Lit Lunch 7-17-13

Fionn:

Nature
Spatiotemporal control of endocytosis by phosphatidylinositol-3,4-bisphosphate

York Posor, Marielle Eichhorn-Gruenig, Dmytro Puchkov, Johannes Schöneberg, Alexander Ullrich, André Lampe, Rainer Müller, Sirus Zarbakhsh, Federico Gulluni, Emilio Hirsch, Michael Krauss, Carsten Schultz, Jan Schmoranzer, Frank Noé & Volker Haucke

Phosphoinositides serve crucial roles in cell physiology, ranging from cell signalling to membrane traffic1, 2. Among the seven eukaryotic phosphoinositides the best studied species is phosphatidylinositol-4,5-bisphosphate (PI(4,5)P2), which is concentrated at the plasma membrane where, among other functions, it is required for the nucleation of endocytic clathrin-coated pits3, 4, 5, 6. No phosphatidylinositol other than PI(4,5)P2 has been implicated in clathrin-mediated endocytosis, whereas the subsequent endosomal stages of the endocytic pathway are dominated by phosphatidylinositol-3-phosphates(PI(3)P)7. How phosphatidylinositol conversion from PI(4,5)P2-positive endocytic intermediates to PI(3)P-containing endosomes is achieved is unclear. Here we show that formation of phosphatidylinositol-3,4-bisphosphate (PI(3,4)P2) by class II phosphatidylinositol-3-kinase C2? (PI(3)K C2?) spatiotemporally controls clathrin-mediated endocytosis. Depletion of PI(3,4)P2 or PI(3)K C2? impairs the maturation of late-stage clathrin-coated pits before fission. Timed formation of PI(3,4)P2 by PI(3)K C2? is required for selective enrichment of the BAR domain protein SNX9 at late-stage endocytic intermediates. These findings provide a mechanistic framework for the role of PI(3,4)P2 in endocytosis and unravel a novel discrete function of PI(3,4)P2 in a central cell physiological process.

Damian:

Multiple tubulins: evolutionary aspects and biological implications
Diego Breviario*, Silvia Gian_ı and Laura Morello
Istituto Biologia e Biotecnologia Agraria, Via Bassini 15, 20133 Milano, Italy
Received 28 November 2012; revised 3 May 2013; accepted 9 May 2013; published online 13 May 2013.
*For correspondence (e-mail diego.breviario@ibba.cnr.it).
The Plant Journal (2013) 75, 202–218
SUMMARY
Plant tubulin is a dimeric protein that contributes to formation of microtubules, major intracellular structures that are involved in the control of fundamental processes such as cell division, polarity of growth, cell-wall deposition, intracellular trafficking and communications. Because it is a structural protein whose function is confined to the role of microtubule formation, tubulin may be perceived as an uninteresting gene product, but such a perception is incorrect. In fact, tubulin represents a key molecule for studying fundamental biological issues such as (i) microtubule evolution (also with reference to prokaryotic precursors and the formation of cytomotive filaments), (ii) protein structure with reference to the various biochemical

features of members of the FstZ/tubulin superfamily, (iii) isoform variations contributed by the existence of multi-gene families and various kinds of post-translational modifications, (iv) anti-mitotic drug interactions and mode of action, (v) plant and cell symmetry, as determined using a series of tubulin mutants, (vi) multiple and sophisticated mechanisms of gene regulation, and (vii) intron molecular evolution. In this review, we present and discuss many of these issues, and offer an updated interpretation of the multi-tubulin hypothesis.

Catastrophic Nuclear Envelope Collapse in Cancer Cell Micronuclei

Emily M. Hatch,1 Andrew H. Fischer,2 Thomas J. Deerinck,3 and Martin W. Hetzer1,*
1Molecular and Cell Biology Laboratory, Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
2Department of Pathology, University of Massachusetts Medical School, 55 Lake Avenue, Worcester, MA 01655, USA
3Department of Neurosciences, National Center for Microscopy and Imaging Research, and Center for Research in Biological Systems,
University of California, San Diego, La Jolla, CA, 92093-0608, USA
*Correspondence: hetzer@salk.edu
http://dx.doi.org/10.1016/j.cell.2013.06.007
Cell 154, 47–60, July 3, 2013

SUMMARY

During mitotic exit, missegregated chromosomes can recruit their own nuclear envelope (NE) to form micronuclei (MN). MN have reduced functioning compared to primary nuclei in the same cell, although the two compartments appear to be structurally comparable. Here we show that over 60% of MN undergo an irreversible loss of compartmentalization during interphase due to NE collapse. This disruption of the MN, which is induced by defects in nuclear lamina assembly, drastically reduces nuclear functions and can trigger massive DNA damage. MN disruption is associated with chromatin compaction and invasion of endoplasmic reticulum (ER) tubules into the chromatin. We identified disrupted MN in both major subtypes of human non-smallcell lung cancer, suggesting that disrupted MN could be a useful objective biomarker for genomic instability in solid tumors. Our study shows that NE collapse is a key event underlying MN dysfunction and establishes a link between aberrant NE organization and aneuploidy.

Caffeine suppresses homologous recombination through interference with RAD51-mediated joint molecule formation

Alex N. Zelensky1, Humberto Sanchez1, Dejan Ristic1, Iztok Vidic1,
Sari E. van Rossum-Fikkert1,2, Jeroen Essers1,2,3, Claire Wyman1,2 and
Roland Kanaar1,2,*
1Department of Cell Biology and Genetics, Cancer Genomics Center, Erasmus Medical Center, PO Box 2040, 3000 CA, Rotterdam, The Netherlands, 2Department of Radiation Oncology, Erasmus Medical Center, PO Box 2040, 3000 CA, Rotterdam, The Netherlands and 3Department of Vascular Surgery, Erasmus Medical Center, PO Box 2040, 3000 CA, Rotterdam, The Netherlands
Received January 23, 2013; Revised April 12, 2013; doi:10.1093/nar/gkt375
Nucleic Acids Research, 2013, Vol. 41, No. 13 6475–6489

ABSTRACT

Caffeine is a widely used inhibitor of the protein kinases that play a central role in the DNA damage response. We used chemical inhibitors and genetically deficient mouse embryonic stem cell lines to study the role of DNA damage response in stable integration of the transfected DNA and found that caffeine rapidly, efficiently and reversibly inhibited homologous integration of the transfected DNA

as measured by several homologous recombination mediated gene-targeting assays. Biochemical and structural biology experiments revealed that caffeine interfered with a pivotal step in homologous recombination, homologous joint molecule formation, through increasing interactions of the RAD51 nucleoprotein filament with non-homologous DNA. Our results suggest that recombination pathways dependent on extensive homology search are caffeine-sensitive and stress the importance of considering direct checkpoint-independent mechanisms in the interpretation of the effects of caffeine on DNA repair.

Stephanie Article:

from PLOS ONE

Effects of the Plant Growth-Promoting Bacterium Burkholderia phytofirmans PsJN throughout the Life Cycle of Arabidopsis thaliana

María Josefina Poupin 1* , Tania Timmermann 1, Andrea Vega 2 , Ana Zuñiga 1 , Bernardo González 11 Laboratorio de Bioingeniería, Facultad de Ingeniería y Ciencias, Universidad Adolfo Ibáñez, Santiago, Chile, 2Departamento de Ciencias Vegetales, Facultad de Agronomía e Ingeniería Forestal, Pontificia Universidad Católica de Chile, Santiago, Chile

Abstract
Plant growth-promoting rhizobacteria (PGPR) induce positive effects in plants, such as increased growth or reduced stress susceptibility. The mechanisms behind PGPR/plant interaction are poorly understood, as most studies have described short-term responses on plants and only a few studies have analyzed plant molecular responses under PGPR colonization. Here, we studied the effects of the PGPR bacterial model Burkholderia phytofirmans PsJN onthe whole life cycle of Arabidopsis thaliana plants. We reported that at different plant developmental points, strain PsJN can be found in the rhizosphere and also colonizing their internal tissues. In early ontogeny, strain PsJN increased several growth parameters and accelerated growth rate of the plants. Also, an rabidopsis transcriptome analysis revealed that 408 genes showed differential expression in PsJN-inoculated plants; some of these genes are involved in stress response and hormone pathways. Specifically, genes implicated in auxin and gibberellin pathways were induced. Quantitative transcriptional analyses of selected genes in different developmental stages revealed that the beginning of these changes could be evidenced early in development, especially among the down-regulated genes. The inoculation with heat-killed bacteria provoked a more severe transcriptional response in plants, but was not able to induce plant growth-promotion. Later in ontogeny, the growth rates of inoculated plants decreased with respect to the non-inoculated group and, interestingly, the inoculation accelerated the flowering time and the appearance of senescence signs in plants; these modifications correlate with the early up-regulation of flowering control genes. Then, we show that a single inoculation with a PGPR could affect the whole life cycle of a plant, accelerating its growth rate and shortening its vegetative period, both effects relevant for most crops. Thus, these findings provide novel and interesting aspects of these relevant biological interactions.

Ariel:

FEBS Lett. 2013 Jul 3. pii: S0014-5793(13)00496-1. doi: 10.1016/j.febslet.2013.06.038.

Suppression of Arabidopsis RING E3 ubiquitin ligase AtATL78 increases tolerance to cold stress and decreases tolerance to drought stress.

Kim SJ, Kim WT.

Source

Department of Systems Biology, College of Life Science and Biotechnology, Yonsei University, Seoul 120-749, Korea.

Abstract

AtATL78 is an Arabidopsis RING E3 ubiquitin ligase. RT-PCR and promoter-GUS assays revealed that AtATL78 was up-regulated by cold stress and down-regulated by drought. AtATL78 was localized at the plasma-membrane. Suppression of AtATL78 increased tolerance to cold stress but decreased tolerance to drought. Our data suggests that AtATL78 is a negative regulator of cold stress response and a positive regulator of drought stress response in Arabidopsis. These results further suggest that AtATL78 plays opposing roles in cold and drought stress responses.

Nathen:

Molecular cell

The Hierarchy of the 3D Genome

Johan H. Gibcus1 and Job Dekker1,

* 1 Program in Systems Biology, Department of Biochemistry and Molecular Pharmacology, University of Massachusetts Medical School,

364 Plantation Street, Worcester, MA 01605-0103, USA

*Correspondence: job.dekker@umassmed.edu

http://dx.doi.org/10.1016/j.molcel.2013.02.011

Mammalian genomes encode genetic information in their linear sequence, but appropriate expression of their genes requires chromosomes to fold into complex three-dimensional structures. Transcriptional control involves the establishment of physical connections among genes and regulatory elements, both along and between chromosomes. Recent technological innovations in probing the folding of chromosomes are providing new insights into the spatial organization of genomes and its role in gene regulation. It is emerging that folding of large complex chromosomes involves a hierarchy of structures, from chromatin loops that connect genes and enhancers to larger chromosomal domains and nuclear compartments. The larger these structures are along this hierarchy, the more stable they are within cells, while becoming more stochastic between cells.

Here, we review the experimental and theoretical data on this hierarchy of structures and propose a key role for the recently discovered topologically associating domains.

New Insights from Existing Sequence Data:

Generating Breakthroughs without a Pipette

Alex M. Plocik1 and Brenton R. Graveley1,* 1

Department of Genetics and Developmental Biology, Institute for Systems Genomics, University of Connecticut Health Center, Farmington, CT 06030, USA

*Correspondence: graveley@neuron.uchc.edu

http://dx.doi.org/10.1016/j.molcel.2013.01.031

With the rapidly declining cost of data generation and the accumulation of massive data sets, molecular biology is entering an era in which incisive analysis of existing data will play an increasingly prominent role in the discovery of new biological phenomena and the elucidation of molecular mechanisms. Here, we discuss resources of publicly available sequencing data most useful for interrogating the mechanisms of gene expression. Existing next-generation sequence data sets, however, come with significant challenges in the form of technical and bioinformatic artifacts, which we discuss in detail. We also recount several breakthroughs made largely through the analysis of existing data, primarily in the RNA field.

Indu:

1. Science. 2013 Jul 5;341(6141):84-7. doi: 10.1126/science.1233606.

Monitoring drug target engagement in cells and tissues using the cellular thermal shift assay.

Molina DM, Jafari R, Ignatushchenko M, Seki T, Larsson EA, Dan C, Sreekumar L, Cao Y, Nordlund P.

Department of Medical Biochemistry and Biophysics, Karolinska Institute, Stockholm, Sweden.

The efficacy of therapeutics is dependent on a drug binding to its cognate target. Optimization of target engagement by drugs in cells is often challenging,

because drug binding cannot be monitored inside cells. We have developed a method for evaluating drug binding to target proteins in cells and tissue samples. This cellular thermal shift assay (CETSA) is based on the biophysical principle of ligand-induced thermal stabilization of target proteins. Using this assay, we validated drug binding for a set of important clinical targets and monitored processes of drug transport and activation, off-target effects and drug resistance in cancer cell lines, as well as drug distribution in tissues. CETSA is likely to become a valuable tool for the validation and optimization of drug target engagement.

PMID: 23828940 [PubMed - indexed for MEDLINE]

Yichen:

J Mol Biol. 2013 Aug 9;425(15):2795-812. doi: 10.1016/j.jmb.2013.04.019. Epub 2013 Apr 29.

E. coli ClpA Catalyzed Polypeptide Translocation Is Allosterically Controlled by the Protease ClpP.

Miller JM, Lin J, Li T, Lucius AL.

Source

Department of Chemistry, The University of Alabama at Birmingham, 1530 Third Avenue South, Birmingham, AL 35294-1240, USA.

Abstract

There are five known ATP-dependent proteases in Escherichia coli (Lon, ClpAP, ClpXP, HslUV, and the membrane-associated FtsH) that catalyze the removal of both misfolded and properly folded proteins in cellular protein quality control pathways. Hexameric ClpA rings associate with one or both faces of the cylindrically shaped tetradecameric ClpP protease. ClpA catalyzes unfolding and translocation of polypeptide substrates into the proteolytic core of ClpP for degradation through repeated cycles of ATP binding and hydrolysis at two nucleotide binding domains on each ClpA monomer. We previously reported a molecular mechanism for ClpA catalyzed polypeptide translocation in the absence of ClpP, including elementary rate constants, overall rate, and the kinetic step size. However, the potential allosteric effect of ClpP on the mechanism of ClpA catalyzed translocation remains unclear. Using single-turnover fluorescence stopped-flow methods, here we report that ClpA, when associated with ClpP, translocates polypeptide with an overall rate of ~35 aa s(-1) and, on average, traverses ~5 aa between two rate-limiting steps with reduced cooperativity between ATP binding sites in the hexameric ring. This is in direct contrast to our previously reported observation that, in the absence of ClpP, ClpA translocates polypeptide substrates with a maximum translocation rate of ~20 aa s(-1) with cooperativity between ATPase sites. Our results demonstrate that ClpP allosterically impacts the polypeptide translocation activity of ClpA by reducing the cooperativity between ATP binding sites.

Proc Natl Acad Sci U S A. 2013 Jul 2;110(27):E2441-50. doi: 10.1073/pnas.1309499110. Epub 2013 Jun 17.

MuB is an AAA+ ATPase that forms helical filaments to control target selection for DNA transposition.

Mizuno N, Dramicanin M, Mizuuchi M, Adam J, Wang Y, Han YW, Yang W, Steven AC, Mizuuchi K, Ramón-Maiques S.

Source

Laboratory of Structural Biology, National Institute of Arthritis, Musculoskeletal, and Skin Diseases and Laboratory of Molecular Biology, National Institute of Diabetes and Digestive and Kidney Diseases, National Institutes of Health, Bethesda, MD 20892.

Abstract

MuB is an ATP-dependent nonspecific DNA-binding protein that regulates the activity of the MuA transposase and captures target DNA for transposition. Mechanistic understanding of MuB function has previously been hindered by MuB's poor solubility. Here we combine bioinformatic, mutagenic, biochemical, and electron microscopic analyses to unmask the structure and function of MuB. We demonstrate that MuB is an ATPase associated with diverse cellular activities (AAA+ ATPase) and forms ATP-dependent filaments with or without DNA. We also identify critical residues for MuB's ATPase, DNA binding, protein polymerization, and MuA interaction activities. Using single-particle electron microscopy, we show that MuB assembles into a helical filament, which binds the DNA in the axial channel. The helical parameters of the MuB filament do not match those of the coated DNA. Despite this protein-DNA symmetry mismatch, MuB does not deform the DNA duplex. These findings, together with the influence of MuB filament size on strand-transfer efficiency, lead to a model in which MuB-imposed symmetry transiently deforms the DNA at the boundary of the MuB filament and results in a bent DNA favored by MuA for transposition.

Keith:

Supersite of immune vulnerability on the glycosylated face of HIV-1 envelope glycoprotein gp120

Nature Structural & Molecular Biology 20, 796–803 (2013)

Leopold Kong, Jeong Hyun Lee, Katie J Doores, Charles D Murin, Jean-Philippe Julien, Ryan McBride, Yan Liu, Andre Marozsan, Albert Cupo, Per-Johan Klasse, Simon Hoffenberg, Michael Caulfield, C Richter King, Yuanzi Hua, Khoa M Le, Reza Khayat, Marc C Deller, Thomas Clayton, Henry Tien, Ten Feizi, Rogier W Sanders, James C Paulson, John P Moore, Robyn L Stanfield, Dennis R Burton

A substantial proportion of the broadly neutralizing antibodies (bnAbs) identified in certain HIV-infected donors recognize glycan-dependent epitopes on HIV-1 gp120. Here we elucidate how the bnAb PGT 135 binds its Asn332 glycan–dependent epitope from its 3.1-Å crystal structure with gp120, CD4 and Fab 17b. PGT 135 interacts with glycans at Asn332, Asn392 and Asn386, using long CDR loops H1 and H3 to penetrate the glycan shield and access the gp120 protein surface. EM reveals that PGT 135 can accommodate the conformational and chemical diversity of gp120 glycans by altering its angle of engagement. Combined structural studies of PGT 135, PGT 128 and 2G12 show that this Asn332-dependent antigenic region is highly accessible and much more extensive than initially appreciated, which allows for multiple binding modes and varied angles of approach; thereby it represents a supersite of vulnerability for antibody neutralization.

Identification of a Novel Endoplasmic Reticulum Stress Response Element Regulated by XBP1*

July 12, 2013 The Journal of Biological Chemistry, 288, 20378-20391.

Michael Misiewicz, Marc-André Déry, Bénédicte Foveau, Julie Jodoin, Derek Ruths and Andréa C. LeBlanc

Understanding the regulatory mechanisms mediating PRNP gene expression is highly relevant to elucidating normal cellular prion protein (PrP) function(s) and the transmissibility of prion protein neurodegenerative diseases. Here, luciferase reporter assays showed that an endoplasmic reticulum stress element (ERSE)-like element, CCAAT-N26-CCACG in the human PRNP promoter, is regulated by ER stress and X-box-binding protein 1 (XBP1) but not by activating transcription factor 6 α (ATF6α). Bioinformatics identified the ERSE-26 motif in 37 other human genes in the absence of canonical ERSE sites except for three genes. Several of these genes are associated with a synaptic function or are involved in oxidative stress. Brefeldin A, tunicamycin, and thapsigargin ER stressors induced gene expression of PRNP and four randomly chosen ERSE-26-containing genes, ERLEC1, GADD45B, SESN2, and SLC38A5, in primary human neuron cultures or in the breast carcinoma MCF-7 cell line, although the level of the response depends on the gene analyzed, the genetic background of the cells, the cell type, and the ER stressor. Overexpression of XBP1 increased, whereas siRNA knockdown of XBP1 considerably reduced, PRNP and ERLEC1 mRNA levels in MCF-7 cells. Taken together, these results identify a novel ER stress regulator, which implicates the ER stress response in previously unrecognized cellular functions.

Liyaun:

The Arabidopsis ETHYLENE RESPONSE FACTOR1
Regulates Abiotic Stress-Responsive Gene Expression
by Binding to Different cis-Acting Elements in Response to Different Stress Signals
1[W][OA] Mei-Chun Cheng, Po-Ming Liao, Wei-Wen Kuo, and Tsan-Piao Lin*
Institute of Plant Biology, National Taiwan University, Taipei 10617, Taiwan

ORCID IDs: 0000-0003-2443-2847 (M.-C.C.); 0000-0002-4350-9574 (T.-P.L.).
ETHYLENE RESPONSE FACTOR1(ERF1) is an upstream component in both jasmonate (JA) and ethylene (ET) signaling and is involved in pathogen resistance. Accumulating evidence suggests thatERF1might be related to the salt stress response through ethylene signaling. However, the specific role ofERF1in abiotic stress and the molecular mechanism underlying the signaling cross talk still need to be elucidated. Here, we report thatERF1was highly induced by high salinity and drought stress in Arabidopsis (Arabidopsis thaliana). The salt stress induction required both JA and ET signaling but was inhibited by abscisic acid. ERF1-overexpressing lines (35S:ERF1) were more tolerant to drought and salt stress. They also displayed constitutively smaller stomatal aperture and less transpirational water loss. Surprisingly, 35S:ERF1also showed enhanced heat tolerance and upregulation of heat tolerance genes compared with the wild type. Several suites of genes activated by JA, drought, salt, and heat were found in microarray analysis of35S:ERF1. Chromatin immunoprecipitation assays found that ERF1 up-regulates specific suites of genes in response to different abiotic stresses by stress-specific binding to GCC or DRE/CRT. In response to biotic stress, ERF1 bound to GCC boxes but not DRE elements; conversely, under abiotic stress, we observed specific binding of ERF1 to DRE elements. Furthermore, ERF1 bound preferentially to only one among several GCC box or DRE/CRT elements in the promoter region of its target genes. ERF1 plays a positive role in salt, drought, and heat stress tolerance by stress-specific gene regulation, which integrates JA, ET, and abscisic acid signals.

Phytochrome-Interacting Factors (PIFs) as
Bridges between Environmental Signals and the
Circadian Clock: Diurnal Regulation of Growth
and Development
Jieun Shin a , Muhammad Usman Anwer a and Seth Jon Davis a,b,1
aMax Planck Institute for Plant Breeding Research, 50829, Cologne, Germany
bDepartment of Biology, University of York, York, UK

The rotation of the Earth around its axis results in distinct changes in light and temperature during a 24-h day/ night cycle. Plants being sessile are constantly and predictably exposed to these environmental changes. It is therefore critical for them to properly perceive environmental signals in order to effectively manage growth and development.
Indeed, plants have developed an anticipation mechanism
that enables them to keep track of time and to integratethis with the perception of external environmental cues to synchronize the internal metabolism to the most appropriate time in a day?night cycle. This internal time-keeping system is known as the circadian clock.

Elizabeth:

July 17 2013

Nature Genetics Contents: May 2013 pp 467 - 578

A battle between genomes in plant male fertility pp472 - 473
Hong Ma

doi:10.1038/ng.2618
Analyses of a new male sterility gene from a well-known rice cytoplasmic sterile line reveal inhibition of a nucleus-encoded protein and counteractions by nuclear fertility restorer factors. The existence of these genes in wild rice populations suggests that they may confer selective advantages.

A detrimental mitochondrial-nuclear interaction causes cytoplasmic male sterility in rice pp573 - 577

Dangping Luo, Hong Xu, Zhenlan Liu, Jingxin Guo, Heying Li, Letian Chen, Ce Fang, Qunyu Zhang, Mei Bai, Nan Yao, Hong Wu, Hao Wu, Chonghui Ji, Huiqi Zheng, Yuanling Chen, Shan Ye, Xiaoyu Li, Xiucai Zhao, Riqing Li and Yao-Guang Liu

doi:10.1038/ng.2570

Yao-Guang Liu and colleagues identify the molecular basis of male sterility in the Wild Abortive CMS (CMS-WA) system that has been widely used for hybrid rice breeding. They report that a new mitochondrial gene, *WA532*, confers male sterility because its protein product interacts with the mitochondrial protein COX11 and leads to cytoplasmic-nuclear incompatibility.

Nature Genetics Contents: April 2013 pp 339 - 465

The draft genome of the fast-growing non-timber forest species moso bamboo (*Phyllostachys heterocycla*) OPEN pp456 - 461

Zhenhua Peng, Ying Lu, Lubin Li, Qiang Zhao, Qi Feng, Zhimin Gao, Hengyun Lu, Tao Hu, Na Yao, Kunyan Liu, Yan Li, Danlin Fan, Yunli Guo, Wenjun Li, Yiqi Lu, Qijun Weng, CongCong Zhou, Lei Zhang, Tao Huang, Yan Zhao, Chuanrang Zhu, Xinge Liu, Xuewen Yang, Tao Wang, Kun Miao, Caiyun Zhuang, Xiaolu Cao, Wenli Tang, Guanshui Liu, Yingli Liu, Jie Chen, Zhenjing Liu, Licai Yuan, Zhenhua Liu, Xuehui Huang, Tingting Lu, Benhua Fei, Zemin Ning, Bin Han & Zehui Jiang

doi:10.1038/ng.2569

Bin Han and colleagues report the draft genome of moso bamboo, an important non-timber forest product. RNA sequencing analysis of bamboo flowering tissues suggests a connection between drought-responsive genes and potential flowering genes.

FEBS Journal Content Alert (New Articles)
MiniReviews

NAD and ADP-ribose metabolism in mitochondria
Christian Dölle, Johannes G.M. Rack and Mathias Ziegler
Accepted manuscript online: 25 APR 2013 10:38AM EST | DOI: 10.1111/febs.12304

Review Article

Redox regulation of protein kinases (pages 1944–1965)
Aoife Corcoran and Thomas G. Cotter
Article first published online: 21 MAR 2013 | DOI: 10.1111/febs.12224

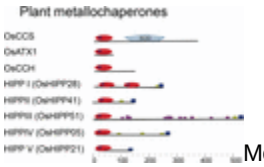
The recognition of ROS as mediators of cellular communications has led to their re-classification as signalling molecules. Identification of redox-sensitive kinases such as Src has prompted the emergence of a role for redox regulation of kinases. This review assesses the evidence for kinase regulation by direct oxidation, and proposes future directions for this crucial aspect of redox biology.

Heavy metal-associated isoprenylated plant protein (HIPP): characterization of a family of proteins exclusive

to plants (pages 1604–1616)

João Braga de Abreu-Neto, Andreia C. Turchetto-Zolet, Luiz Felipe Valter de Oliveira, Maria Helena Bodanese Zanettini and Marcia Margis-Pinheiro

Article first published online: 28 FEB 2013 | DOI: 10.1111/febs.12159



Metallochaperones are key proteins for the safe transport of metallic ions inside the cell. HIPPs are metallochaperones that contain a metal binding domain (HMA) and an isoprenylation motif. They are found only in vascular plants and can be separated into five clusters. HIPPs may be involved in: heavy metal homeostasis mechanisms; transcriptional responses to cold and drought, and plant-pathogen interactions

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Cell: Alert 1 July-7 July

lincRNAs: Genomics, Evolution, and Mechanisms Review Article
Pages 26-46
Igor Ulitsky, David P. Bartel

SnapShot: Mass Spectrometry for Protein and Proteome Analyses

Pages 252-252.e1

Alexander Leitner, Ruedi Aebersold

Plant Cell & Environment

Interactive effects of water, light and heat stress on photosynthesis in Fremont cottonwood (pages 1423–1434)

EMILY S. TOZZI, HSIEN MING EASLON and JAMES H. RICHARDS

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Along many western North American rivers, human-altered flow patterns have led to reduced cottonwood seeding recruitment, and seedling death is often attributed to water stress. This study examined photosynthetic responses of Fremont cottonwood to the interactive effects of water, light, and heat stresses, which were hypothesized to be more important than water stress alone on the exposed point bar environments where seedlings establish. Our results show that interactions of heat stress, surprisingly mediated by reduced photosynthetic capacity and not damage to photosystems, water limitation and leaf orientation are important in determining stress to cottonwood leaves that leads to leaf death and eventual seedling mortality. Application of these results to modeling efforts is needed because current models of riparian seedling establishment use water stress alone as a limiting factor.

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Molecular Cell

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Arabidopsis *MSI1 connects LHP1 to PRC2 complexes*

The *Arabidopsis* protein MSI1 is an essential component of the Polycomb repressive complex 2, PRC2, and links PRC2 to the polycomb group protein LHP1 to promote the inheritance of H3K27me3 during DNA replication.

Maria Derkacheva, Yvonne Steinbach, Thomas Wildhaber, Iva Mozgová, Walid Mahrez, Paolo Nanni, Sylvain Bischof, Wilhelm Gruissem and Lars Hennig

Crowdsourcing to kick-start comeback from ash dieback

A team from The Sainsbury Laboratory and the JIC became the first to publish the RNA sequence data on the ash dieback fungus. They released the data via a website to a system designed for "social coding" of software called GitHub, which allow contributions from other scientists to be attributed and tracked. The move enabled experts from around the world to access the RNA sequence and start to analyse it immediately, speeding up the process of discovery.