Lit Lunch 7_17_15

Damian:

Antibodies to influenza nucleoprotein cross-react with human hypocretin receptor 2

Syed Sohail Ahmed,1*† Wayne Volkmuth,2 José Duca,3 Lorenzo Corti,4 Michele Pallaoro,4 Alfredo Pezzicoli,5 Anette Karle,6 Fabio Rigat,7 Rino Rappuoli,8 Vas Narasimhan,9 Ilkka Julkunen,10,11 Arja Vuorela,10 Outi Vaarala,10 Hanna Nohynek,10 Franco Laghi Pasini,12,13 Emanuele Montomoli,14,15 Claudia Trombetta,14 Christopher M. Adams,16 Jonathan Rothbard,17 Lawrence Steinman18*
Science Translational Medicine 01 Jul 2015: Vol. 7, Issue 294, pp. 294ra105 DOI: 10.1126/scitranslmed.aab2354

The sleep disorder narcolepsy is linked to the HLA-DQB1*0602 haplotype and dysregulation of the hypocretin ligand-hypocretin receptor pathway. Narcolepsy was associated with Pandemrix vaccination (an adjuvanted, influenza pandemic vaccine) and also with infection by influenza virus during the 2009 A(H1N1) influenza pandemic.
In contrast, very few cases were reported after Focetria vaccination (a differently manufactured adjuvanted influenza pandemic vaccine). We hypothesized that differences between these vaccines (which are derived from inactivated influenza viral proteins) explain the association of narcolepsy with Pandemrix-vaccinated subjects. A mimic peptide was identified from a surface-exposed region of influenza nucleoprotein A that shared protein residues in common with a fragment of the first extracellular domain of hypocretin receptor 2. A significant proportion of sera from HLA-DQB1*0602 haplotype–positive narcoleptic Finnish patients with a history of Pandemrix vaccination (vaccine-associated narcolepsy) contained antibodies to hypocretin receptor 2 compared to sera from nonnarcoleptic individuals with either 2009 A(H1N1) pandemic influenza infection or history of Focetria vaccination.
Antibodies from vaccine-associated narcolepsy sera cross-reacted with both influenza nucleoprotein and hypocretin receptor 2, which was demonstrated by competitive binding using 21-mer peptide (containing the identified nucleoprotein mimic) and 55-mer recombinant peptide (first extracellular domain of hypocretin receptor 2) on cell lines expressing human hypocretin receptor 2. Mass spectrometry indicated that relative to Pandemrix,
Focetria contained 72.7% less influenza nucleoprotein. In accord, no durable antibody responses to nucleoprotein were detected in sera fromFocetria-vaccinated nonnarcoleptic subjects. Thus, differences in vaccine nucleoprotein content and respective immune response may explain the narcolepsy association with Pandemrix.

A Constitutively Active Allele of Phytochrome B Maintains Circadian Robustness in the Absence of Light

1. **Matthew A Jones (**majonea@essex.ac.uk**),**
2. **Wei Hu (**weihu@ucdavis.edu**),**
3. **Suzanne Litthauer(**slitth@essex.ac.uk**),**
4. **J. Clark Lagarias (**jclagarias@ucdavis.edu**) and**
5. **Stacey Harmer(**slharmer@ucdavis.edu**)**

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The sensitivity of the circadian system to light allows entrainment of the clock, permitting coordination of plant metabolic function and flowering time across seasons. Light affects the circadian system both via photoreceptors, such as phytochromes and cryptochromes, and sugar

production by photosynthesis. In the present studies, we introduce a constitutively active version of phytochrome B (phyB-Y276H, YHB) into both wild-type and phytochrome null backgrounds of Arabidopsis thaliana to distinguish the effects of photoreceptor signalling on clock function from those of photosynthesis. We find that the YHB mutation is sufficient to phenocopy red light input into the circadian mechanism and to sustain robust rhythms in steady-state mRNA levels even in plants grown without light or exogenous sugars. The pace of the clock is insensitive to light intensity in YHB plants, indicating that light input to the clock is constitutively activated by this allele. Mutation of YHB so that it is retained in the cytoplasm abrogates its effects on clock function, indicating that nuclear localization of phytochrome is necessary for its clock regulatory activity. We also demonstrate a role for phytochrome C as part of the red light sensing network that modulates phytochrome B signalling input into the circadian system. Our findings indicate that phytochrome signaling in the nucleus plays a critical role in sustaining robust clock function under red light, even in the absence of photosynthesis or exogenous sources of energy.

Extra-Large G proteins (XLGs) expand the repertoire of subunits in Arabidopsis heterotrimeric G protein signaling

1. **David Chakravorty (**duc16@psu.edu**),**
2. **Timothy E. Gookin (**tegookin@psu.edu**),**
3. **Matthew Milner (**matthew.milner@niab.com**),**
4. **Yunqing Yu (**yxy151@psu.edu**) and**
5. **Sarah M. Assmann(**sma3@psu.edu**)**

Published online before print July 2015, doi: http://dx.doi.org/10.1104/pp.15.00251Plant Physiology July 2015 pp.00251.2015

Heterotrimeric G proteins, consisting of Gα, Gβ and Gγ subunits, are a conserved signal transduction mechanism in eukaryotes. However, G protein subunit numbers in diploid plant genomes are greatly reduced as compared to animals, and do not correlate with the diversity of functions and phenotypes in which heterotrimeric G proteins have been implicated. In addition to GPA1, the sole canonical Arabidopsis thaliana Gα subunit, Arabidopsis has three related proteins: the extra-large GTP-binding proteins XLG1, XLG2 and XLG3. We demonstrate that the XLGs can bind Gβγ dimers (AGB1 plus a Gγ subunit: AGG1, AGG2, or AGG3) with differing specificity, in yeast 3-hybrid assays. Our in silico structural analysis shows that XLG3 aligns closely to the crystal structure of GPA1, and XLG3 also competes with GPA1 for Gβγ binding in yeast. We observed interaction of the XLGs with all three Gβγ dimers at the plasma membrane in planta by BiFC. Bioinformatic and localization studies identified and confirmed nuclear localization signals in XLG2 and XLG3, and a nuclear export signal in XLG3, which may facilitate intracellular shuttling. We found that tunicamycin, salt, and glucose hypersensitivity, and increased stomatal density are agb1 specific phenotypes that are not observed in gpa1 mutants but are recapitulated in xlg mutants. Thus, XLG-Gβγ heterotrimers provide additional signaling modalities for tuning plant G protein responses, and increase the repertoire of G protein heterotrimer combinations from three to twelve. The potential for signal partitioning and competition between the XLGs and GPA1 is a new paradigm for plant-specific cell signaling.

Plastidial glycolytic glyceraldehyde-3-phosphate dehydrogenase is an important determinant in the carbon and nitrogen metabolism of heterotrophic cells in Arabidopsis

1. **Armand, Djoro Anoman (**armand.anoman@uv.es**),**
2. **Jesus Muñoz-Bertomeu(**jesus.munoz@ibmcp.upv.es**),**
3. **Sara Rosa-Téllez (**sara.rosa@uv.es**),**
4. **María Flores-Tornero(**maria.flores@uv.es**),**
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6. **Eduardo Bueso(**edbuero@ibmcp.upv.es**),**
7. **Alisdair, R. Fernie (**fernie@mpimp-golm.mpg.de**),**
8. **Juan Segura(**juan.segura@uv.es**) and**
9. **Roc Ros (**roc.ros@uv.es**)**

Published online before print July 2015, doi: http://dx.doi.org/10.1104/pp.15.00696Plant Physiology July 2015 pp.00696.2015

This study functionally characterizes the Arabidopsis thaliana plastidial glycolytic isoforms of glyceraldehyde-3-phosphate dehydrogenase (GAPCp) in photosynthetic and heterotrophic cells. We expressed the enzyme in gapcp double mutants (gapcp1gapcp2) under the control of photosynthetic (RUBISCO small subunit RBCS2B; RBCS), or heterotrophic (phosphate transporter PHT1.2; PHT), cell-specific promoters. Expression of GAPCp1 under the control of RBCS in gapcp1gapcp2 had no significant effect on the metabolite profile or growth in the aerial part (AP). GAPCp1 expression under the control of PHT promoter clearly affected Arabidopsis development, by increasing the number of lateral roots and having a major effect on the AP growth and metabolite profile. Our results indicate that GAPCp1 is not functionally important in photosynthetic cells, but plays a fundamental role in roots and in heterotrophic cells of the AP. Specifically GAPCp activity may be required in root meristems and the root cap for normal primary root growth. Transcriptomic and metabolomic analyses indicate that lack of GAPCp activity affects nitrogen and carbon metabolism as well as mineral nutrition, and that glycerate and glutamine are the main metabolites responding to GAPCp activity. Thus GAPCp could be an important metabolic connector of glycolysis with other pathways such as the phosphorylated pathway of serine biosynthesis, the ammonium assimilation pathway or the metabolism of GABA which in turn affect plant development.

A Potential Role for Mitochondrial Produced Reactive Oxygen Species in Salicylic Acid-Mediated Plant Acquired Thermotolerance

1. **Shengjun Nie (**nieshj@scnu.edu.cn**),**
2. **Haiyun Yue (**haiyun1314@126.com**) and**
3. **Da Xing(**xingda@scnu.edu.cn**)**

Published online before print June 2015, doi: http://dx.doi.org/10.1104/pp.15.00719Plant Physiology June 2015 pp.00719.2015

To characterize the function of salicylic acid (SA) in acquired thermotolerance, the effects of heat shock (HS) on wild-type and sid2 (for SA induction deficient 2) was investigated. After HS treatment, the survival ratio of sid2 mutant was lower than that of wild-type. However, pretreatment with hydrogen peroxide (H2O2) rescued the sid2 heat sensitivity. HsfA2 is a key component of acquired thermotolerance in Arabidopsis. The expression of HsfA2 induced by SA was highest among those of heat-inducible Hsfs (HsfA2, HsfA7a, HsfA3, HsfB1, and HsfB2) in response to HS. Furthermore, the application of AsA, an H2O2 scavenger, significantly reduced

the expression level of HsfA2 induced by SA. Although SA enhanced the survival of sid2 mutant, no significant effect on the hsfA2 mutant was observed, suggesting that HsfA2 is responsible for SA-induced acquired thermotolerance as a downstream factor. Further, real-time PCR analysis revealed that after HS treatment, SA also up-regulated mRNA transcription of HS protein (Hsp) genes through AtHsfA2. Time course experiments showed an increase in the fluorescence intensity of DCF in the mitochondria occurred earlier than in other regions of the protoplasts in response to SA. The cytochrome reductase activity analysis in isolated mitochondria demonstrated that SA-induced mitochondrial ROS possibly originated from complex III in the respiration chain. Collectively, our data suggest that SA functions and acts upstream of AtHsfA2 in acquired thermotolerance, which requires a pathway with H2O2 production involved and is dependent on increased expression of Hsp genes.

mTERF6, a Member of the Arabidopsis Mitochondrial Transcription Termination Factor Family, Is Required for Maturation of Chloroplast tRNAIle(GAU)

Isidora Romani, Nikolay Manavski, Arianna Morosetti, Luca Tadini, Swetlana Maier, Kristina Kühn, Hannes Ruwe, Christian Schmitz-Linneweber, Gerhard Wanner, Dario Leister, and Tatjana Kleine
Plant Physiol. pp.15.00964; First Published on July 7, 2015; doi:10.1104/pp.15.00964
http://www.plantphysiol.org/content/early/2015/07/07/pp.15.00964.abstract

Stephanie:

Heterosis and inbreeding depression of epigenetic *Arabidopsis* hybrids

Mélanie Dapp, **Jon Reinders**, **Alexis Bédiée**, **Crispulo Balsera**, **Etienne Bucher**, **Gregory Theiler**, **Christine Granier** & **Jerzy Paszkowski**

We have addressed the possible epigenetic contribution to heterosis using epigenetic inbred lines (epiRILs) with varying levels and distributions of DNA methylation. One line consistently displayed parent-of-origin heterosis for growth-related traits. Genome-wide transcription profiling followed by a candidate gene approach revealed 33 genes with altered regulation in crosses of this line that could contribute to the observed heterosis. Although none of the candidate genes could explain hybrid vigour, we detected intriguing, hybrid-specific transcriptional regulation of the RPP5 gene, encoding a growth suppressor. RPP5 displayed intermediate transcript levels in heterotic hybrids; surprisingly however, with global loss of fitness of their F2 progeny, we observed striking under-representation of the hybrid-like intermediate levels. Thus, in addition to genetic factors contributing to heterosis, our results

strongly suggest that epigenetic diversity and epigenetic regulation of transcription play a role in hybrid vigour and inbreeding depression, and also in the absence of parental genetic diversity.

Minsoo:

1. Hum Mol Genet. 2015 Jul 9. pii: ddv265. [Epub ahead of print]

COA6 is a mitochondrial complex IV assembly factor critical for biogenesis of mtDNA-encoded COX2.

Stroud DA(1), Maher MJ(2), Lindau C(2), Vögtle FN(3), Frazier AE(4), Surgenor E(1), Mountford H(4), Singh AP(2), Bonas M(2), Oeljeklaus S(5), Warscheid B(5), Meisinger C(6), Thorburn DR(3), Ryan MT(7).

Author information:

(1)Department of Biochemistry and Molecular Biology, Monash University, Clayton 3800, Melbourne, Australia. (2)Department of Biochemistry and Genetics, La Trobe Institute for Molecular Science, La Trobe University 3086, Melbourne, Australia.

Biogenesis of complex IV of the mitochondrial respiratory chain requires assembly factors for subunit maturation, co-factor attachment and stabilization of intermediate assemblies. **A pathogenic mutation in COA6, leading to substitution of a conserved tryptophan for a cysteine residue, results in a loss of complex IV activity and cardiomyopathy.** Here we demonstrate that the complex IV defect correlates with a severe loss in complex IV assembly in patient heart but not fibroblasts. Complete loss of COA6 activity using gene-editing in HEK293T cells resulted in a profound growth defect due to complex IV deficiency, caused **by impaired biogenesis of the copper-bound mtDNA encoded subunit COX2 and subsequent accumulation of complex IV assembly intermediates.** We show that the pathogenic mutation in COA6 does not affect its import into mitochondria but impairs its maturation and stability. Furthermore we show that **COA6 has the capacity to bind copper and can associate with newly translated COX2 and the mitochondrial copper chaperone SCO1.** Our data reveals that COA6 is intricately involved in the copper-dependent biogenesis of COX2.

2. PLoS One. Mar 26, 2015; 10(3): e0119853.

Mitochondrial-Derived Reactive Oxygen Species Play a Vital Role in the Salicylic Acid Signaling Pathway in Arabidopsis thaliana

Shengjun Nie, Haiyun Yue, Jun Zhou, and Da Xing*

Abstract

Plant mitochondria constitute a major source of ROS and are proposed to act as signaling organelles in the orchestration of defense response. At present, the signals generated and then integrated by mitochondria are still limited. Here, fluorescence techniques were used to monitor the events of mitochondria in vivo, as well as the induction of mitochondrial signaling by a natural defensive signal chemical salicylic acid (SA). **An inhibition of respiration was observed in isolated mitochondria subjected to SA.** The cytochrome reductase activity analysis in isolated mitochondria demonstrated that **SA might act directly on the complex III in the respiration chain by inhibiting the activity.** With this alteration, a quick burst of mitochondrial ROS (mtROS) was stimulated. **SA-induced mtROS caused mitochondrial morphology transition in leaf tissue or protoplasts expressing mitochondria-GFP (43C5) and depolarization of membrane potential**. However, **the application of AsA, an H2O2 scavenger, significantly prevented both events, indicating that both of them are attributable to ROS accumulation.** In parallel, SA-induced mtROS up-regulated AOX1a transcript abundance and this induction was correlated with the disease resistance, whereas AsA-pretreatment interdicted this effect. It is concluded that mitochondria play an essential role in the signaling pathway of SA-induced ROS generation, which possibly provided new insight into the SA-mediated biological processes, including plant defense response.

3. Plant Physiol. 2015 Jun 22.

A Potential Role for Mitochondrial Produced Reactive Oxygen Species in Salicylic Acid-Mediated Plant Acquired Thermotolerance.

Nie S1, Yue H1, Xing D2.

Abstract

To characterize the function of salicylic acid (SA) in acquired thermotolerance, the effects of heat shock (HS) on wild-type and sid2 (for SA induction deficient 2) was investigated. After HS treatment, the survival ratio of sid2 mutant was lower than that of wild-type. However, **pretreatment with hydrogen peroxide (H2O2) rescued the sid2 heat sensitivity.** HsfA2 is a key component of acquired thermotolerance in Arabidopsis. **The expression of HsfA2 induced by SA** was highest among those of heat-inducible Hsfs (HsfA2, HsfA7a, HsfA3, HsfB1, and HsfB2) in response to HS. Furthermore, **the application of AsA, an H2O2 scavenger, significantly reduced the expression level of HsfA2 induced by SA**. Although SA enhanced the survival of sid2 mutant, no significant effect on the hsfA2 mutant was observed, suggesting that **HsfA2 is responsible for SA-induced acquired thermotolerance as a downstream factor.** Further, real-time PCR analysis revealed that after HS treatment, SA also up-regulated mRNA transcription of HS protein (Hsp) genes through AtHsfA2. Time course experiments showed an increase in the fluorescence intensity of DCF in the mitochondria occurred earlier than in other regions of the protoplasts in response to SA. The cytochrome reductase activity analysis in isolated mitochondria demonstrated that SA-induced mitochondrial ROS possibly originated from complex III in the respiration chain. Collectively, our data suggest that **SA functions and acts upstream of AtHsfA2 in**

acquired thermotolerance, which requires a pathway with H2O2 production involved and is dependent on increased expression of Hsp genes.

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Bradner
JE. DRUG DEVELOPMENT. Phthalimide conjugation as a strategy for in vivo
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Keith:

Structural Mechanisms of Mutant Huntingtin Aggregation Suppression by the Synthetic Chaperonin-like CCT5 Complex Explained by Cryoelectron Tomography

July 10, 2015 The Journal of Biological Chemistry, 290, 17451-17461.

Michele C. Darrow[‡1], Oksana A. Sergeeva[§], Jose M. Isas[¶], Jesús G. Galaz-Montoya[‡], Jonathan A. King[§], Ralf Langen[¶], Michael F. Schmid[‡], and Wah Chiu[‡2]

[‡]*National Center for Macromolecular Imaging, Verna and Marrs McLean Department of Biochemistry and Molecular Biology, Baylor College of Medicine, Houston, Texas 77030, the* [§]*Department of Biology, Massachusetts Institute of Technology, Cambridge, Massachusetts 02139, and the* [¶]*Zilkha Neurogenetic Institute, Keck School of Medicine, University of Southern California, Los Angeles, California 90033*

Huntington disease, a neurodegenerative disorder character- ized by functional deficits and loss of striatal neurons, is linked to an expanded and unstable CAG trinucleotide repeat in the huntingtin gene (*HTT*). This DNA sequence translates to a poly- glutamine repeat in the protein product, leading to mutant huntingtin (mHTT) protein aggregation. The aggregation of mHTT is inhibited *in vitro* and *in vivo* by the TCP-1 ring complex (TRiC) chaperonin. Recently, a novel complex comprised of a single type of TRiC subunit has been reported to inhibit mHTT aggre- gation. Specifically, the purified CCT5 homo-oligomer com- plex, when compared with TRiC, has a similar structure, ATP use, and substrate refolding activity, and, importantly, it also inhibits mHTT aggregation. Using an aggregation suppression assay and cryoelectron tomography coupled with a novel com- putational classification method, we uncover the interactions between the synthetic CCT5 complex (□1 MDa) and aggregates of mutant huntingtin exon 1 containing 46 glutamines (mHTTQ46- Ex1). We find that, in a similar fashion to TRiC, synthetic CCT5 complex caps mHTT fibrils at their tips and encapsulates mHTT oligomers, providing a structural description of the inhibition of mHTTQ46-Ex1 by CCT5 complex and a shared mechanism of mHTT inhibition between TRiC chaperonin and the CCT5 complex: cap and contain.

Mary:

Stressing out over long noncoding RNA

Timothy E. Audas,
Stephen Lee

Abstract

Genomic studies have revealed that humans possess far fewer protein-encoding genes than originally predicted. These over-estimates were drawn from the inherent developmental and stimuli-responsive complexity found in humans and other mammals, when compared to lower eukaryotic organisms. This left a conceptual void in many cellular networks, as a new class of functional molecules was necessary for “fine-tuning” the basic proteomic machinery. Transcriptomics analyses have determined that the vast majority of the genetic material is transcribed as noncoding RNA, suggesting that these molecules could provide the functional diversity initially sought from proteins. Indeed, as discussed in this review, long noncoding RNAs (lncRNAs), the largest family of noncoding transcripts, have emerged as common regulators of many cellular stressors; including heat shock, metabolic deprivation and DNA damage. These stimuli, while divergent in nature, share some common stress-responsive pathways, notably inhibition of cell proliferation. This role intrinsically makes stress-responsive lncRNA regulators potential tumor suppressor or proto-oncogenic genes. As the list of functional RNA

molecules continues to rapidly expand it is becoming increasingly clear that the significance and functionality of this family may someday rival that of proteins.

Natural alleles of a proteasome α subunit gene contribute to thermotolerance and adaptation of African rice pp827 - 833

Xin-Min Li, Dai-Yin Chao, Yuan Wu, Xuehui Huang, Ke Chen, Long-Gang Cui, Lei Su, Wang-Wei Ye, Hao Chen, Hua-Chang Chen, Nai-Qian Dong, Tao Guo, Min Shi, Qi Feng, Peng Zhang, Bin Han, Jun-Xiang Shan, Ji-Ping Gao & Hong-Xuan Lin

doi:10.1038/ng.3305

Hong-Xuan Lin, Ji-Ping Gao, Jun-Xiang Shan and colleagues show that natural variation in a proteasome α subunit gene contributes to thermotolerance in African rice. Their follow-up studies suggest that the variant allele protects cells from heat stress by enhancing the elimination of cytotoxic denatured proteins and maintaining heat-response processes.

July 1-14, 2015

Advances in Botanical Research Volume 74 , Pages 1-306, 2015

Land Plants – Trees – a whole issue about advances in the genomics of trees Very cool.

Chapter Two – Forest Tree Genomics: Review of Progress

Geneviève J. Parent*, Elie Raherison*, Juliana Sena*, John J. MacKay*,†,
Centre for Forest Research and Institute for Systems and Integrative Biology, Université Laval, Quebec, QC, Canada
Present address: Department of Plant Sciences, University of Oxford, Oxford, UK

Not4-dependent translational repression is important for cellular protein homeostasis in yeast

Steffen Preissler, Julia Reuther, Miriam Koch, Annika Scior, Michael Bruderek, Tancred Frickey, and Elke Deuerling

http://EMBOJ.embopress.org/content/34/14/1905?etoc

Not4, a component of the CCR4-NOT complex, triggers translational repression of mRNAs carrying transiently stalled ribosomes and contributes to the maintenance of protein homeostasis during cellular stress.

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Arabidopsis QTLs Associated with Reduction of Fertility in Response to Heat Stress
Jennifer Mach
Plant Cell 2015 tpc.15.00561; First Published on July 10, 2015; doi:10.1105/tpc.15.00561
http://www.plantcell.org/content/early/2015/07/10/tpc.15.00561

Genome-Wide Association Mapping of Fertility Reduction upon Heat Stress Reveals Developmental Stage-Specific QTLs in *Arabidopsis thaliana*
Johanna A. Bac-Molenaar, Emilie F. Fradin, Frank F.M. Becker, Juriaan A. Rienstra, J. van der Schoot, Dick Vreugdenhil, and Joost J.B. Keurentjes
Plant Cell 2015 tpc.15.00248; First Published on July 10, 2015; doi:10.1105/tpc.15.00248
http://www.plantcell.org/content/early/2015/07/10/tpc.15.00248.abstract
Genome-wide association mapping identified four stage-specific QTLs that affect the Arabidopsis heat response and analysis of QTLs revealed candidate genes.

Journal of Photochemistry and Photobiology B: Biology: Alert 3 July-9 July

Effects of elevated ultraviolet radiation on primary metabolites in selected alpine algae and cyanobacteria Original Research Article
Pages 149-155 Anja Hartmann, Andreas Albert, Markus Ganzera

Cell Host & Microbe: Alert 3 July-9 July
Absolute Proteome Composition and Dynamics during Dormancy and Resuscitation of *Mycobacterium tuberculosis* Original Research Article
Pages 96-108
Olga T. Schubert, Christina Ludwig, Maria Kogadeeva, Michael Zimmermann, George Rosenberger, Martin Gengenbacher, Ludovic C. Gillet, Ben C. Collins, Hannes L. Rost, Stefan H.E. Kaufmann, Uwe Sauer, Ruedi Aebersold

Plant Cell Table of Contents for June 2015; Vol. 27, No. 6
The Elegant Simplicity of the Liverwort *Marchantia polymorpha*
Jennifer Lockhart
Plant Cell 2015 27: 1565. First Published on June 2, 2015; doi:10.1105/tpc.15.00431
http://www.plantcell.org/content/27/6/1565

Nature Biotechnology Contents: Volume 33 pp 671 - 780
First stress-tolerant soybean gets go-ahead in Argentina - p682 Emily Waltz doi:10.1038/nbt0715-682
Full Text - First stress-tolerant soybean gets go-ahead in Argentina | PDF (476 KB)

Illuminating the dark matter of shotgun proteomics - pp717 - 718
Owen S Skinner & Neil L Kelleher doi:10.1038/nbt.3287
Many of the unassignable spectra in proteomics data represent peptides with post-translational modifications.

Full Text - Illuminating the dark matter of shotgun proteomics | PDF (255 KB) - Illuminating the dark matter of shotgun proteomics

See also: Research by Chick et al.

A mass-tolerant database search identifies a large proportion of unassigned spectra in shotgun proteomics as modified peptides - pp743 - 749
Joel M Chick, Deepak Kolippakkam, David P Nusinow, Bo Zhai, Ramin Rad, Edward L Huttlin & Steven P Gygi
doi:10.1038/nbt.3267

In shotgun proteomics experiments, modified peptides account for a large part of the unassigned spectra and can be identified using ultra-tolerant database searches.

Abstract - | Full Text - A mass-tolerant database search identifies a large proportion of unassigned spectra in shotgun proteomics as modified peptides | PDF (1,978 KB) - A mass-tolerant database search identifies a large proportion of unassigned spectra in shotgun proteomics as modified peptides | Supplementary information

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Mitochondrial Dihydrolipoyl Dehydrogenase Activity Shapes Photosynthesis and Photorespiration of *Arabidopsis thaliana*
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Large-Scale Conformational Transitions and Dimerization Are Encoded in the Amino-Acid Sequences of Hsp70 Chaperones Duccio Malinverni, Simone Marsili, Alessandro Barducci, Paolo De Los Rios

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Multilayered Organization of Jasmonate Signalling in the Regulation of Root Growth
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Transfer RNAs Mediate the Rapid Adaptation of *Escherichia coli* to Oxidative Stress
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Does a Warmer World Mean a Greener World? Not Likely!
Jonathan Chase

While ongoing climate change can increase the number of days above freezing, changes in other climatic conditions will lead to fewer days when plants can grow, which in turn will affect biodiversity and people. Read the Research Article.

Suitable Days for Plant Growth Disappear under Projected Climate Change: Potential Human and Biotic Vulnerability
Camilo Mora, Iain R. Caldwell, Jamie M. Caldwell, Micah R. Fisher, Brandon M. Genco, Steven W. Running

While ongoing climate change can increase the number of days above freezing, changes in other climatic conditions will lead to fewer days when plants can grow, which in turn will affect biodiversity and people. See the Synopsis.

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Cerebral nitric oxide represses choroid plexus NFκB-dependent gateway activity for leukocyte trafficking
Kuti Baruch, Alexander Kertser, Ziv Porat, and Michal Schwartz Published online 04.05.2015
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Neurodegenerative disorders are associated with excessive nitric oxide (NO) production. New findings show here that NO represses leukocyte trafficking to the CNS via inhibition of the NFκB/p65 signaling pathway.

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Proteostasis control by the unfolded protein response - pp829 – 838 **Claudio Hetz, Eric Chevet & Scott A. Oakes**

Plant Breeding Content Alert (New Articles)
Overexpression of a small heat-shock-protein gene enhances tolerance to abiotic stresses in rice
Anquan Wang, Xiaohong Yu, Yun Mao, Ying Liu, Guoqing Liu, Yongsheng Liu and Xiangli Niu
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Global, *in situ*, site-specific analysis of protein *S*-sulfenylation **pp1022 - 1037**
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A nuclear role for the respiratory enzyme CLK-1 in regulating mitochondrial stress responses and longevity - pp782 - 792
Richard M. Monaghan, Robert G. Barnes, Kate Fisher, Tereza Andreou, Nicholas Rooney, Gino B. Poulin & Alan J. Whitmarsh doi:10.1038/ncb3170
Whitmarsh and colleagues identify a nuclear form of the mitochondrial enzyme, CLK-1 in *C. elegans* and COQ7 in human cells, respectively, that senses reactive oxygen species and regulates gene expression.
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The Phyre2 web portal for protein modeling, prediction and analysis - pp845 - 858
Lawrence A Kelley, Stefans Mezulis, Christopher M Yates, Mark N Wass & Michael J E Sternberg
doi:10.1038/nprot.2015.053

Phyre2 is a web-based tool for predicting and analyzing protein structure and function. Phyre2 uses advanced remote homology detection methods to build 3D models, predict ligand binding sites, and analyze amino acid variants in a protein equence.

Abstract - The Phyre2 web portal for protein modeling, prediction and analysis | Full Text - The Phyre2 web portal for protein modeling, prediction and analysis | PDF (3,362 KB)

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Rapid, optimized interactomic screening pp553 - 560
Zhanna Hakhverdyan, Michal Domanski, Loren E Hough, Asha A Oroskar, Anil R Oroskar *et al.*
doi:10.1038/nmeth.3395
Extraction conditions can have a substantial effect on protein complexes isolated from within cells. A platform for rapid, systematic screening of these conditions is described, which should enable the identification of biologically relevant complexes.