between PDCD5 and CCT. PDCD5 formed a complex with CCT and β -tubulin, a key CCT-folding substrate, and specifically inhibited β -tubulin folding. Cryo-electron microscopy studies of the PDCD5·CCT complex suggested a possible mechanism of inhibition of β -tubulin folding. PDCD5 bound the apical domain of the CCT β subunit, projecting above the folding cavity without entering it. Like PDCD5, β -tubulin also interacts with the CCT β apical domain, but a second site is found at the sensor loop deep within the folding cavity. These orientations of PDCD5 and β -tubulin suggest that PDCD5 sterically interferes with β -tubulin binding to the CCT β apical domain and inhibits β -tubulin folding. Given the importance of tubulins in cell division and proliferation, PDCD5 might exert its apoptotic function at least in part through inhibition of β -tubulin folding.

Ribosomal Protein S6, a Target of Rapamycin, Is Involved in the Regulation of rRNA Genes by Possible Epigenetic Changes in *Arabidopsis*

February 14, 2014 The Journal of Biological Chemistry, 289, 3901-3912.

Yun-Kyoung Kim^{‡1}, Sunghan Kim^{§,¶1}, Yun-jeong Shin[‡], Yoon-Sun Hur[‡], Woo-Young Kim^{||}, Myung-Sok Lee[‡], Choong-Ill Cheon^{‡2} and Desh Pal S. Verma^{§3}

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The target of rapamycin (TOR) kinase pathway regulates various biological processes, including translation, synthesis of ribosomal proteins, and transcription of rRNA. The ribosomal protein S6 (RPS6) is one of the well known downstream components of the TOR pathway. Ribosomal proteins have been known to have diverse functions in regulating cellular metabolism as well as protein synthesis. So far, however, little is known about other possible role(s) of RPS6 in plants, besides being a component of the 40 S ribosomal subunit and acting as a target of TOR. Here, we report that RPS6 may have a novel function via interaction with histone deacetylase 2B (AtHD2B) that belongs to the plant-specific histone deacetylase HD2 family. RPS6 and AtHD2B were localized to the nucleolus. Co-expression of RPS6 and AtHD2B caused a change in the location of both RPS6 and AtHD2B to one or several nucleolar spots. ChIP analysis suggests that RPS6 directly interacts with the rRNA gene promoter. Protoplasts overexpressing both AtHD2B and RPS6 exhibited down-regulation of pre-18 S rRNA synthesis with a concomitant decrease in transcription of some of the ribosomal proteins, suggesting their direct role in ribosome biogenesis and plant development. This is consistent with the mutation in *rps6b* that results in reduction in 18 S rRNA transcription and decreased root growth. We propose that the interaction between RPS6 and AtHD2B brings about a change in the chromatin structure of rDNA and thus plays an important role in linking TOR signaling to rDNA transcription and ribosome biogenesis in plants.

Damian:

A Positive Feedback Loop between HSP101 and HSA32 Modulates Long-Term Acquired Thermotolerance Illustrating Diverse Heat Stress Responses in Rice Varieties

Meng-yi Lin^{1,2,#}, Kuo-hsing Chai^{1,3}, Swee-suak Ko⁴, Lin-yun Kuang⁵, Hui-Sheng Lur³, Yee-yung Charng^{1*} Plant Physiology Preview.

Scavenging iron: a novel mechanism of plant immunity activation by 12 microbial siderophores

Aude Aznar^{1, 2}, Nicolas W. G. Chen^{1,§}, Martine Rigault^{1, 2}, Nassima Riache³, Delphine Joseph³, Didier Desmaële⁴, Gregory Mouille², Stéphanie Boutet², Ludivine Soubigou¹⁻⁷, Taconnat⁵, Jean-Pierre Renou⁵, †, Sébastien Thomine⁶, Dominique Expert¹, Alia Dellagi^{1, 2,*} Plant Physiology Preview.

Activity-Driven Local ATP Synthesis Is Required for Synaptic Function

Vidhya Rangaraju^{1,2}, Nathaniel Calloway² and Timothy A. Ryan^{2,*} Cell 156, 825–835, February 13, 2014

Indu:

1. Science. 2014 Jan 3;343(6166):35-6. doi: 10.1126/science.1248110.

Ecology. On tropical forests and their pests.

Coley PD(1), Kursar TA.

Author information:

(1)Department of Biology, University of Utah, Salt Lake City, UT 84112, USA, and Smithsonian Tropical Research Institute, Panama City, Panama.

PMID: 24385624 [PubMed - indexed for MEDLINE]

2. Science. 2014 Jan 17;343(6168):290-4. doi: 10.1126/science.1248110.

Identification of a plant receptor for extracellular ATP.

Choi J(1), Tanaka K, Cao Y, Qi Y, Qiu J, Liang Y, Lee SY, Stacey G.

Author information:

(1)Divisions of Biochemistry and Plant Sciences, Christopher S. Bond Life Sciences Center, University of Missouri, Columbia, MO 65211, USA.

Erratum in

Science. 2014 Feb 14;343(6172):730.

Extracellular adenosine 5'-triphosphate (ATP) is an essential signaling molecule that is perceived in mammals by plasma membrane P2-type purinoceptors. Similar ATP receptors do not exist in plants, although extracellular ATP has been shown to play critical roles in plant growth, development, and stress responses. Here, we identify an ATP-insensitive Arabidopsis mutant, dorn1 (Does not Respond to Nucleotides 1), defective in lectin receptor kinase 1.9 (Arabidopsis Information Resource accession code At5g60300). DORN1 binds ATP with high affinity (dissociation constant of 45.7 ± 3.1 nanomolar) and is required for ATP-induced calcium response, mitogen-activated protein kinase activation, and gene expression. Ectopic expression of DORN1 increased the plant response to physical wounding. We propose that DORN1 is essential for perception of extracellular ATP and likely plays a variety of roles in plant stress resistance.

PMID: 24436418 [PubMed - indexed for MEDLINE]

Fionn:

Plant cell

The Protein Phosphatase RCF2 and Its Interacting Partner NAC019 Are Critical for Heat Stress-Responsive Gene Regulation and Thermotolerance in Arabidopsis[W]

Qingmei Guan, Xiule Yue, Haitao Zeng and Jianhua Zhu¹

Abstract

Heat stress is a major environmental constraint for crop production worldwide. To respond to and cope with heat stress, plants synthesize heat shock proteins (HSPs), which are often molecular chaperones and are under the control of heat stress transcription factors (HSFs). Very little is known about the upstream regulators of HSFs. In a forward genetic screen for regulators of C-REPEAT BINDING

FACTOR (CBF) gene expression (RCFs), we identified RCF2 and found that it is allelic to CPL1/FIERY2, which encodes a homolog of C-terminal domain phosphatase. Our results also showed that, in addition to being critical for cold stress tolerance, RCF2 is required for heat stress-responsive gene regulation and thermotolerance, because, compared with the wild type, the *rcf2-1* mutant is hypersensitive to heat stress and because the reduced thermotolerance is correlated with lower expression of most of the 21 HSFs and some of the HSPs in the mutant plants. We found that RCF2 interacts with the NAC transcription factor NAC019 and that RCF2 dephosphorylates NAC019 in vivo. The *nac019* mutant is more sensitive to heat stress than the wild type, and chromatin immunoprecipitation followed by quantitative PCR analysis revealed that NAC019 binds to the promoters of HSFA1b, HSFA6b, HSFA7a, and HSFC1. Overexpression of RCF2 or NAC019 in *Arabidopsis thaliana* increases thermotolerance. Together, our results suggest that, through dephosphorylation of NAC019, RCF2 is an integrator of high-temperature signal transduction and a mechanism for HSF and HSP activation.

Plant cell and environment

Histone chaperone ASF1 is involved in gene transcription activation in response to heat stress in *Arabidopsis thaliana*

MINJIE WENG1,?, YUE YANG1,?, HAIYANG FENG1, ZONGDE PAN1, WEN-HUI SHEN1,2, YAN ZHU1,*, AIWU DONG1,*

Abstract

ANTI-SILENCING FUNCTION 1 (ASF1) is an evolutionarily conserved histone chaperone involved in diverse chromatin-based processes in eukaryotes. Yet, its role in transcription and the underlying molecular mechanisms remain largely elusive, particularly in plants. Here, we show that the *Arabidopsis thaliana* ASF1 homologous genes, AtASF1A and AtASF1B, are involved in gene transcription activation in response to heat stress. The *Atasf1ab* mutant displays defective basal as well as acquired thermotolerance phenotypes. Heat-induced expression of several key genes, including the HEAT SHOCK PROTEIN (HSP) genes Hsp101, Hsp70, Hsa32, Hsp17.6A and Hsp17.6B-C1, and the HEAT SHOCK FACTOR (HSF) gene HsfA2 but not HsfB1 is drastically impaired in *Atasf1ab* as compared to that in wild type. We found that AtASF1A/B proteins are recruited onto chromatin and their enrichment is correlated with nucleosome removal and RNA polymerase II accumulation at the promoter and coding regions of HsfA2 and Hsa32 but not HsfB1. Moreover, AtASF1A/B facilitate H3K56 acetylation (H3K56ac), which is associated with HsfA2 and Hsa32 activation. Taken together, our study unravels an important function of AtASF1A/B in plant heat stress response and suggests that AtASF1A/B participate in transcription activation of some but not all HSF and HSP genes via nucleosome removal and H3K56ac stimulation.

Yichen:

Microbiology. 2014 Feb 3. doi: 10.1099/mic.0.073478-0. [Epub ahead of print]

Cyanobacterial Heat Shock Response: Role and Regulation of Molecular Chaperones.

Rajaram H1, Chaurasia AK, Apte SK.

Author information

Abstract

Cyanobacteria constitute a morphologically diverse group of oxygenic photoautotrophic microbes which range from unicellular to multicellular, and non-nitrogen-fixing to nitrogen-fixing types. Sustained long term

exposure to changing environmental conditions, during their three billion years of evolution, has presumably led to their adaptation to diverse ecological niches. The ability to maintain protein conformational homeostasis (folding-misfolding-refolding or aggregation-degradation) by molecular chaperones holds the key to the stress adaptability of cyanobacteria. Though cyanobacteria possess several genes encoding DnaK and DnaJ family proteins, these are not the most abundant Hsps, as is the case in other bacteria. Instead, the Hsp60 family of proteins, comprising two phylogenetically conserved proteins, and small Hsps are more abundant during heat stress. The contribution of the Hsp100 (ClpB) family of proteins and of small Hsps in the unicellular cyanobacteria (*Synechocystis* and *Synechococcus*) as well as that of Hsp60 proteins in the filamentous cyanobacteria (*Anabaena*) to thermotolerance has been elucidated. The regulation of chaperone genes by several cis elements and trans-acting factors has also been well documented. Recent studies have demonstrated novel transcriptional and translational (mRNA secondary structure) regulatory mechanisms in unicellular cyanobacteria. This article provides an insight into the heat shock response (HSR); its organisation, and eco-physiological regulation and role of molecular chaperones, in unicellular and filamentous nitrogen-fixing cyanobacterial strains.

Nat Methods, 2014 Jan 30;11(2):121-2. doi: 10.1038/nmeth.2811.

BoxPlotR: a web tool for generation of box plots.

Spitzer M1, Wildenhain J2, Rappsilber J3, Tyers M4.

Umaru:

Nat Struct Mol Biol. 2014 Feb;21(2):126-32. doi: 10.1038/nsmb.2746. Epub 2014 Jan 12.

Temporal orchestration of repressive chromatin modifiers by circadian clock Period complexes.

Duong HA, Weitz CJ.

Author information



Abstract

The mammalian circadian clock is built on a molecular feedback loop in which the Period (PER) proteins, acting in a large, poorly understood complex, repress Clock-Bmal1, the transcription factor driving their expression. We found that mouse PER complexes include the histone methyltransferase HP1 γ -Suv39h. PER proteins recruited HP1 γ -Suv39h to the Per1 and Per2 promoters, and HP1 γ -Suv39h proved important for circadian di- and trimethylation of histone H3 Lys9 (H3K9) at the Per1 promoter, feedback repression and clock function. HP1 γ -Suv39h was recruited to the Per1 and Per2 promoters ~4 h after recruitment of HDAC1, a PER-associated

protein previously implicated in clock function and H3K9 deacetylation at the Per1 promoter. PER complexes containing HDAC1 or HP1 γ -Suv39h appeared to be physically separable. Circadian clock negative feedback by the PER complex thus involves dynamic, ordered recruitment of repressive chromatin modifiers to DNA-bound Clock-Bmal1.

Stephanie:

1) Polyphosphate Is a Primordial Chaperone

Michael J. Gray¹, Wei-Yun Wholey^{1,2}, Nico O. Wagner¹, Claudia M. Cremers¹, Antje Mueller-Schickert^{1,3}, Nathaniel T. Hock¹, Adam G. Krieger¹, Erica M. Smith¹, Robert A. Bender¹, James C.A. Bardwell^{1,2,3}, Ursula Jakob^{1,2}  

Summary

Composed of up to 1,000 phospho-anhydride bond-linked phosphate monomers, inorganic polyphosphate (polyP) is one of the most ancient, conserved, and enigmatic molecules in biology. Here we demonstrate that polyP functions as a hitherto unrecognized chaperone. We show that polyP stabilizes proteins in vivo, diminishes the need for other chaperone systems to survive proteotoxic stress conditions, and protects a wide variety of proteins against stress-induced unfolding and aggregation. In vitro studies reveal that polyP has protein-like chaperone qualities, binds to unfolding proteins with high affinity in an ATP-independent manner, and supports their productive refolding once nonstress conditions are restored. Our results uncover a universally important function for polyP and suggest that these long chains of inorganic phosphate may have served as one of nature's first chaperones, a role that continues to the present day.

ELIZABETH:

Feb 9, 2014

Chemistry & Biology: Alert 3 February-9 February

[Free Energy Diagrams for Protein Function](#) Review Article Ruth Nussinov, Chung-Jung Tsai

Christou A, Filippou P, Manganaris GA, Fotopoulos V.

Sodium hydrosulfide induces systemic thermotolerance to strawberry plants through transcriptional regulation of heat shock proteins and aquaporin.

BMC Plant Biol. 2014 Feb 5;14(1):42. [Epub ahead of print]

PMID: 24499299 [PubMed - as supplied by publisher]

Rajaram H, Chaurasia AK, Apte SK.

Cyanobacterial Heat Shock Response: Role and Regulation of Molecular Chaperones.

Microbiology. 2014 Feb 3;. [Epub ahead of print]
PMID: 24493248 [PubMed - as supplied by publisher]

Klus P, Bolognesi B, Agostini F, Marchese D, Zanzoni A, Tartaglia GG. The cleverSuite Approach for Protein Characterization: Predictions of Structural Properties, Solubility, Chaperone Requirements and RNA-Binding Abilities.

Bioinformatics. 2014 Feb 3;. [Epub ahead of print]
PMID: 24493033 [PubMed - as supplied by publisher]

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Chaperone and protease functions of LON protease 2 modulate the peroxisomal transition and degradation with autophagy. Plant Cell Physiol. 2014 Feb 2;. [Epub ahead of print]
PMID: 24492254 [PubMed - as supplied by publisher]

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Antiaggregation activity of chaperones and its quantification. Biochemistry (Mosc). 2013 Dec;78(13):1554-66.
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Nitric oxide and hydrogen peroxide are important signals mediating the allelopathic response of Arabidopsis to p-hydroxybenzoic acid. Physiol Plant. 2014 Feb 6;. [Epub ahead of print]
PMID: 24502504 [PubMed - as supplied by publisher]

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LeMAPK1, LeMAPK2, and LeMAPK3 Are Associated with Nitric Oxide-Induced Defense Response against Botrytis cinerea in the Lycopersicon esculentum Fruit.

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PMID: 24490996 [PubMed - as supplied by publisher]

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The thioredoxin superfamily in oxidative protein folding. Antioxid Redox Signal. 2014 Feb 2;. [Epub ahead of print]
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Helix-loop-helix/basic helix-loop-helix transcription factor network represses cell elongation in Arabidopsis through an apparent incoherent feed-forward loop.

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PMID: 24505057 [PubMed - as supplied by publisher]

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The Scanning Mechanism of Eukaryotic Translation Initiation.
Annu Rev Biochem. 2014 Jan 29;. [Epub ahead of print]
PMID: 24499181 [PubMed - as supplied by publisher]

Molecular Cell: Alert 1 February-7 February
[The Intrinsically Disordered Sem1 Protein Functions as a Molecular Tether during Proteasome Lid Biogenesis](#) Original Research Article
Pages 433-443
Robert J. Tomko, Mark Hochstrasser

Cell Stem Cell: Alert 1 February-7 February
[Translational Research: The Path for Bringing Discovery to Patients](#)
Pages 146-148
Leonard Zon

SVR4 (suppressor of variegation 4) and SVR4-like: two proteins with a role in proper organization of the chloroplast genetic machinery (pages 477-492)

Marta Powikrowska, Anastassia Khrouchtchova, Helle Juel Martens, Agnieszka Zygadlo-Nielsen, Joanna Melonek, Alexander Schulz, Karin Krupinska, Steven Rodermeil and Poul Erik Jensen
Article first published online: 16 OCT 2013 | DOI: 10.1111/ppl.12108

Plant, Cell & Environment Content Alert (New Articles)

Interplays between nitric oxide and reactive oxygen species in cryptogeiin signaling
ANNA KULIK, ELODIE NOIROT, VINCENT GRANDPERRET, STÉPHANE BOURQUE, JÉRÔME FROMENTIN, PAULINE SALLOIGNON, CAROLINE TRUNTZER, GRAZYNA DOBROWOLSKA, FRANÇOISE SIMON-PLAS and DAVID WENDEHENNE
Accepted manuscript online: 10 FEB 2014 05:10AM EST | DOI: 10.1111/pce.12295

Cell: Alert 8 February-14 February
[The TPLATE Adaptor Complex Drives Clathrin-Mediated Endocytosis in Plants](#) Original Research Article

Pages 691-704

EMBO Journal (2014) 33, 265-276

[Dom34 - Hbs1 mediated dissociation of inactive 80S ribosomes promotes restart of translation after stress](#)

Stresses such as glucose starvation generate inactive 80S ribosome complexes.
Dom34-Hbs1 together with Rli1 actively

Lin MY, Chai KH, Ko SS, Kuang LY, Lur HS, Charng YY.
A Positive Feedback Loop between HSP101 and HSA32 Modulates Long-Term Acquired Thermotolerance Illustrating Diverse Heat Stress Responses in Rice Varieties.
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Hydrogen Peroxide Acts Upstream of Nitric Oxide in the Heat Shock
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Plant Physiol. 2014 Feb 7;. [Epub ahead of print]
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Nitrogen dioxide is a positive regulator of plant growth.
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Ubiquinone accumulation improves osmotic-stress tolerance in
Escherichia coli.
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rapamycin complex 1 signalling and downstream translation factors.
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PMID: 24526220 [PubMed - as supplied by publisher]