Damian

1. Labbadia, J. and Richard I. Morimoto, *Repression of the Heat Shock Response Is a Programmed Event at the Onset of Reproduction.* Molecular Cell.

The heat shock response (HSR) is essential for proteostasis and cellular health. In metazoans, aging is associated with a decline in quality control, thus increasing the risk for protein conformational disease. Here, we show that in *C. elegans*, the HSR declines precipitously over a 4 hr period in early adulthood coincident with the onset of reproductive maturity. Repression of the HSR occurs due to an increase in H3K27me3 marks at stress gene loci, the timing of which is determined by reduced expression of the H3K27 demethylase *jmjd-3.1*. This results in a repressed chromatin state that interferes with HSF-1 binding and suppresses transcription initiation in response to stress. The removal of germline stem cells preserves *jmjd-3.1*expression, suppresses the accumulation of H3K27me3 at stress gene loci, and maintains the HSR. These findings suggest that competing requirements of the germline and soma dictate organismal stress resistance as animals begin reproduction.

2. Wang, F., Y. Yang, Z. Wang, J. Zhou, B. Fan, and Z. Chen, *A Critical Role of LIP5, a Positive Regulator of Multivesicular Body Biogenesis, in Plant Responses to Heat and Salt Stresses.* Plant Physiol, 2015.

Multivesicular bodies (MVBs) are unique endosomes containing vesicles in the lumens and play critical roles in many cellular processes. We have recently shown that Arabidopsis LIP5, a positive regulator of the SKD1 AAA ATPase in MVB biogenesis, is a critical target of mitogen-activated protein kinases MPK3 and MPK6 and plays an important role in plant immune system. In the present study, we report that LIP5-regulated MVB pathway also plays a critical role in plant responses to abiotic stresses. Disruption of LIP5 causes compromised tolerance to both heat and salt stresses. The critical role of LIP5 in plant tolerance to abiotic stresses is dependent on its ability to interact with SKD1. When compared with wild-type plants, lip5 mutants accumulate increased levels of ubiquitinated protein aggregates and NaCl under heat and salt stresses, respectively. Further analysis using fluorescent dye and MVB marker reveal that abiotic stress increases formation of endocytic vesicles and MVBs in a LIP5-dependent manner. LIP5 is also required for salt-induced increase of intracellular reactive oxygen species, which have been implicated in signaling of salt stress responses. Basal levels of LIP5 phosphorylation by MPKs and stability of LIP5 were elevated by salt stress and mutation of MPK phosphorylation sites in LIP5 reduces the stability and compromises the ability to complement the lip5 salt-sensitive mutant phenotype. These results collectively indicate that the MVB pathway is positively regulated by pathogen/stress-responsive MPK3/6 through LIP5 phosphorylation and plays a critical role in broad plant responses to biotic and abiotic stresses.

3. Correa-Aragunde, N., F.J. Cejudo, and L. Lamattina, *Nitric oxide is required for the auxin-induced activation of NADPH-dependent thioredoxin reductase and protein denitrosylation during root growth responses in arabidopsis.* Annals of Botany, 2015.

Background and Aims Auxin is the main phytohormone controlling root development in plants. This study uses pharmacological and genetic approaches to examine the role of auxin and nitric oxide (NO) in the activation of NADPH-dependent thioredoxin reductase (NTR), and the effect that this activity has on root growth responses in *Arabidopsis thaliana*.

Methods Arabidopsis seedlings were treated with auxin with or without the NTR inhibitors auranofin (ANF) and 1-chloro-2, 4-dinitrobenzene (DNCB). NTR activity, lateral root (LR) formation and *S*-nitrosothiol content were measured in roots. Protein *S*-nitrosylation was analysed by the biotin switch method in wild-type arabidopsis and in the double mutant *ntra ntrb*.

Key Results The auxin-mediated induction of NTR activity is inhibited by the NO scavenger 2-(4-carboxyphenyl)-4,4,5,5-tetramethylimidazoline-1-oxyl-3-oxide (CPTIO), suggesting that NO is downstream of auxin in this regulatory pathway. The NTR inhibitors ANF and DNCB prevent auxin-mediated activation of NTR and LR formation. Moreover, ANF and DNCB also inhibit auxin-induced DR5 : : GUS and BA3 : : GUS gene expression, suggesting that the auxin signalling pathway is compromised without full NTR activity. Treatment of roots with ANF and DNCB increases total nitrosothiols (SNO) content and protein *S*-nitrosylation, suggesting a role of the NTR-thioredoxin (Trx)-redox system in protein denitrosylation. In agreement with these results, the level of *S*-nitrosylated proteins is increased in the arabidopsis double mutant *ntra ntrb* as compared with the wild-type.

Conclusions The results support for the idea that NTR is involved in protein denitrosylation during auxin-mediated root development. The fact that a high NO concentration induces NTR activity suggests that a feedback mechanism to control massive and unregulated protein *S*-nitrosylation could be operating in plant cells.

Mary
Escherichia coli ClpB is a non-processive polypeptide translocase.
Li T et al. 15 August 2015 Biochemical Journal.

Escherichia coli caseinolytic protease (Clp)B is a hexameric AAA + [expanded superfamily of AAA (ATPase associated with various cellular activities)] enzyme that has the unique ability to catalyse protein disaggregation. Such enzymes are essential for proteome maintenance. Based on structural comparisons to homologous enzymes involved in ATP-dependent proteolysis and clever protein engineering strategies, it has been reported that ClpB translocates polypeptide through its axial channel. Using single-turnover fluorescence and anisotropy experiments we show that ClpB is a non-processive polypeptide translocase that catalyses disaggregation by taking one or two translocation steps followed by rapid dissociation. Using single-turnover FRET experiments we show that ClpB containing the IGL loop from ClpA does not translocate substrate through its axial channel and into ClpP for proteolytic degradation. Rather, ClpB containing the IGL loop dysregulates ClpP leading to non-specific proteolysis reminiscent of ADEP (acyldepsipeptide) dysregulation. Our results support a molecular mechanism where ClpB catalyses protein disaggregation by tugging and releasing exposed tails or loops.

Minsoo
1. Proc Natl Acad Sci U S A. 2015 Aug 11;112(32):9908-13. doi: 10.1073/pnas.1508040112. Epub 2015 Jul 27.

Structural basis for inhibition of the histone chaperone activity of SET/TAF-Iβ by cytochrome c. González-Arzola K(1), Díaz-Moreno I(2), Cano-González A(3), Díaz-Quintana A(1), Velázquez-Campoy A(4), Moreno-Beltrán B(1), López-Rivas A(3), De la Rosa MA(2).

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Chromatin is pivotal for regulation of the DNA damage process insofar as it influences access to DNA and serves as a DNA repair docking site. Recent works identify histone chaperones as key regulators of damaged chromatin's transcriptional activity. However, understanding how chaperones are modulated during DNA damage response is still challenging. This study reveals that the histone chaperone SET/TAF-Iβ interacts with cytochrome c following DNA damage. Specifically, cytochrome c is shown to be translocated into cell nuclei upon induction of DNA damage, but not upon stimulation of the death receptor or stress-induced pathways. Cytochrome c was found to competitively hinder binding of SET/TAF-Iβ to core histones, thereby locking its histone-binding domains and inhibiting its nucleosome assembly activity. In addition, we have used NMR spectroscopy, calorimetry, mutagenesis, and molecular docking to provide an insight into the structural features of the formation of the complex between

cytochrome c and SET/TAF-Iβ. Overall, these findings establish a framework for understanding the molecular basis of cytochrome c-mediated blocking of SET/TAF-Iβ, which subsequently may facilitate the development of new drugs to silence the oncogenic effect of SET/TAF-Iβ's histone chaperone activity.

2. Proc Natl Acad Sci U S A. 2015 Aug 11;112(32):10044-9. doi: 10.1073/pnas.1511570112. Epub 2015 Jul 6.

Chloroplasts extend stromules independently and in response to internal redox signals. Brunkard JO(1), Runkel AM(1), Zambryski PC(2).

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A fundamental mystery of plant cell biology is the occurrence of "stromules," stroma-filled tubular extensions from plastids (such as chloroplasts) that are universally observed in plants but whose functions are, in effect, completely unknown. One prevalent hypothesis is that stromules exchange signals or metabolites between plastids and other subcellular compartments, and that stromules are induced during stress. Until now, no signaling mechanisms originating within the plastid have been identified that regulate stromule activity, a critical missing link in this hypothesis. Using confocal and superresolution 3D microscopy, we have shown that stromules form in response to light-sensitive redox signals within the chloroplast. Stromule frequency increased during the day or after treatment with chemicals that produce reactive oxygen species specifically in the chloroplast. Silencing expression of the chloroplast NADPH-dependent thioredoxin reductase, a central hub in chloroplast redox signaling pathways, increased chloroplast stromule frequency, whereas silencing expression of nuclear genes related to plastid genome expression and tetrapyrrole biosynthesis had no impact on stromules. Leucoplasts, which are not photosynthetic, also made more stromules in the daytime. Leucoplasts did not respond to the same redox signaling pathway but instead increased stromule formation when exposed to sucrose, a major product of photosynthesis, although sucrose has no impact on chloroplast stromule frequency. Thus, different types of plastids make stromules in response to distinct signals. Finally, isolated chloroplasts could make stromules independently after extraction from the cytoplasm, suggesting that chloroplast-associated factors are sufficient to generate stromules. These discoveries demonstrate that chloroplasts are remarkably autonomous organelles that alter their stromule frequency in reaction to internal signal transduction pathways.

3. PLoS Genet. 2015 Jun 19;11(6):e1005302. doi: 10.1371/journal.pgen.1005302. eCollection 2015.

Transfer RNAs Mediate the Rapid Adaptation of Escherichia coli to Oxidative Stress. Zhong J(1), Xiao C(2), Gu W(1), Du G(1), Sun X(1), He QY(1), Zhang G(1).
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Translational systems can respond promptly to sudden environmental changes to provide rapid adaptations to environmental stress. Unlike the well-studied translational responses to oxidative stress in eukaryotic systems, little is known regarding how prokaryotes respond rapidly to oxidative stress in terms of translation. In this study, we measured protein synthesis from the entire Escherichia coli proteome and found that protein synthesis was severely slowed down under oxidative stress. With unchanged translation initiation, this slowdown was caused by decreased translation elongation speed. We further confirmed by tRNA sequencing and qRT-PCR that this deceleration was caused by a global, enzymatic downregulation of almost all tRNA species shortly after exposure to oxidative agents. Elevation in tRNA levels accelerated translation and protected E. coli against oxidative stress caused by hydrogen peroxide and the antibiotic ciprofloxacin. Our results showed that the global regulation of tRNAs mediates the rapid adjustment of the E. coli translation system for prompt adaptation to oxidative stress.

4. 1. Plant Cell. 2015 Jul;27(7):1968-84. doi: 10.1105/tpc.15.00105. Epub 2015 Jun 26.
Mitochondrial Dihydrolipoyl Dehydrogenase Activity Shapes Photosynthesis and Photorespiration of Arabidopsis thaliana. Timm S(1), Wittmiß M(2), Gamlien S(2), Ewald R(2), Florian A(3), Frank M(4), Wirtz M(5), Hell R(5), Fernie AR(3), Bauwe H(2).

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Mitochondrial dihydrolipoyl dehydrogenase (mtLPD; L-protein) is an integral component of several multienzyme systems involved in the tricarboxylic acid (TCA) cycle, photorespiration, and the degradation of branched-chain α-ketoacids. The majority of the mtLPD present in photosynthesizing tissue is used for glycine decarboxylase (GDC), necessary for the high-flux photorespiratory glycine-into-serine conversion. We previously suggested that GDC activity could be a signal in a regulatory network that adjusts carbon flux through the Calvin-Benson cycle in response to photorespiration. Here, we show that elevated GDC L-protein activity significantly alters several diagnostic parameters of cellular metabolism and leaf gas exchange in Arabidopsis thaliana. Overexpressor lines displayed markedly decreased steady state contents of TCA cycle and photorespiratory intermediates as well as elevated NAD(P)(+)-to-NAD(P)H ratios. Additionally, increased rates of CO2 assimilation, photorespiration, and plant growth were observed. Intriguingly, however, day respiration rates remained unaffected. By contrast, respiration was enhanced in the first half of the dark phase but depressed in the second. We also observed enhanced sucrose biosynthesis in the light in combination with a lower diel magnitude of starch accumulation and breakdown. These data thus substantiate our prior hypothesis that facilitating flux through the photorespiratory pathway stimulates photosynthetic CO2 assimilation in the Calvin-Benson cycle. They furthermore suggest that this regulation is, at least in part, dependent on increased light-capture/use efficiency.

Keith
Structure and mechanism of the Rubisco-assembly chaperone Raf1
Nature Structural and Molecular Biology, 03 August 2015
Thomas Hauser, Javaid Y Bhat, Goran Miličić, Petra Wendler, F Ulrich Hartl, Andreas Bracher & Manajit Hayer-Hartl

Department of Cellular Biochemistry, Max Planck Institute of Biochemistry, Martinsried, Germany.
Thomas Hauser, Javaid Y Bhat, Goran Miličić, F Ulrich Hartl, Andreas Bracher & Manajit Hayer-Hartl
Gene Center Munich, Ludwig-Maximilians-Universität München, Munich, Germany.

Biogenesis of the photosynthetic enzyme Rubisco, a complex of eight large (RbcL) and eight small (RbcS) subunits, requires assembly chaperones. Here we analyzed the role of Rubisco accumulation factor1 (Raf1), a dimer of ~40-kDa subunits. We find that Raf1 from *Synechococcus elongatus* acts downstream of chaperonin-assisted RbcL folding by stabilizing RbcL antiparallel dimers for assembly into RbcL8 complexes with four Raf1 dimers bound. Raf1 displacement by RbcS results in holoenzyme formation. Crystal structures show that Raf1 from *Arabidopsis thaliana* consists of a β-sheet dimerization domain and a flexibly linked α-helical domain. Chemical cross-linking and EM reconstruction indicate that the β-domains bind along the equator of each RbcL2 unit, and the α-helical domains embrace the top and bottom edges of RbcL2. Raf1 fulfills a role similar to that of the assembly chaperone RbcX, thus suggesting that functionally redundant factors ensure efficient Rubisco biogenesis.

Crucial HSP70 co-chaperone complex unlocks metazoan protein disaggregation

Nadinath B. Nillegoda[1], Janine Kirstein[2], Anna Szlachcic[1], Mykhaylo Berynskyy[3], Antonia Stank[3,4], Florian Stengel[5], Kristin Arnsburg[2], Xuechao Gao[1], Annika Scior[2], Ruedi Aebersold[5,6], D. Lys Guilbride[1], Rebecca C. Wade[1,3,7], Richard I. Morimoto[8], Matthias P. Mayer[1] & Bernd Bukau[1]

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Protein aggregates are the hallmark of stressed and ageing cells, and characterize several pathophysiological states[1,2]. Healthy metazoan cells effectively eliminate intracellular protein aggregates[3,4], indicating that efficient disaggregation and/or degradation mechanisms exist. However, metazoans lack the key heat-shock protein disaggregase HSP100 of non-metazoan HSP70-dependent protein disaggregation systems[5,6], and the human HSP70 system alone, even with the crucial HSP110 nucleotide exchange factor, has poor disaggregation activity in vitro[4,7]. This unresolved con- undrum is central to protein quality control biology. Here we show that synergic cooperation between complexed J-protein co-chaperones of classes A and B unleashes highly efficient protein disaggregation activity in human and nematode HSP70 systems. Metazoan mixed-class J-protein complexes are transient, involve complementary charged regions conserved in the J-domains and carboxy-terminal domains of each J-protein class, and are flexible with respect to subunit composition. Complex formation allows J-proteins to initiate transient higher order chaperone structures involving HSP70 and interacting nucleotide exchange factors. A network of cooperative class A and B J-protein interactions therefore provides the metazoan HSP70 machinery with powerful, flexible, and finely regulatable disaggregase activity and a further level of regulation crucial for cellular protein quality control.

Fionn
Nature. 2015 Aug 5;
Authors: Nillegoda NB, Kirstein J, Szlachcic A, Berynskyy M, Stank A, Stengel F, Arnsburg K, Gao X, Scior A, Aebersold R, Guilbride DL, Wade RC, Morimoto RI, Mayer MP, Bukau B
Protein aggregates are the hallmark of stressed and ageing cells, and characterize several pathophysiological states. Healthy metazoan cells effectively eliminate intracellular protein aggregates, indicating that efficient disaggregation and/or degradation mechanisms exist. However, metazoans lack the key heat-shock protein disaggregase HSP100 of non-metazoan HSP70-dependent protein disaggregation systems, and the human HSP70 system alone, even with the crucial

HSP110 nucleotide exchange factor, has poor disaggregation activity in vitro. This unresolved conundrum is central to protein quality control biology. Here we show that synergic cooperation between complexed J-protein co-chaperones of classes A and B unleashes highly efficient protein disaggregation activity in human and nematode HSP70 systems. Metazoan mixed-class J-protein complexes are transient, involve complementary charged regions conserved in the J-domains and carboxy-terminal domains of each J-protein class, and are flexible with respect to subunit composition. Complex formation allows J-proteins to initiate transient higher order chaperone structures involving HSP70 and interacting nucleotide exchange factors. A network of cooperative class A and B J-protein interactions therefore provides the metazoan HSP70 machinery with powerful, flexible, and finely regulatable disaggregase activity and a further level of regulation crucial for cellular protein quality control.

Plant breeding
Anquan Wang, Xiaohong Yu, Yun Mao, Ying Liu, Guoqing Liu, Yongsheng Liu and Xiangli Niu
Overexpression of a small heat-shock-protein gene enhances tolerance to abiotic stresses in rice (pages 384–393)

AbstractRice (Oryza sativa L.) is one of the most important crops in the world which survives from various abiotic stresses in natural environments with specific stress-involved genes expressed. Plant sHSPs (small heat-shockproteins) were reported to respond to abiotic stresses. To improve theunderstanding of sHSPs in rice, we characterized heat-shock-protein geneOsHSP18.6 here. OsHSP18.6 could be induced by diverse stresses, suchas drought, salt and cold, especially under heat. The gene was foundexpressed in root, stem, leaf, internode and spikelet. Overexpression ofOsHSP18.6 results in increased thermotolerance and exhibits universal tolerance to stresses tested, including heat, drought, salt and cold. Lowerlevels of malondialdehyde (MDA) and greater activities of catalase(CAT) and superoxide dismutase (SOD) were observed in OsHSP18.6-overexpression rice under heat and drought. OsHSP18.6-overexpressionlines indicated decreased sterile rates under hot weather without remark-able changes in most of other agronomic traits compared with wild-typeplants.

J Biol Chem
A two-step protein quality control pathway for a misfolded DJ-1 variant in fission yeast.
Mathiassen SG1, Larsen IB1, Poulsen EG1, Madsen CT1, Papaleo E1, Lindorff-Larsen K1, Kragelund BB1, Nielsen ML1, Kriegenburg F1, Hartmann-Petersen R2
Abstract
A mutation, L166P, in the cytosolic protein, PARK7/DJ-1, causes protein misfolding and is linked to Parkinson's disease. Here, we identify the fission yeast protein Sdj1 as the orthologue of DJ-1 and calculate by in silico saturation mutagenesis the effects of point mutants on its structural stability. We also map the degradation pathways for Sdj1-L169P, the fission yeast orthologue of the disease-causing DJ-1 L166P protein. Sdj1-L169P forms inclusions, which are enriched for the Hsp104 disaggregase. Hsp104 and Hsp70-type chaperones are required for efficient degradation of Sdj1-L169P. This also depends on the ribosome-associated E3 ligase Ltn1 and its co-factor Rqc1. While Hsp104 is absolutely required for proteasomal degradation of Sdj1-L169P aggregates, the degradation of already aggregated Sdj1-L169P occurs independently of Ltn1 and Rqc1. Thus, our data point to soluble Sdj1-L169P being targeted early by Ltn1 and Rqc1. The fraction of Sdj1-L169P that escapes this first inspection then forms aggregates that are subsequently cleared via an Hsp104- and proteasome-dependent pathway.

INDU
Articles from Science:
1. Science. 2015 Jul 17;349(6245):324-8. doi: 10.1126/science.1260031. Epub 2015 Jun 25.
Circadian rhythms. A protein fold switch joins the circadian oscillator to clock output in cyanobacteria.
Chang YG(1), Cohen SE(2), Phong C(3), Myers WK(4), Kim YI(2), Tseng R(5), Lin J(3), Zhang L(1), Boyd JS(2), Lee Y(6), Kang S(6), Lee D(7), Li S(7), Britt RD(4), Rust MJ(3), Golden SS(8), LiWang A(9).

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Jolla, CA 92093, USA. (9)School of Natural Sciences, University of California, Merced, CA 95343, USA. Center for Circadian Biology, University of California, San Diego, La Jolla, CA 92093, USA. Quantitative and Systems Biology, University of California, Merced, CA 95343, USA. Chemistry and Chemical Biology, University of California, Merced, CA 95343, USA. Health Sciences Research Institute,University of California, Merced, CA 95343, USA. aliwang@ucmerced.edu.

Organisms are adapted to the relentless cycles of day and night, because theyevolved timekeeping systems called circadian clocks, which regulate biological activities with ~24-hour rhythms. The clock of cyanobacteria is driven by a three-protein oscillator composed of KaiA, KaiB, and KaiC, which together generate a circadian rhythm of KaiC phosphorylation. We show that KaiB flips between two distinct three-dimensional folds, and its rare transition to an active state provides a time delay that is required to match the timing of the oscillator to that of Earth's rotation. Once KaiB switches folds, it binds phosphorylated KaiC and captures KaiA, which initiates a phase transition of the circadian cycle, and it regulates components of the clock-output pathway, which provides the link that joins the timekeeping and signaling functions of the oscillator.

PMCID: PMC4506712 [Available on 2016-07-17]
PMID: 26113641 [PubMed - in process]

2. Science. 2015 Jul 31;349(6247):500-6. doi: 10.1126/science.aaa0079.
METABOLISM. S-Nitrosylation links obesity-associated inflammation to endoplasmic reticulum dysfunction.
Yang L(1), Calay ES(1), Fan J(1), Arduini A(1), Kunz RC(2), Gygi SP(2), Yalcin A(1), Fu S(1), Hotamisligil GS(3).
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The association between inflammation and endoplasmic reticulum (ER) stress has been observed in many diseases. However, if and how chronic inflammation regulates the unfolded protein response (UPR) and alters ER homeostasis in general, or in the context of chronic disease, remains unknown. Here, we show that, in the setting of obesity, inflammatory input through increased inducible nitric oxide synthase (iNOS) activity causes S-nitrosylation of a key UPR regulator, IRE1α, which leads to a progressive decline in hepatic IRE1α-mediated XBP1 splicing activity in both genetic (ob/ob) and dietary (high-fat diet-induced) models of obesity. Finally, in obese mice with liver-specific IRE1α deficiency, reconstitution of IRE1α expression with a nitrosylation-resistant variant restored IRE1α-mediated XBP1 splicing and improved glucose homeostasis in vivo. Taken together, these data describe a mechanism by which inflammatory pathways compromise UPR function through iNOS-mediated S-nitrosylation of IRE1α, which contributes to defective IRE1α activity, impaired ER function, and prolonged ER stress in obesity.

PMID: 26228140 [PubMed - in process]

3. Science. 2015 Jul 31;349(6247):535-9. doi: 10.1126/science.aab4090.
ACTIN-DIRECTED TOXIN. ACD toxin-produced actin oligomers poison formin-controlled actin polymerization.
Heisler DB(1), Kudryashova E(2), Grinevich DO(3), Suarez C(4), Winkelman JD(4),Birukov KG(5), Kotha SR(6), Parinandi NL(6), Vavylonis D(7), Kovar DR(8),Kudryashov DS(9).
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The actin cross-linking domain (ACD) is an actin-specific toxin produced by several pathogens, including life-threatening spp. of Vibrio cholerae, Vibrio vulnificus, and Aeromonas hydrophila. Actin cross-linking by ACD is thought to lead to slow cytoskeleton failure owing to a gradual sequestration of actin in the form of nonfunctional oligomers. Here, we found that ACD converted cytoplasmic actin into highly toxic oligomers that potently "poisoned" the ability of major actin assembly proteins, formins, to sustain actin polymerization. Thus, ACD can target the most abundant cellular protein by using actin oligomers as secondary toxins to efficiently subvert cellular functions of actin while functioning at very low doses.

PMID: 26228148 [PubMed - in process]

4. Science. 2015 Jul 31;349(6247):540-3. doi: 10.1126/science.aab1140.
PLANT EVOLUTION. Convergent evolution of strigolactone perception enabled host detection in parasitic plants.
Conn CE(1), Bythell-Douglas R(2), Neumann D(1), Yoshida S(3), Whittington B(4),Westwood JH(4), Shirasu K(3), Bond CS(2), Dyer KA(1), Nelson DC(1).
(1)Department of Genetics, University of Georgia, Athens, GA 30602, USA.(2)School of Chemistry and Biochemistry, The University of Western Australia,Crawley, Western Australia 6009, Australia. (3)RIKEN Center for Sustainable Resource Science, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan. (4)Department of Plant Pathology, Physiology, and Weed Science, Virginia Tech, Blacksburg, VA 24061, USA.

Obligate parasitic plants in the Orobanchaceae germinate after sensing plant hormones, strigolactones, exuded from host roots. In Arabidopsis thaliana, the α/β-hydrolase D14 acts as a strigolactone receptor that controls shoot branching, whereas its ancestral paralog, KAI2, mediates karrikin-specific germination responses. We observed that KAI2, but not D14, is present at higher copy numbers in parasitic species than in nonparasitic relatives. KAI2 paralogs in parasites are distributed into three phylogenetic clades. The fastest-evolving clade, KAI2d, contains the majority of KAI2 paralogs. Homology models predict that the ligand-binding pockets of KAI2d resemble D14. KAI2d transgenes confer strigolactone-specific germination responses to Arabidopsis thaliana. Thus, the KAI2 paralogs D14 and KAI2d underwent convergent evolution of strigolactone recognition, respectively enabling developmental responses to strigolactones in angiosperms and host detection in parasites.

PMID: 26228149 [PubMed - in process]

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Plant Cell Table of Contents for July 2015; Vol. 27, No. 7
Mitochondrial Dihydrolipoyl Dehydrogenase Activity Shapes Photosynthesis and Photorespiration of *Arabidopsis thaliana*
Stefan Timm, Maria Wittmiß, Sabine Gamlien, Ralph Ewald, Alexandra Florian, Marcus Frank, Markus Wirtz, Rüdiger Hell, Alisdair R. Fernie, and Hermann Bauwe
Plant Cell 2015 27: 1968-1984. First Published on June 26, 2015; doi:10.1105/tpc.15.00105
http://www.plantcell.org/content/27/7/1968.abstract
The activity of the mitochondrial dihydrolipoyl dehydrogenase improves photorespiration and in turn stimulates photosynthetic carbon assimilation and plant growth.

Mitochondrial dihydrolipoyl dehydrogenase (mtLPD; L-protein) is an integral component of several multienzyme systems involved in the tricarboxylic acid (TCA) cycle, photorespiration, and the degradation of branched-chain α-ketoacids. The majority of the mtLPD present in photosynthesizing tissue is used for glycine decarboxylase (GDC), necessary for the high-flux photorespiratory glycine-into-serine conversion. We previously suggested that GDC activity could be a signal in a regulatory network that adjusts carbon flux through the Calvin-Benson cycle in response to photorespiration. Here, we show that elevated GDC L-protein activity significantly alters several diagnostic parameters of cellular metabolism and leaf gas exchange in *Arabidopsis thaliana*. Overexpressor lines displayed markedly decreased steady state contents of TCA cycle and photorespiratory intermediates as well as elevated $NAD(P)^+$-to-NAD(P)H ratios. Additionally, increased

rates of CO_2 assimilation, photorespiration, and plant growth were observed. Intriguingly, however, day respiration rates remained unaffected. By contrast, respiration was enhanced in the first half of the dark phase but depressed in the second. We also observed enhanced sucrose biosynthesis in the light in combination with a lower diel magnitude of starch accumulation and breakdown. These data thus substantiate our prior hypothesis that facilitating flux through the photorespiratory pathway stimulates photosynthetic CO_2 assimilation in the Calvin-Benson cycle. They furthermore suggest that this regulation is, at least in part, dependent on increased light-capture/use efficiency.

Sasaki K, Liu Y, Kim MH, Imai R.
An RNA chaperone, AtCSP2, negatively regulates salt stress tolerance.
Plant Signal Behav. 2015 Aug 7;:0. [Epub ahead of print] PMID: 26252779 [PubMed - as supplied by publisher]

Tapken W, Ravet K, Shahbaz M, Pilon M.
Regulation of Cu delivery to chloroplast proteins.
Plant Signal Behav. 2015 Jul 3;10(7):e1046666. PMID: 26251885 [PubMed - in process]

Maruyama D, Endo T, Nishikawa S.
BiP3 supports the early stages of female gametogenesis in the absence of BiP1 and BiP2 in Arabidopsis thaliana.
Plant Signal Behav. 2015 Jul 3;10(7):e1035853. PMID: 26251880 [PubMed - in process]

Li T, Weaver CL, Lin J, Duran EC, Miller JM, Lucius AL.
Escherichia coli ClpB is a non-processive polypeptide translocase.
Biochem J. 2015 Aug 15;470(1):39-52. PMID: 26251445 [PubMed - in process]

Yu HY, Ziegelhoffer T, Craig EA.
Functionality of Class A and Class B J-protein co-chaperones with Hsp70.
FEBS Lett. 2015 Aug 3;. [Epub ahead of print] PMID: 26247431 [PubMed - as supplied by publisher]

Nillegoda NB, Kirstein J, Szlachcic A, Berynskyy M, Stank A, Stengel F, Arnsburg K, Gao X, Scior A, Aebersold R, Guilbride DL, Wade RC, Morimoto RI, Mayer MP, Bukau B.
Crucial HSP70 co-chaperone complex unlocks metazoan protein disaggregation.
Nature. 2015 Aug 5;. [Epub ahead of print] PMID: 26245380 [PubMed - as supplied by publisher]

Crucial HSP70 co-chaperone complex unlocks metazoan protein disaggregation.
Nature. 2015 Aug 5;

Authors: Nillegoda NB, Kirstein J, Szlachcic A, Berynskyy M, Stank A, Stengel F, Arnsburg K, Gao X, Scior A, Aebersold R, Guilbride DL, Wade RC, Morimoto RI, Mayer MP, Bukau B

Protein aggregates are the hallmark of stressed and ageing cells, and characterize several pathophysiological states. Healthy metazoan cells effectively eliminate intracellular protein aggregates, indicating that efficient disaggregation and/or degradation mechanisms exist. However, metazoans lack the key heat-shock protein disaggregase HSP100 of non-metazoan HSP70-dependent protein disaggregation systems, and the human HSP70 system alone, even with the crucial HSP110 nucleotide exchange factor, has poor disaggregation activity in vitro. This unresolved conundrum is central to protein quality control biology. Here we show that synergic cooperation between complexed J-protein co-chaperones of classes A and B unleashes highly efficient protein disaggregation activity in human and nematode HSP70 systems. Metazoan mixed-class J-protein complexes are transient, involve complementary charged regions conserved in the J-domains and carboxy-terminal domains of each J-protein class, and are flexible with respect to subunit composition. Complex formation allows J-proteins to initiate transient higher order chaperone structures involving HSP70 and interacting nucleotide exchange factors. A network of cooperative class A and B J-protein interactions therefore provides the metazoan HSP70 machinery with powerful, flexible, and finely regulatable disaggregase activity and a further level of regulation crucial for cellular protein quality control.

Rajagopal P, Liu Y, Shi L, Clouser AF, Klevit RE.
Structure of the Î±-crystallin domain from the redox-sensitive chaperone, HSPB1.
J Biomol NMR. 2015 Aug 5;. [Epub ahead of print]
PMID: 26243512 [PubMed - as supplied by publisher]

The Plant Journal Content Alert: 83, 4 (August 2015)

A tetratricopeptide repeat domain-containing protein SSR1 located in mitochondria is involved in root development and auxin polar transport in Arabidopsis (pages 582–599)

Min Zhang, Cuiping Wang, Qingfang Lin, Aihua Liu, Ting Wang, Xuanjun Feng, Jie Liu, Huiling Han, Yan Ma, Diana Bonea, Rongmin Zhao and Xuejun Hua Article first published online: 4 JUL 2015 | DOI: 10.1111/tpj.12911

Current Opinion in Microbiology: Alert 2 August-8 August

Exploration of extremophiles for high temperature biotechnological processes Review Article *Pages 113-119*

Skander Elleuche, Christian Schäfers, Saskia Blank, Carola Schröder, Garabed Antranikian

Industrial processes often take place under harsh conditions that are hostile to microorganisms and their biocatalysts. Microorganisms surviving at temperatures above 60 °C represent a chest of biotechnological treasures for high-temperature bioprocesses by producing a large portfolio of biocatalysts (thermozymes). Due to the unique requirements to cultivate thermophilic (60–80 °C) and hyperthermophilic (80–110 °C) Bacteria and Archaea, less than 5% are cultivable in the laboratory. Therefore, other approaches including sequence-based screenings and metagenomics have been successful in providing novel thermozymes. In particular, polysaccharide-degrading enzymes (amylolytic enzymes, hemicellulases, cellulases, pectinases and chitinases), lipolytic enzymes and proteases from thermophiles have attracted interest due to their potential for versatile applications in pharmaceutical, chemical, food, textile, paper, leather and feed industries as well as in biorefineries.

Molecular Cell: Alert 1 August-7 August

Acute Activation of Oxidative Pentose Phosphate Pathway as First-Line Response to Oxidative Stress in Human Skin Cells Original Research Article *Pages 359-371*

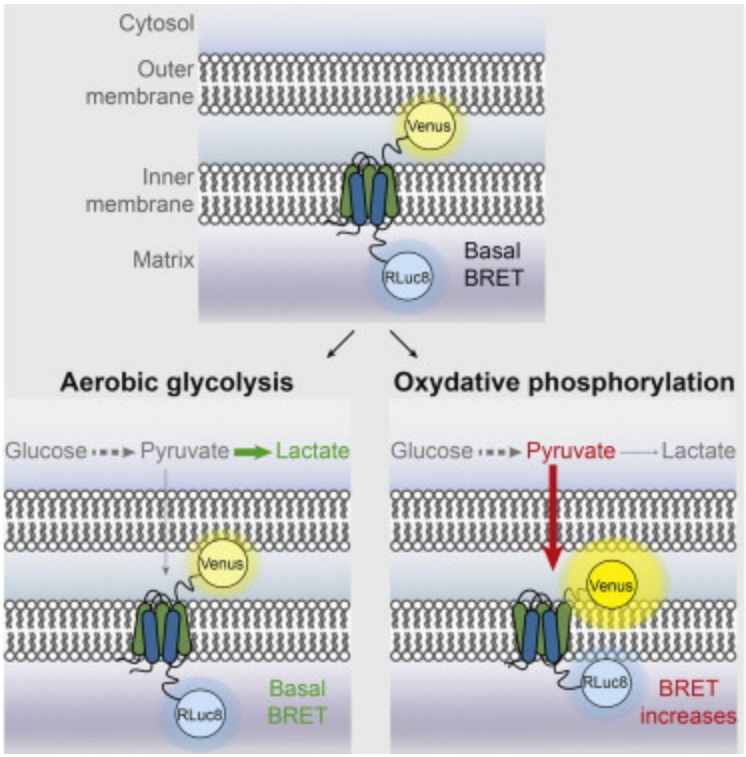
Andreas Kuehne, Hila Emmert, Joern Soehle, Marc Winnefeld, Frank Fischer, Horst Wenck, Stefan Gallinat, Lara Terstegen, Ralph Lucius, Janosch Hildebrand, Nicola Zamboni

Conformational Differences between Open and Closed States of the Eukaryotic Translation Initiation Complex Original Research Article *Pages 399-412*

Jose L. Llácer, Tanweer Hussain, Laura Marler, Colin Echeverría Aitken, Anil Thakur, Jon R. Lorsch, Alan G. Hinnebusch, V. Ramakrishnan

Monitoring Mitochondrial Pyruvate Carrier Activity in Real Time Using a BRET-Based Biosensor: Investigation of the Warburg Effect Original Research Article *Pages 491-501*

Vincent Compan, Sandra Pierredon, Benoît Vanderperre, Petra Krznar, Ibtissam Marchiq, Nicola Zamboni, Jacques Pouyssegur, Jean-Claude Martinou



Nture Biotechnolgy

Flexible guide-RNA design for CRISPR applications using Protospacer Workbench **pp805 - 806**
Cameron Ross MacPherson and Artur Scherfvvoi:10.1038/nbt.3291

The emergence of agbiogenerics **pp819 - 823**
David J Jefferson, Gregory D Graff, Cecilia L Chi-Ham and Alan B Bennettvdoi:10.1038/nbt.3306
Although the first major agbiotech product patent has expired, regulatory requirements could continue to allot a significant degree of control to the original right holder.

A time and a place for sugar in your ears **pp827 - 828**
Jiahn-Chou Guan and Karen E Koch doi:10.1038/nbt.3315
Targeting trehalose metabolism improves maize yield under a range of water-deficit conditions.

Expression of trehalose-6-phosphate phosphatase in maize ears improves yield in well-watered and drought conditions **pp862 - 869**
Michael L Nuccio, Jeff Wu, Ron Mowers, Hua-Ping Zhou, Moez Meghji *et al.* doi:10.1038/nbt.3277
Expression of a single trehalose transgene in maize improves yield in field trials in both well-watered and drought conditions.

The *OsSPL16-GW7* regulatory module determines grain shape and simultaneously improves rice yield and grain quality Wang, S. *et al. Nat. Genet.* doi:10.1038/ng.3352 (6 July 2015)

Plant, Cell & Environment Content Alert: 38, 9 (September 2015)

Rice responses to rising temperatures – challenges, perspectives and future directions (pages 1686–1698)
S. V. K. JAGADISH, M. V. R. MURTY and W. P. QUICK Article first published online: 9 OCT 2014 | DOI: 10.1111/pce.12430
In tropical rice growing regions higher temperatures know to negatively affect sensitive reproductive processes under fully flooded conditions can potentially induce greater damage under scenarios wherein water-saving technologies would be adopted. The rapid increase in night temperature compared to the day temperature both at the regional and global scale necessitates the need to understand the differential responses of rice, with the trend projected to continue in the future. Our review provides an analysis of the above aspects and in addition the need to establish a reliable and high throughput marker for estimating pollen viability; possible routes inducing yield and quality losses due to poor grain filling under

increasing temperatures are highlighted. Finally we quantify the heat stress induced reduction in spikelet fertility taking South Asia as a case study and provide future research directions that would help minimize heat stress induced damage.

Responses of tree species to heat waves and extreme heat events (pages 1699–1712)
ROBERT TESKEY, TIMOTHY WERTIN, INGVAR BAUWERAERTS, MAARTEN AMEYE, MARY ANNE MCGUIRE and KATHY STEPPE Article first published online: 1 SEP 2014 | DOI: 10.1111/pce.12417
The number and intensity of heat waves has increased in recent decades and this trend is likely to continue throughout the 21st Century. This review summarizes our current understanding of how extreme heat events affect tree functions from the cellular to the whole plant scale. When drought stress accompanies heat waves, heat stress is exacerbated and can lead to tree mortality. Although there have been only few studies to date, there is evidence of within-species genetic variation that could be exploited to increase heat stress resistance in trees. Understanding the mechanisms of tree responses to extreme temperature events may be critically important for understanding how tree species will be affected by climate change.

Prospects of engineering thermotolerance in crops through modulation of heat stress transcription factor and heat shock protein networks (pages 1881–1895)
SOTIRIOS FRAGKOSTEFANAKIS, SASCHA RÖTH, ENRICO SCHLEIFF and KLAUS-DIETER SCHARF Article first published online: 6 AUG 2014 | DOI: 10.1111/pce.12396
The review compiles recent studies on model and crop plants which suggest that genetic engineering of Hsf-chaperone networks can improve thermotolerance. Although conserved in their basic functions, species-specific variations in the composition and interaction of the two central networks involved in regulation of stress response and maintenance of protein homeostasis under stressful but also normal growth conditions have been described. Hence, manipulations on the molecular level guided only by model plant-specific knowledge transfer might cause unexpected pleiotropic effects. Detailed knowledge of the multi-level regulatory mechanisms controlling the availability and activity of Hsf-chaperone networks undoubtedly is required to unravel promising targets for manipulation and selection of cultivars that can combine both high productivity and enhanced thermotolerance.

Alzheimer's and Parkinson's diseases: The prion concept in relation to assembled Aβ, tau, and α-synuclein Michel Goedert *Science 7 August 2015: 1255555* Full Text (PDF)

Parkinson's disease and Alzheimer's disease are progressive neurodegenerative diseases with increasing prevalence in our aging populations. Recent evidence suggests that some of the molecular mechanisms involved in the pathology of these diseases have similarities to those observed in infectious prion diseases such as bovine spongiform encephalopathy (mad cow disease). Goedert reviews how the spread of a variety of pathological protein aggregates is involved in neurodegenerative disease.

Current Opinion in Plant Biology: Alert 31 July-6 August
New insights into redox control of starch degradation Review Article *Pages 1-9*
Diana Santelia, Paolo Trost, Francesca Sparla

The increasing importance of distinguishing among plant nitrogen sources Review Article *Pages 10-16*
Arnold J Bloom

Metabolites and chloroplast retrograde signaling Review Article *Pages 32-38*
Wei Chi, Peiqiang Feng, Jinfang Ma, Lixin Zhang

Crop yield: challenges from a metabolic perspective Review Article *Pages 79-89*
Magdalena Rossi, Luisa Bermudez, Fernando Carrari

Measurement of plant growth in view of an integrative analysis of regulatory networks Review Article *Pages 90-97* Nathalie Wuyts, Stijn Dhondt, Dirk Inzé

Plant nitrogen assimilation and its regulation: a complex puzzle with missing pieces Review Article *Pages 115-122* Anne Krapp
Science 24 April 2015: Vol. 348 no. 6233 pp. 442-444 DOI: 10.1126/science.aaa5945

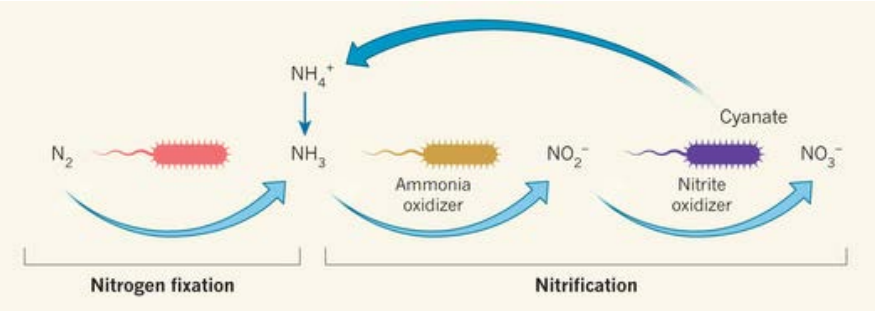
The mutagenic chain reaction: A method for converting heterozygous to homozygous mutations Valentino M. Gantz*, Ethan Bier*

An organism with a single recessive loss-of-function allele will typically have a wild-type phenotype, whereas individuals homozygous for two copies of the allele will display a mutant phenotype. We have developed a method called the mutagenic chain reaction (MCR), which is based on the CRISPR/Cas9 genome-editing system for generating autocatalytic mutations, to produce homozygous loss-of-function mutations. In *Drosophila*, we found that MCR mutations efficiently spread from their chromosome of origin to the homologous chromosome, thereby converting heterozygous mutations to homozygosity in the vast majority of somatic and germline cells. MCR technology should have broad applications in diverse organisms.

Nature

Cyanate as an energy source for nitrifiers Marton Palatinszky, Craig Herbold, Nico Jehmlich, Mario Pogoda, Ping Han+ et al.

The ammonia-oxidizing archaeon *Nitrososphaera gargensis* can utilize cyanate as the only source of energy for growth due to the presence of a cyanase enzyme, and cyanase-encoding nitrite-oxidizing bacteria can work together with cyanase-negative ammonia oxidizers to collectively grow on cyanate via reciprocal feeding; cyanases are widespread in the environment according to metagenomic data sets, pointing to the potential importance of cyanate in the nitrogen cycle.



Nitrification is a two-step process. First, one set of microorganisms (bacteria and archaea) oxidize ammonia (NH_3) to nitrite (NO_2^-); the ammonia is provided by bacteria that fix nitrogen gas (N_2). Nitrite is then oxidized to nitrate (NO_3^-) by other bacteria. Both sets of organisms gain energy from these reactions, which they use to produce new biomass; the carbon for this is obtained through carbon dioxide fixation by the ammonia oxidizers. Palatinszky *et al.*[3] show that this fuel provision also occurs in the opposite direction. They find that nitrite-oxidizing bacteria express the enzyme cyanase, which allows them to convert cyanate — a breakdown product of environmental cyanide — into ammonium (NH_4^+) and CO_2. The ammonium is converted to ammonia by normal environmental pH conditions. Thus, ammonia-oxidizing bacteria need not rely solely on nitrogen-fixing bacteria to provide their ammonia substrate.

Protein synthesis by ribosomes with tethered subunits
Cédric Orelle,Erik D. Carlson, Teresa Szal, Tanja Florin, Michael C. Jewett & Alexander S. Mankin

Nature 524, 119–124 (06 August 2015) doi:10.1038/nature14862 PDF

The ribosome is a ribonucleoprotein machine responsible for protein synthesis. In all kingdoms of life it is composed of two subunits, each built on its own ribosomal RNA (rRNA) scaffold. The independent but coordinated functions of the subunits, including their ability to associate at initiation, rotate during elongation, and dissociate after protein release, are an established model of protein synthesis. Furthermore, the bipartite nature of the ribosome is presumed to be essential for biogenesis, since dedicated assembly factors keep immature ribosomal subunits apart and prevent them from translation initiation[1]. Free exchange of the subunits limits the development of specialized orthogonal genetic systems that could be evolved for novel functions without interfering with native translation. Here we show that ribosomes with tethered and thus inseparable subunits (termed Ribo-T) are capable of successfully carrying out protein synthesis. By engineering a hybrid rRNA composed of both small and large subunit rRNA sequences, we produced a functional ribosome in which the subunits are covalently linked into a single entity by short RNA linkers. Notably, Ribo-T was not only functional *in vitro*, but was also able to support the growth of *Escherichia coli* cells even in the absence of wild-type ribosomes. We used Ribo-T to create the first fully orthogonal ribosome–messenger RNA system, and demonstrate its evolvability by selecting otherwise dominantly lethal rRNA mutations in the peptidyl transferase centre that facilitate the translation of a problematic protein sequence. Ribo-T can be used for exploring poorly understood functions of the ribosome, enabling orthogonal genetic systems, and engineering ribosomes with new functions.

Current Opinion in Cell Biology: Alert 29 July-4 August

The mitochondria–plasma membrane contact site Review Article *Pages 1-6* Benedikt Westermann

Mitochondria are dynamic organelles that are highly motile and frequently fuse and divide. It has recently become clear that their complex behavior is governed to a large extent by interactions with other cellular structures. This review will focus on a mitochondria–plasma membrane tethering complex that was recently discovered and molecularly analyzed in budding yeast, the Num1/Mdm36 complex. This complex attaches mitochondria to the cell cortex and ensures that a portion of the organelles is retained in mother cells during cell division. At the same time, it supports mitochondrial division and integrates mitochondrial dynamics into cellular architecture. Recent evidence suggests that similar mechanisms might exist also in mammalian cells.

Overexpression of a small heat-shock-protein gene enhances tolerance to abiotic stresses in rice (pages 384–393)

Anquan Wang, Xiaohong Yu, Yun Mao, Ying Liu, Guoqing Liu, Yongsheng Liu and Xiangli Niu

Article first published online: 25 JUN 2015 | DOI: 10.1111/pbr.12289

PLOS Biology New Articles Published

The BEACH Domain Protein SPIRRIG Is Essential for Arabidopsis Salt Stress Tolerance and Functions as a Regulator of Transcript Stabilization and Localization

Alexandra Steffens, Andrea Bräutigam, Marc Jakoby, Martin Hülskamp

Members of the highly conserved class of BEACH domain containing proteins (BDCPs) have been established as broad facilitators of protein–protein interactions and membrane dynamics in the context of human diseases like albinism, bleeding diathesis, impaired cellular immunity, cancer predisposition, and neurological dysfunctions. Also, the Arabidopsis thaliana BDCP SPIRRIG (SPI) is important for membrane integrity, as *spi* mutants exhibit split vacuoles. In this work, we report a novel molecular function of the BDCP SPI in ribonucleoprotein particle formation. We show that SPI interacts with the P-body core component DECAPPING PROTEIN 1 (DCP1), associates to mRNA processing bodies (P-bodies), and regulates their assembly upon salt stress. The finding that *spi* mutants exhibit salt hypersensitivity suggests that the local function of SPI at P-bodies is of biological relevance. Transcriptome-wide analysis revealed qualitative differences in the salt stress-regulated transcriptional response of Col-0 and *spi*. We show that SPI regulates the salt stress-dependent post-transcriptional stabilization, cytoplasmic agglomeration, and localization to P-bodies of a subset of salt stress-regulated mRNAs. Finally, we show that the PH-BEACH domains of SPI and its human homolog FAN (Factor Associated with Neutral sphingomyelinase activation) interact with DCP1 isoforms from plants, mammals, and yeast, suggesting the evolutionary conservation of an association of BDCPs and P-bodies.

Sirt1-deficiency causes defective protein quality control.
Sci Rep. 2015 Jul 29;5:12613. PMID: 26219988 [PubMed - in process]

Correa-Aragunde N, Cejudo FJ, Lamattina L.
Nitric oxide is required for the auxin-induced activation of NADPH-dependent thioredoxin reductase and protein denitrosylation during root growth responses in arabidopsis.
Ann Bot. 2015 Jul 30;. [Epub ahead of print]
PMID: 26229066 [PubMed - as supplied by publisher]

CELL

Evolution of the Grain Dispersal System in Barley *Cell, Volume 162, Issue 3, 30 July 2015, Pages 527-539*

Selection and domestication of plants with genes that prevent grains from shattering in cereals was essential for human civilization's transition to agriculture-based societies. In this issue, Pourkheirandish et al. show that domestication of barley required evolution of a molecular system distinct from other grains, such as rice and maize, and reveal that present-day cultivars derive from two ancient domestication centers.

An Essential Role of the Mitochondrial Electron Transport Chain in Cell Proliferation Is to Enable Aspartate Synthesis Original Research Article *Pages 540-551*

Kıvanç Birsoy, Tim Wang, Walter W. Chen, Elizaveta Freinkman, Monther Abu-Remaileh, David M. Sabatini

Supporting Aspartate Biosynthesis Is an Essential Function of Respiration in Proliferating Cells *Pages 552-563*

Lucas B. Sullivan, Dan Y. Gui, Aaron M. Hosios, Lauren N. Bush, Elizaveta Freinkman, Matthew G. Vander Heiden

The Plant Journal Content Alert (New Articles)

Increased glutathione contributes to stress tolerance and global translational changes in Arabidopsis

Mei-Chun Cheng, Ko Ko, Wan-Ling Chang, Wen-Chieh Kuo, Guan-Hong Chen and Tsan-Piao Lin
Accepted manuscript online: 25 JUL 2015 07:16AM EST | DOI: 10.1111/tpj.12940

Thornell E, Aquilina A.
Regulation of Î±A- and Î±B-crystallins via phosphorylation in cellular homeostasis.
Cell Mol Life Sci. 2015 Jul 26;. [Epub ahead of print] PMID: 26210153 [PubMed - as supplied by publisher]

Caspeta L, Nielsen J.
Thermotolerant Yeast Strains Adapted by Laboratory Evolution Show Trade-Off at Ancestral Temperatures and Preadaptation to Other Stresses. MBio. 2015 Jul 21;6(4). PMID: 26199325 [PubMed - as supplied by publisher]

Zhang B, Zheng J, Peng Y, Liu X, Hoffmann AA, Ma CS.
Stress Responses of Small Heat Shock Protein Genes in Lepidoptera Point to Limited Conservation of Function across Phylogeny. PLoS One. 2015;10(7):e0132700. PMID: 26196395 [PubMed - as supplied by publisher]

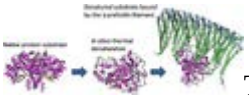
Zhang J, Ieong KW, Johansson M, Ehrenberg M.
Accuracy of initial codon selection by aminoacyl-tRNAs on the mRNA-programmed bacterial ribosome.
Proc Natl Acad Sci U S A. 2015 Jul 20;. [Epub ahead of print]
PMID: 26195797 [PubMed - as supplied by publisher]

The Plant Journal Content Alert (New Articles)
A tomato phloem-mobile protein regulates the shoot:root ratio by mediating auxin response in distant organs
Ziv Spiegelman, Byung-Kook Ham, Zhaoliang Zhang, Ted W. Toal, Siobhan M. Brady, Yi Zheng, Zhangjun Fei, William J. Lucas and Shmuel Wolf Accepted manuscript online: 14 JUL 2015 11:09AM EST | DOI: 10.1111/tpj.12932

The proteolysis adaptor, NblA, is essential for degradation of the core pigment of the cyanobacterial light harvesting complex Eleonora Sendersky, Noga Kozer, Mali Levi, Michael Moizik, Yuval Garini, Yaron Shav-Tal and Rakefet Schwarz Accepted manuscript online: 14 JUL 2015 10:54AM EST | DOI: 10.1111/tpj.12931

Functional characterization of mutants affected in the carbonic anhydrase domain of the respiratory complex I in Arabidopsis thaliana Débora Soto, Juan Pablo Córdoba, Fernando Villarreal, Carlos Bartoli, Jessica Schmitz, Veronica G. Maurino, Hans Peter Braun, Gabriela C. Pagnussat and Eduardo Zabaleta
Accepted manuscript online: 3 JUL 2015 08:51AM EST | DOI: 10.1111/tpj.12930

FEBS Journal Content Alert: 282, 15 (August 2015)
Oligomeric assembly is required for chaperone activity of the filamentous γ-prefoldin (pages 2985–2997)
Dominic J. Glover and Douglas S. Clark Article first published online: 2 JUL 2015 | DOI: 10.1111/febs.13341



This study investigates the relationship between the structure and morphology of a filamentous chaperone, γ-prefoldin (γPFD), and its ability to prevent protein aggregation. A combination of molecular dynamic simulations and chaperone assays were used to show that the number of γPFD subunits required to stabilize a substrate from thermal aggregation is dependent upon the size of the substrate.

The Plant Journal Content Alert: 83, 3 (August 2015)
***PAY1* improves plant architecture and enhances grain yield in rice (pages 528–536)**
Lei Zhao, Lubin Tan, Zuofeng Zhu, Langtao Xiao, Daoxin Xie and Chuanqing Sun
Article first published online: 7 JUL 2015 | DOI: 10.1111/tpj.12905
This study describes the identification and functional analysis of the *PLANT ARCHITECTURE AND YIELD 1* (*PAY1*) gene in rice, which affects plant architecture and grain yield in rice. *PAY1* can optimize plant architecture through altering auxin polar transport and distribution, leading to more desirable plant architecture and increased grain yield in rice.

Journal of Agronomy and Crop Sci... Content Alert (New Articles)
Heat Stress Effects are Stronger on Spikelets Than on Flag Leaves in Rice Due to Differences in Dissipation Capacity
C. X. Zhang, G. F. Fu, X. Q. Yang, Y. J. Yang, X. Zhao, T. T. Chen, X. F. Zhang, Q. Y. Jin and L. X. Tao
Article first published online: 28 JUL 2015 | DOI: 10.1111/jac.12138