Keith

The Populus trichocarpa PtHSP17.8 involved in heat and salt stress tolerances

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5State Key Laboratory of Tree Genetics and Breeding, Key Laboratory of Tree Breeding and Cultivation of the State Forestry Administration, Research Institute of Forestry, Chinese Academy of Forestry, Beijing, 100091, China.
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PtHSP17.8 was regulated by various abiotic stresses. Overexpression of PtHSP17.8 enhanced the tolerance to heat and salt stresses through maintain ROS homeostasis and cooperate with stress-related genes in Arabidopsis. Small heat shock proteins (sHSPs) play important roles in response to diverse biotic and abiotic stresses, especially in heat tolerance. However, limited information is available on the stress tolerance roles of sHSPs in woody species. To explore the function of sHSPs in poplar, we isolated and characterized PtHSP17.8 from Populus trichocarpa. Phylogenetic analysis and subcellular localization revealed that PtHSP17.8 was a cytosolic class I sHSP. The gene expression profile of PtHSP17.8 in various tissues showed that it was significantly accumulated in stem and root, which was consistent with the GUS expression pattern driven by promoter of PtHSP17.8. The expression of PtHSP17.8 could be induced by various abiotic stresses and significantly activated by heat stress. Overexpression of PtHSP17.8 enhanced the tolerance to heat and salt stresses in Arabidopsis. The seedling survival rate, root length, relative water content, antioxidative enzyme activities, proline, and soluble sugar content were increased in transgenic Arabidopsis under heat and salt stresses, but not in normal condition. The co-expression network of PtHSP17.8 were constructed and demonstrated many stress responsive genes included. The stress-related genes in the co-expression network were up-regulated in the PtHSP17.8 overexpression seedlings. These results suggest that PtHSP17.8 confers heat and salt tolerances in plants.

Gene Expression Profile in the Long-Living Lotus: Insights into the Heat Stress Response Mechanism

PLoS One. 2016 Mar 28;11(3):e0152540.

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Lotus (Nelumbo Adans) is an aquatic perennial plant that flourished during the middle Albian stage. In this study, we characterized the digital gene expression signatures for China Antique lotus under conditions of heat shock stress. Using RNA-seq technology, we sequenced four libraries, specifically, two biological replicates for control plant samples and two for heat stress samples. As a result, 6,528,866 to 8,771,183 clean reads were mapped to the reference genome, accounting for 92-96% total clean reads. A total of 396 significantly altered genes were detected across the genome, among which 315 were upregulated and 81 were downregulated by heat shock stress. Gene ontology (GO) enrichment of differentially expressed genes revealed protein folding, cell morphogenesis and cellular component morphogenesis as the top three functional terms under heat shock stress. Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis led to the identification of protein processing in endoplasmic reticulum, plant-pathogen interactions, spliceosome, endocytosis, and protein export as significantly enriched pathways. Among the upregulated genes, small heat shock proteins (sHsps) and genes related to cell morphogenesis were particularly abundant under heat stress. Data from the current study provide valuable clues that may help elucidate the molecular events underlying heat stress response in China Antique lotus.

Arabidopsis AtDjA3 Null Mutant Shows Increased Sensitivity to Abscisic Acid, Salt, and Osmotic Stress in Germination and Post-germination Stages.

Front Plant Sci. 2016 Feb 25;7:220.

Salas-Muñoz S1, Rodríguez-Hernández AA1, Ortega-Amaro MA1, Salazar-Badillo FB1, Jiménez-Bremont JF1.

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DnaJ proteins are essential co-chaperones involved in abiotic and biotic stress responses. Arabidopsis AtDjA3 gene encodes a molecular co-chaperone of 420

amino acids, which belongs to the J-protein family. In this study, we report the functional characterization of the AtDjA3 gene using the Arabidopsis knockout line designated j3 and the 35S::AtDjA3 overexpression lines. Loss of AtDjA3 function was associated with small seed production. In fact, j3 mutant seeds showed a reduction of 24% in seed weight compared to Col-0 seeds. Expression analysis showed that the AtDjA3 gene was modulated in response to NaCl, glucose, and abscisic acid (ABA). The j3 line had increased sensitivity to NaCl and glucose treatments in the germination and cotyledon development in comparison to parental Col-0. Furthermore, the j3 mutant line exhibited higher ABA sensitivity in comparison to parental Col-0 and 35S::AtDjA3 overexpression lines. In addition, we examined the expression of ABI3 gene, which is a central regulator in ABA signaling, in j3 mutant and 35S::AtDjA3 overexpression lines. Under 5 μM ABA treatment at 24 h, j3 mutant seedlings displayed higher ABI3 expression, whereas in 35S::AtDjA3 overexpression lines, ABI3 gene expression was repressed. Taken together, these results demonstrate that the AtDjA3 gene is involved in seed development and abiotic stress tolerance.

Transcriptional induction of the heat shock protein B8 mediates the clearance of misfolded proteins responsible for motor neuron diseases.

Sci Rep. 2016 Mar 10;6:22827.

Crippa V1, D'Agostino VG2, Cristofani R3, Rusmini P3, Cicardi ME3, Messi E3, Loffredo R2, Pancher M2, Piccolella M3, Galbiati M3, Meroni M3, Cereda C1, Carra S4, Provenzani A2, Poletti A3,5.

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Neurodegenerative diseases (NDs) are often associated with the presence of misfolded protein inclusions. The chaperone HSPB8 is upregulated in mice, the human brain and muscle structures affected during NDs progression. HSPB8 exerts a potent pro-degradative activity on several misfolded proteins responsible for familial NDs forms. Here, we demonstrated that HSPB8 also counteracts accumulation of aberrantly localized misfolded forms of TDP-43 and its 25 KDa fragment involved in most sporadic cases of Amyotrophic Lateral Sclerosis (sALS) and of Fronto Lateral Temporal Dementia (FLTD). HSPB8 acts with BAG3 and the

HSP70/HSC70-CHIP complex enhancing the autophagic removal of misfolded proteins. We performed a high-through put screening (HTS) to find small molecules capable of inducing HSPB8 in neurons for therapeutic purposes. We identified two compounds, colchicine and doxorubicin, that robustly up-regulated HSPB8 expression. Both colchicine and doxorubicin increased the expression of the master regulator of autophagy TFEB, the autophagy linker p62/SQSTM1 and the autophagosome component LC3. In line, both drugs counteracted the accumulation of TDP-43 and TDP-25 misfolded species responsible for motoneuronal death in sALS. Thus, analogs of colchicine and doxorubicin able to induce HSPB8 and with better safety and tolerability may result beneficial in NDs models.

Oligomers of Heat-Shock Proteins: Structures That Don't Imply Function

PLoS Comput Biol. 2016 Feb 29;12(2):e1004756.

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Most proteins must remain soluble in the cytosol in order to perform their biological functions. To protect against undesired protein aggregation, living cells maintain a population of molecular chaperones that ensure the solubility of the proteome. Here we report simulations of a lattice model of interacting proteins to understand how low concentrations of passive molecular chaperones, such as small heat-shock proteins, suppress thermodynamic instabilities in protein solutions. Given fixed concentrations of chaperones and client proteins, the solubility of the proteome can be increased by tuning the chaperone-client binding strength. Surprisingly, we find that the binding strength that optimizes solubility while preventing irreversible chaperone binding also promotes the formation of weakly bound chaperone oligomers, although the presence of these oligomers does not significantly affect the thermodynamic stability of the solution. Such oligomers are commonly observed in experiments on small heat-shock proteins, but their connection to the biological function of these chaperones has remained unclear. Our simulations suggest that this clustering may not have any essential biological function, but rather emerges as a natural side-effect of optimizing the thermodynamic stability of the proteome.

An atomistic view of Hsp70 allosteric crosstalk: from the nucleotide to the substrate binding domain and back.

Sci Rep. 2016 Mar 30;6:23474.

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The Hsp70 is an allosterically regulated family of molecular chaperones. They consist of two structural domains, NBD and SBD, connected by a flexible linker. ATP hydrolysis at the NBD modulates substrate recognition at the SBD, while peptide binding at the SBD enhances ATP hydrolysis. In this study we apply Molecular Dynamics (MD) to elucidate the molecular determinants underlying the allosteric communication from the NBD to the SBD and back. We observe that local structural and dynamical modulation can be coupled to large-scale rearrangements, and that different combinations of ligands at NBD and SBD differently affect the SBD domain mobility. Substituting ADP with ATP in the NBD induces specific structural changes involving the linker and the two NBD lobes. Also, a SBD-bound peptide drives the linker docking by increasing the local dynamical coordination of its C-terminal end: a partially docked DnaK structure is achieved by combining ATP in the NBD and peptide in the SBD. We propose that the MD-based analysis of the inter domain dynamics and structure modulation could be used as a tool to computationally predict the allosteric behaviour and functional response of Hsp70 upon introducing mutations or binding small molecules, with potential applications for drug discovery.

Lens regeneration using endogenous stem cells with gain of visual function

Nature **531**, 323–328 (17 March 2016)

Haotian Lin, Hong Ouyang, Jie Zhu, Shan Huang, Zhenzhen Liu, Shuyi Chen, Guiqun Cao, Gen Li, Robert A. J. Signer, Yanxin Xu, Christopher Chung, Ying Zhang, Danni Lin, Sherrina Patel, Frances Wu, Huimin Cai, Jiayi Hou, Cindy Wen, Maryam Jafari, Xialin Liu, Lixia Luo, Jin Zhu, Austin Qiu, Rui Hou, Baoxin Chen *et al.*

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Clinical and Translational Research Institute, University of California, San Diego, La Jolla, California 92093, USA
Veterans Administration Healthcare System, San Diego, California 92093, USA

The repair and regeneration of tissues using endogenous stem cells represents an ultimate goal in regenerative medicine. To our knowledge, human lens regeneration has not yet been demonstrated. Currently, the only treatment for cataracts, the leading cause of blindness worldwide, is to extract the cataractous lens and implant an artificial intraocular lens. However, this procedure poses notable risks of complications. Here we isolate lens epithelial stem/progenitor cells (LECs) in mammals and show that *Pax6* and *Bmi1* are required for LEC renewal. We design a surgical method of cataract removal that preserves endogenous LECs and achieves functional lens regeneration in rabbits and macaques, as well as in human infants with cataracts. Our method differs conceptually from current practice, as it preserves endogenous LECs and their natural environment maximally, and regenerates lenses with visual function. Our approach demonstrates a novel treatment strategy for cataracts and provides a new paradigm for tissue regeneration using endogenous stem cells.

Damian

Eroglu, E., Gottschalk, B., Charoensin, S., Blass, S., Bischof, H., Rost, R., Madreiter-Sokolowski, C. T., Pelzmann, B., Bernhart, E., Sattler, W., Hallstrom, S., Malinski, T., Waldeck-Weiermair, M., Graier, W. F., and Malli, R. (2016) Development of novel FP-based probes for live-cell imaging of nitric oxide dynamics, *Nat. Commun. 7*.

Trabjerg, E., Jakobsen, R. U., Mysling, S., Christensen, S., Jørgensen, T. J. D., and Rand, K. D. (2015) Conformational Analysis of Large and Highly Disulfide-Stabilized Proteins by Integrating Online Electrochemical Reduction into an Optimized H/D Exchange Mass Spectrometry Workflow, *Anal. Chem. 87*, 8880-8888.

Jarrett

Elimination of HIV-1 Genomes from Human T-lymphoid Cells by CRISPR/Cas9 Gene Editing
Rafal Kaminski, Yilan Chen, Tracy Fischer, Ellen Tedaldi, Alessandro Napoli, Yonggang Zhang, Jonathan Karn, Wenhui Hu & Kamel Khalili
NATURE Scientific Reports 6, Article number: 22555 (2016)
http://www.nature.com/articles/srep22555

Boreal and temperate trees show strong acclimation of respiration to warming
Peter B. Reich, Kerrie M. Sendall, Artur Stefanski, Xiaorong Wei,Roy L. Rich & Rebecca A. Montgomery
Nature **531**, 633–636 (31 March 2016)
http://www.nature.com/nature/journal/v531/n7596/pdf/nature17142.pdf
Structure of promoter-bound TFIID and model of human pre-initiation complex assembly
Robert K. Louder, Yuan He, José Ramón López-Blanco, Jie Fang, Pablo Chacón & Eva Nogales

Nature **531**, 604–609 (31 March 2016)
http://www.nature.com/nature/journal/v531/n7596/full/nature17394.html

Minsoo

1. Mol Cell. 2016 Mar 17;61(6):914-24. doi: 10.1016/j.molcel.2016.02.030.

Digital Quantification of Proteins and mRNA in Single Mammalian Cells.

Albayrak C(1), Jordi CA(1), Zechner C(1), Lin J(1), Bichsel CA(1), Khammash M(1), Tay S(2).

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Absolute quantification of macromolecules in single cells is critical for understanding and modeling biological systems that feature cellular heterogeneity. Here we show extremely sensitive and absolute quantification of both proteins and mRNA in single mammalian cells by a very practical workflow that combines proximity ligation assay (PLA) and digital PCR. This digital PLA method has femtomolar sensitivity, which enables the quantification of very small protein concentration changes over its entire 3-log dynamic range, a quality necessary for accounting for single-cell heterogeneity. We counted both endogenous (CD147) and exogenously expressed (GFP-p65) proteins from hundreds of
single cells and determined the correlation between CD147 mRNA and the protein it encodes. Using our data, a stochastic two-state model of the central dogma was constructed and verified using joint mRNA/protein distributions, allowing us to estimate transcription burst sizes and extrinsic noise strength and calculate the transcription and translation rate constants in single mammalian cells.

2. Nat Methods. 2016 Mar 28. doi: 10.1038/nmeth.3810. [Epub ahead of print]

**Robust transcriptome-wide discovery of RNA-binding protein binding sites with
enhanced CLIP (eCLIP).**

Van Nostrand EL(1,)(2,)(3), Pratt GA(1,)(2,)(3,)(4), Shishkin AA(5), Gelboin-Burkhart C(1,)(2,)(3), Fang MY(1,)(2,)(3), Sundararaman B(1,)(2,)(3), Blue SM(1,)(2,)(3), Nguyen TB(1,)(2,)(3), Surka C(5), Elkins K(1,)(2,)(3), Stanton R(1,)(2,)(3), Rigo F(6), Guttman M(5), Yeo GW(1,)(2,)(3,)(4,)(7,)(8).

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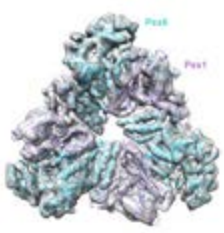
As RNA-binding proteins (RBPs) play essential roles in cellular physiology by interacting with target RNA molecules, binding site identification by UV crosslinking and immunoprecipitation (CLIP) of ribonucleoprotein complexes is critical to understanding RBP function. However, current CLIP protocols are technically demanding and yield low-complexity libraries with high experimental failure rates. We have developed an enhanced CLIP (eCLIP) protocol that decreases requisite amplification by ~1,000-fold, decreasing discarded PCR duplicate reads by ~60% while maintaining single-nucleotide binding resolution. By simplifying the generation of paired IgG and size-matched input controls, eCLIP improves specificity in the discovery of authentic binding sites. We generated 102 eCLIP experiments for 73 diverse RBPs in HepG2 and K562 cells (available at https://www.encodeproject.org), demonstrating that eCLIP enables large-scale and robust profiling, with amplification and sample requirements similar to those of ChIP-seq. eCLIP enables integrative analysis of diverse RBPs to reveal factor-specific profiles, common artifacts for CLIP and RNA-centric perspectives on RBP activity.

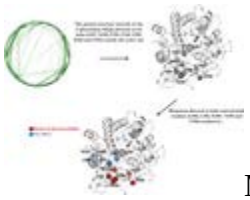
March 28 2016
A proposal regarding best practices for validating the identity of genetic stocks and the effects of genetic variants
Detlef Weigel, Joy Bergelson, Edward S. Buckler, Joseph R. Ecker, and Magnus Nordborg
Plant Cell 2016 tpc.15.00502; Advance Publication March 8, 2016;
doi:10.1105/tpc.15.00502 **OPEN**
http://www.plantcell.org/content/early/2016/03/08/tpc.15.00502
FEBS Journal Content Alert: 283, 6 (March 2016)

Structures of the double-ring AAA ATPase Pex1–Pex6 involved in peroxisome biogenesis (pages 986–992)
Dongyan Tan, Neil B. Blok, Tom A. Rapoport and Thomas Walz
Article first published online: 12 NOV 2015 | DOI: 10.1111/febs.13569



The Pex1/Pex6 complex is a member of the AAA family of ATPases that is involved in peroxisome biogenesis. Recently, cryo-electron microscopy structures have been determined of the Pex1/Pex6 complex in different nucleotide states. This Structural Snapshot describes the structural features of the complex, their implications for its function, as well as questions that still await answers.

Protein thermal denaturation is modulated by central residues in the protein structure network (pages 1124–1138)
Valquiria P. Souza, Cecília M. Ikegami, Guilherme M. Arantes and Sandro R. Marana
Article first published online: 2 FEB 2016 | DOI: 10.1111/febs.13659



Mutations directed to seven hubs of the protein structure network of the β-glucosidase Sfβgly reduced its thermostability. Moreover, mutations directed to the vicinity of a hub residue also caused significant decreases in the Sfβgly thermostability. On the contrary mutations directed to non-hub residues had no effect. These results show that protein structure networks are robust, whereas attacks on central nodes cause network failure.

The Plant Journal Content Alert (New Articles)
Bacterial Microcompartments as Metabolic Modules for Plant Synthetic Biology
C. Raul Gonzalez-Esquer, Sarah E. Newnham and Cheryl A. Kerfeld
Accepted manuscript online: 16 MAR 2016 08:51AM EST | DOI: 10.1111/tpj.13166

Transcriptome dynamics of Arabidopsis during sequential biotic and abiotic stresses
Silvia Coolen, Silvia Proietti, Richard Hickman, Nelson H. Davila Olivas, Ping-Ping Huang, Marcel C. Van Verk, Johan A. Van Pelt, Alexander H.J. Wittenberg, Martin De Vos, Marcel Prins, Joop J.A. Van Loon, Mark G.M. Aarts, Marcel Dicke, Corné M.J. Pieterse and Saskia C.M. Van Wees
Accepted manuscript online: 15 MAR 2016 10:40PM EST | DOI: 10.1111/tpj.13167

Journal of Agronomy and Crop Sci... Content Alert (New Articles)
Susceptibility of Faba Bean (***Vicia faba*** L.) to Heat Stress During Floral Development and Anthesis
J. Bishop, S. G. Potts and H. E. Jones
Article first published online: 21 MAR 2016 | DOI: 10.1111/jac.12172

***Science*, March 25 p. 10.1126/science.aad6253**
Designing and building a minimal genome

A goal in biology is to understand the molecular and biological function of every gene in a cell. One way to approach this is to build a minimal genome that includes only the genes essential for life. In 2010, a 1079-kb genome based on the genome of *Mycoplasma mycoides* (JCV-syn1.0) was chemically synthesized and supported cell growth when transplanted into cytoplasm. Hutchison III *et al.* used a design, build, and test cycle to reduce this genome to 531 kb (473 genes). The resulting JCV-syn3.0 retains genes involved in key processes such as transcription and translation, but also contains 149 genes of unknown function.

The Plant Journal Content Alert (New Articles)

Large-scale atlas of microarray data reveals the distinct expression landscape of different tissues in Arabidopsis
Fei He, Shinjae Yoo, Daifeng Wang, Sunita Kumari, Mark Gerstein, Doreen Ware and Sergei Maslov
Accepted manuscript online: 25 MAR 2016 09:45AM EST | DOI: 10.1111/tpj.13175

Current Opinion in Chemical Biology: Alert 25 March-31 March
Dynamics of co-translational protein targeting Review Article
Pages 79-86
Margaret M Elvekrog, Peter Walter
Development of novel FP-based probes for live-cell imaging of nitric oxide dynamics
Emrah Eroglu, Benjamin Gottschalk, Suphachai Charoensin, et al
Nature Communications 7,Article number:10623 doi:10.1038/ncomms10623
Nitric oxide ($^{NO\bullet}$) is a free radical with a wide range of biological effects, but practically impossible to visualize in single cells. Here we report the development of novel multicoloured fluorescent quenching-based $^{NO\bullet}$probes by fusing a bacteria-derived $^{NO\bullet}$-binding domain close to distinct fluorescent protein variants. These genetically encoded $^{NO\bullet}$probes, referred to as geNOps, provide a selective, specific and real-time read-out of cellular $^{NO\bullet}$dynamics and, hence, open a new era of $^{NO\bullet}$bioimaging. The combination of geNOps with a Ca^{2+} sensor allowed us to visualize $^{NO\bullet}$and Ca^{2+} signals simultaneously in single endothelial cells. Moreover, targeting of the $^{NO\bullet}$probes was used to detect $^{NO\bullet}$ signals within mitochondria. The geNOps are useful new tools to further investigate and understand the complex patterns of $^{NO\bullet}$signalling on the single (sub)cellular level.

Starting too soon: upstream reading frames repress downstream translation
Anna M McGeachy and Nicholas T Ingolia

http://EMBOJ.embopress.org/content/35/7/699?etoc

The analysis of ribosome profiling data across three vertebrate species demonstrates the global effect of uORF-dependent translational control of gene expression.

Upstream ORFs are prevalent translational repressors in vertebrates
Timothy G Johnstone, Ariel A Bazzini, and Antonio J Giraldez

Published online 19.02.2016

http://EMBOJ.embopress.org/content/35/7/706?etoc

Upstream open reading frames (uORFs) are found in many genes, but their functional impact is unclear. This study explores their abundant translation, conservation, and potent role in shaping the vertebrate
translational landscape.

The chloroplast NADPH thioredoxin reductase C, NTRC, controls non-photochemical quenching of light energy and photosynthetic electron transport in ***Arabidopsis*** (pages 804–822)
Belén Naranjo, Clara Mignée, Anja Krieger-Liszkay, Dámaso Hornero-Méndez, Lourdes Gallardo-Guerrero, Francisco Javier Cejudo and Marika Lindahl
Article first published online: 18 JAN 2016 | DOI: 10.1111/pce.12652

Excess excitation and the means by which plants respond to defend themselves against light-induced damage have been extensively studied, and the importance of qE is well documented. Nevertheless, the success of a plant also depends on the capacity to restrict the induction of acclimation mechanisms, such as qE, in order to avoid wasting the energy absorbed. Given the possible redox control and implication of thioredoxins in protection mechanisms against excess light, we have investigated the role of the chloroplast NADPH-dependent thioredoxin reductase NTRC. This enzyme has been previously implied in peroxide detoxification and abiotic stress tolerance. Surprisingly, NTRC proved to be essential, not for the induction of protection mechanisms under strong irradiance, but for the maintenance of optimal photosynthetic efficiency under normal-light conditions and down-regulation of qE through control of the trans-thylakoid pH gradient.


Analysis of the sodium chloride-dependent respiratory kinetics of wheat mitochondria reveals differential effects on phosphorylating and non-phosphorylating electron transport pathways (pages 823–833)
R. P. Jacoby, M. H. Che-Othman, A. H. Millar and N. L. Taylor
Article first published online: 11 DEC 2015 | DOI: 10.1111/pce.12653

A number of previous studies have documented the gross response of mitochondrial respiration to salinity treatment, but it is unclear how NaCl directly affects the kinetics of plant phosphorylating and non-phosphorylating electron transport pathways. This study investigates the direct effects of NaCl upon different respiratory pathways in wheat, by measuring rates of isolated mitochondrial oxygen consumption across different substrate oxidation pathways in saline media. These data deepen our understanding of how plant respiration responds to NaCl, offering new mechanistic explanations for the divergent salinity responses of whole-plant respiratory rate in the literature.

Nature Genetics Contents: April 2016 pp 343 - 473
***OsSPL13* controls grain size in cultivated rice** **pp447 - 456**
Lizhen Si, Jiaying Chen, Xuehui Huang, Hao Gong, Jianghong Luo *et al.*

doi:10.1038/ng.3518
Bin Han and colleagues present a genome-wide association analysis of grain size and shape in cultivated rice and identify a major locus for grain size encoding the transcription factor OsSPL13. They find that the large-grain allele in tropical *japonica* cultivars was introgressed from *indica* varieties during selection for improved grain yield.

FEBS Journal Content Alert (New Articles)
Sequestration of cellular interacting partners by protein aggregates: implication in a loss-of-function pathology
Hui Yang and Hong-Yu Hu
Accepted manuscript online: 26 MAR 2016 06:40AM EST | DOI: 10.1111/febs.13722

Protein misfolding and aggregation are a hallmark of several neurodegenerative diseases (NDs). However, how protein aggregation leads to cytotoxicity and neurodegeneration is still controversial. Emerging evidence demonstrates that sequestration of cellular interacting partners by protein aggregates contributes to the pathogenesis of these diseases. Here, we review current research on sequestration of cellular proteins by protein aggregates and its relation to proteinopathies. Based on different interaction modes, we classify these protein sequestrations into four types: protein co-aggregation, domain/motif-mediated sequestration, RNA-assisted sequestration, and sequestration of molecular chaperones. Thus, the cellular essential proteins and/or RNAs hijacked by protein aggregates may lose their biological functions, consequently resulting in cytotoxicity and neurodegeneration. We have proposed a hijacking model recapitulating the sequestration process and the loss-of-function pathology of ND.

Mitochondria and senescence: new actors for an old play
Nicolás Herranz and Jesús Gil Published online 23.02.2016
http://EMBOJ.embopress.org/content/35/7/701?etoc
A new study reveals a causal role of mitochondria for cellular senescence phenotypes and ageing.

Mack KL, Shorter J.
Engineering and Evolution of Molecular Chaperones and Protein Disaggregases with Enhanced Activity.
Front Mol Biosci. 2016;3:8. PMID: 27014702 [PubMed]

MoliÃ¨re N, HoÃŸmann J, SchÃ¤fer H, Turgay K.
Role of Hsp100/Clp Protease Complexes in Controlling the Regulation of Motility in Bacillus subtilis.
Front Microbiol. 2016;7:315. PMID: 27014237 [PubMed]

Arosio P, Michaels TC, Linse S, MÃ¥nsson C, Emanuelsson C, Presto J, Johansson J, Vendruscolo M, Dobson CM, Knowles TP.
Kinetic analysis reveals the diversity of microscopic mechanisms through which molecular chaperones suppress amyloid formation.
Nat Commun. 2016 Mar 24;7:10948. PMID: 27009901 [PubMed - in process]

Cuevas-Velazquez CL, Saab-RincÃ³n G, Reyes JL, Covarrubias AA.

The unstructured N-terminal region of Arabidopsis group 4 Late Embryogenesis Abundant Proteins (LEA) is required for folding and for chaperone-like activity under water deficit.
J Biol Chem. 2016 Mar 22;. [Epub ahead of print]
PMID: 27006402 [PubMed - as supplied by publisher]

Kang CH, Lee YM, Park JH, Nawkar GM, Oh HT, Kim MG, Lee SI, Kim WY, Yun DJ, Lee SY.
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The Plant Journal Content Alert (New Articles)
Extending the biosynthetic repertoires of cyanobacteria and chloroplasts
Agnieszka Zygadlo Nielsen, Silas Busck Mellor, Konstantinos Vavitsas, Artur Jacek Wlodarczyk, Thiyagarajan Gnanasekaran, Maria Perestrello Ramos H de Jesus, Brian Christopher King, Kamil Bakowski and Poul Erik Jensen
Accepted manuscript online: 23 MAR 2016 01:11AM EST | DOI: 10.1111/tpj.13173
Advances in Botanical Research: Alert 19 March-25 March
Coevolution of Organelle RNA Editing and Nuclear Specificity Factors in Early Land Plants Original Research Article
Pages 37-93
M. Schallenberg-Rüdinger, V. Knoop
Cell: Alert 19 March-25 March
Types of Ubiquitin Ligases
Pages 248-248.e1
Francesca Ester Morreale, Helen Walden
Current Opinion in Cell Biology: Alert 18 March-24 March
Shaping the multi-scale architecture of mitochondria Review Article
Pages 45-51
Vaishali Jayashankar, Irina A Mueller, Susanne M Rafelski

Plant, Cell & Environment Content Alert (New Articles)

Ribosomal P3 protein AtP3B of Arabidopsis acts as both protein and RNA chaperone to increase tolerance of heat and cold stresses

Chang Ho Kang, Young Mee Lee, Joung Hun Park, Ganesh M. Nawkar, Hun Taek Oh, Min Gap Kim, Soo In Lee, Woe Yeon Kim, Dae-Jin Yun and Sang Yeol Lee

Accepted manuscript online: 23 MAR 2016 05:15AM EST | DOI: 10.1111/pce.12742

A dual system formed by the ARC and NR molybdoenzymes mediates nitrite-dependent NO production in ***Chlamydomonas***

Alejandro Chamizo-Ampudia, Emanuel Sanz-Luque, Ángel Llamas, Francisco Ocaña-Calahorro, Vicente Mariscal, Alfonso Carreras, Juan B. Barroso, Aurora Galván and Emilio Fernández

Accepted manuscript online: 17 MAR 2016 05:05AM EST | DOI: 10.1111/pce.12739

FEBS Journal Content Alert (New Articles)

To deliver or to degrade: an interplay of the ubiquitin–proteasome system, autophagy and vesicular transport in plants

Katarzyna Zientara-Rytter and Agnieszka Sirko

Accepted manuscript online: 17 MAR 2016 01:00AM EST | DOI: 10.1111/febs.13712

Nature Reviews Molecular Cell Biology contents January 2016 Volume 17 Number 4 pp 201-262

Mitonuclear communication in homeostasis and stress

Pedro M. Quirós, Adrienne Mottis & Johan Auwerx

p213 | doi:10.1038/nrm.2016.23

As most mitochondrial proteins are encoded in the nucleus, mitochondrial activity requires efficient communication between the nuclear and mitochondrial genomes. This is mediated by nucleus-to-mitochondria (anterograde), mitochondria-to-nucleus (retrograde) and mitonuclear feedback signalling, as well as the integrated stress response and extracellular communication, which regulate homeostasis and, consequently, healthspan and lifespan.

Abstract | Full Text | **PDF**

Molecular Cell: Alert 12 March-18 March

Resources for the Comprehensive Discovery of Functional RNA Elements Original Research Article

Pages 903-913

Balaji Sundararaman, Lijun Zhan, Steven M. Blue, Rebecca Stanton, Keri Elkins, Sara Olson, Xintao Wei, Eric L. Van Nostrand, Gabriel A. Pratt, Stephanie C. Huelga, Brendan M. Smalec, Xiaofeng Wang, Eurie L. Hong, Jean M. Davidson, Eric Lécuyer, Brenton R. Graveley, Gene W. Yeo