Lit Lunch 10/3/12

Plant Journal

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Targeted inactivation of transcription factors by overexpression of their truncated forms in plants.

Summary
Transcription factors are central constituents of gene regulatory networks that control diverse aspects of plant development and environmental adaptability. Therefore they have been explored for decades as primary targets for agricultural biotechnology. A gene of interest can readily be introduced into many crop plants, whereas targeted gene inactivation is practically difficult in many cases. Here, we developed an artificial small interfering peptide (a-siPEP) approach, which is based on overexpression of specific protein domains, and evaluated its application for the targeted inactivation of transcription factors in the dicot model, Arabidopsis, and monocot model, Brachypodium. We designed potential a-siPEPs of two representative MADS box transcription factors, SUPPRESSOR OF OVEREXPRESSOR OF CONSTANS 1 (SOC1) and AGAMOUS (AG), and a MYB transcription factor, LATE ELONGATED HYPOCOTYL (LHY). Transgenic plants overproducing the a-siPEPs displayed phenotypes comparable to those of gene-deficient mutants. The a-siPEPs attenuate nuclear import and DNA-binding of target transcription factors. Our data demonstrate that the a-siPEP tool is an efficient genetic means of inactivating specific transcription factors in plants.

Complementary Proteome and Transcriptome Profiling in Phosphate-Deficient Arabidopsis Roots Reveals Multiple Levels of Gene Regulation

Ping Lan, Wenfeng Li and Wolfgang Schmidt*

Molecular & Cellular Proteomics 10.1074/mcp.M112.020461

Phosphate (Pi) deficiency impairs plant growth and productivity in many agricultural ecosystems, causing severe reductions in crop yield. To uncover novel aspects in acclimation to Pi starvation, we investigated the correlation between Pi deficiency-induced changes in transcriptome and proteome profiles in Arabidopsis roots. Using exhaustive tandem mass spectrometry-based shotgun proteomics and whole-genome RNA sequencing to generate a nearly complete catalogue of expressed mRNAs and proteins, we reliably identified 13,298 proteins and 24,591 transcripts, subsets of 356 proteins and 3,106 mRNAs were differentially expressed during Pi deficiency. Most dramatic changes were noticed for genes involved in Pi acquisition and in processes that either liberate Pi or bypass Pi/ATP-consuming metabolic steps, for example during membrane lipid remodeling and glycolytic carbon flux. The concordance between the abundance of mRNA and its encoded protein was generally high for highly up-

regulated genes, but the analysis also revealed numerous discordant changes in mRNA/protein pairs, indicative of divergent regulation of transcription and post-transcriptional processes. In particular, a decreased abundance of proteins upon Pi deficiency was not closely correlated with changes in the corresponding mRNAs. In several cases, up-regulation of gene activity was observed solely at the protein level, adding novel aspects to key processes in the adaptation to Pi deficiency. We conclude that integrated measurement and interpretation of changes in protein and transcript abundance are mandatory for generating a complete inventory of the components that are critical in the response to environmental stimuli.

A gain-of-function mutation in IAA16 confers reduced responses to auxin and abscisic acid and impedes plant growth and fertility

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Plant Molecular Biology

Volume 79, Numbers 4-5 (2012), 359-373

Auxin regulates many aspects of plant development, in part, through degradation of the Aux/IAA family of transcriptional repressors. Consequently, stabilizing mutations in several Aux/IAA proteins confer reduced auxin responsiveness. However, of the 29 apparent Aux/IAA proteins in Arabidopsis thaliana, fewer than half have roles established through mutant analysis. We identified iaa16-1, a dominant gain-of-function mutation in IAA16 (At3g04730), in a novel screen for reduced root responsiveness to abscisic acid. The iaa16-1 mutation also confers dramatically reduced auxin responses in a variety of assays, markedly restricts growth of adult plants, and abolishes fertility when homozygous. We compared iaa16-1 phenotypes with those of dominant mutants defective in the closely related IAA7/AXR2, IAA14/SLR, and IAA17/AXR3, along with the more distantly related IAA28, and found overlapping but distinct patterns of developmental defects. The identification and characterization of iaa16-1 provides a fuller understanding of the IAA7/IAA14/IAA16/IAA17 clade of Aux/IAA proteins and the diverse roles of these repressors in hormone response and plant development.

1. Science. 2012 Sep 21;337(6101):1546-50.

Unicellular cyanobacterium symbiotic with a single-celled eukaryotic alga.

Thompson AW, Foster RA, Krupke A, Carter BJ, Musat N, Vaulot D, Kuypers MM, Zehr
JP.

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Symbioses between nitrogen (N)(2)-fixing prokaryotes and photosynthetic

eukaryotes are important for nitrogen acquisition in N-limited environments. Recently, a widely distributed planktonic uncultured nitrogen-fixing cyanobacterium (UCYN-A) was found to have unprecedented genome reduction, including the lack of oxygen-evolving photosystem II and the tricarboxylic acid cycle, which suggested partnership in a symbiosis. We showed that UCYN-A has a symbiotic association with a unicellular prymnesiophyte, closely related to calcifying taxa present in the fossil record. The partnership is mutualistic, because the prymnesiophyte receives fixed N in exchange for transferring fixed carbon to UCYN-A. This unusual partnership between a cyanobacterium and a unicellular alga is a model for symbiosis and is analogous to plastid and organismal evolution, and if calcifying, may have important implications for past and present oceanic N(2) fixation.

PMID: 22997339 [PubMed - in process]

2. Science. 2012 Sep 21;337(6101):1460-1.

Structural biology. Versatility from protein disorder.

Babu MM, Kriwacki RW, Pappu RV.

MRC Laboratory of Molecular Biology, Hills Road, Cambridge CB2 0QH, UK. madanm@mrc-lmb.cam.ac.uk

PMID: 22997313 [PubMed - in process]

3. Science. 2012 Sep 28;337(6102):1612-4.

Ecology. Insecticide resistance after Silent spring.

Heckel DG.

Department of Entomology, Max Planck Institute for Chemical Ecology, Jena, Germany. heckel@ice.mpg.de

PMID: 23019637 [PubMed - in process]

4. Science. 2012 Sep 28;337(6102):1592.

Scientific community. U.S. study shows unconscious gender bias in academic science.

Mervis J.

PMID: 23019620 [PubMed - in process]

5. Science. 2012 Sep 28;337(6102):1583.

The end of "small science"?

Alberts B.

PMID: 23019614 [PubMed - in process]

6. Science. 2012 Sep 28;337(6102):1665-8. Epub 2012 Aug 30.

Disulfide rearrangement triggered by translocon assembly controls lipopolysaccharide export.

Chng SS, Xue M, Garner RA, Kadokura H, Boyd D, Beckwith J, Kahne D.

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The presence of lipopolysaccharide (LPS) on the cell surface of Gram-negative bacteria is critical for viability. A conserved β-barrel membrane protein LptD (lipopolysaccharide transport protein D) translocates LPS from the periplasm across the outer membrane (OM). In Escherichia coli, this protein contains two disulfide bonds and forms the OM LPS translocon with the lipoprotein LptE. Here,we identified seven in vivo states on the oxidative-folding pathway of LptD.Proper assembly involved a nonfunctional intermediate containing non-native disulfides. Intermediate formation required the oxidase DsbA, and subsequent maturation to the active form with native disulfides was triggered by LptE. Thus,disulfide bond-dependent protein folding of LptD requires the proper assembly of a two-protein complex to promote disulfide bond rearrangement.

PMID: 22936569 [PubMed - in process]

Nature Sept 27

- **Interaction landscape of membrane-protein complexes in *Saccharomyces cerevisiae***

  - Mohan Babu, James Vlasblom, Shuye Pu, Xinghua Guo, Chris Graham+ et al.

A survey of 1,590 putative integral, peripheral and lipid-anchored membrane proteins from *Saccharomyces cerevisiae* reveals unexpected physical associations underlying the membrane biology of eukaryotes and delineates the global topological landscape of the membrane interactome.

Macromolecular assemblies involving membrane proteins (MPs) serve vital biological roles and are prime drug targets in a variety of diseases[1]. Large-scale affinity purification studies of soluble-protein complexes have been accomplished for diverse model organisms, but no global characterization of MP-complex membership has been described so far. Here we report a complete survey of 1,590 putative integral, peripheral and lipid-anchored MPs from *Saccharomyces cerevisiae*, which were affinity purified in the presence of non-denaturing

detergents. The identities of the co-purifying proteins were determined by tandem mass spectrometry and subsequently used to derive a high-confidence physical interaction map encompassing 1,726 membrane protein–protein interactions and 501 putative heteromeric complexes associated with the various cellular membrane systems. Our analysis reveals unexpected physical associations underlying the membrane biology of eukaryotes and delineates the global topological landscape of the membrane interactome.

Genomic analysis of a key innovation in an experimental *Escherichia coli* population

- Zachary D. Blount, Jeffrey E. Barrick, Carla J. Davidson & Richard E. Lenski

By combining full-genome sequencing and 'evolutionary replay' experiments to dissect the origin of aerobic citrate use in an experimental *Escherichia coli* population over 40,000 generations and 2 decades, the authors unveil a 3-step process in which potentiation makes a trait possible, actualization makes the trait manifest and refinement makes it effective.

Evolutionary novelties have been important in the history of life, but their origins are usually difficult to examine in detail. We previously described the evolution of a novel trait, aerobic citrate utilization (Cit$^+$), in an experimental population of *Escherichia coli*. Here we analyse genome sequences to investigate the history and genetic basis of this trait. At least three distinct clades coexisted for more than 10,000 generations before its emergence. The Cit$^+$ trait originated in one clade by a tandem duplication that captured an aerobically expressed promoter for the expression of a previously silent citrate transporter. The clades varied in their propensity to evolve this novel trait, although genotypes able to do so existed in all three clades, implying that multiple potentiating mutations arose during the population's history. Our findings illustrate the importance of promoter capture and altered gene regulation in mediating the exaptation events that often underlie evolutionary innovations.

• Rat study sparks GM furore

Cancer claims put herbicide-resistant transgenic maize in the spotlight.

Nature Sept 20

Sequencing power One of a new generation of DNA sequencers, a benchtop device from US biotech firm Life Technologies, began shipping to customers on 13 September, the company says. The

US$150,000 'Ion Proton' uses $1,000 chips to sequence between 60 million and 80 million DNA fragments, each up to 200 bases long, in 4 hours. The company, based in Carlsbad, California, says that next year it will release a chip that can sequence a full human genome within 4 hours. Its competitor Illumina, headquartered in San Diego, California, says that its own high-throughput instrument, which can complete a full human genome within 24 hours, will be available by the end of this year. See go.nature.com/8g54pj for more.

TREND WATCH

The financial and economic crisis has caused a worldwide drop in spending on research and development, as well as reductions in the creation of companies and venture-capital investment (see chart). Figures in the Organisation for Economic Co-operation and Development's 2012 outlook report, published on 13 September, also suggest that China, South Korea and other emerging Asian economies are out-innovating the Western world.

26–28 September
In Arusha, Tanzania, politicians, firms, farmers and scientists convene at the African Green Revolution Forum to discuss how to invest in the continent's agricultural development.

Chemistry and Biology of Biomolecule Nitration

Review Article
Pages 1086-1092
Lyn H. Jones

Trends in biochemical Sciences.
Bardwell JC, Jakob U.
Conditional disorder in chaperone action.
Trends Biochem Sci. 2012 Sep 24;. [Epub ahead of print]
PMID: 23018052 [PubMed - as supplied by publisher]

Selective translation during stress in *Escherichia coli*

Review Article
In Press, Corrected Proof, *Available online 30 August 2012*
Isabella Moll, Hanna Engelberg-Kulka

Intrinsically disordered proteins: a 10-year recap

Review Article
In Press, Corrected Proof, *Available online 16 September 2012*
Peter Tompa

Mitochondrial quality control: an integrated network of pathways

Review Article
Pages 284-292
Fabian Fischer, Andrea Hamann, Heinz D. Osiewacz

Ribosome-associated chaperones as key players in proteostasis

Review Article
Pages 274-283
Steffen Preissler, Elke Deuerling

RNA–protein interactions *in vivo*: global gets specific

Review Article
Pages 255-262
Minna-Liisa Änkö, Karla M. Neugebauer

Atomic structures of the eukaryotic ribosome

Review Article
Pages 189-198
Sebastian Klinge, Felix Voigts-Hoffmann, Marc Leibundgut, Nenad Ban

RINGs hold the key to ubiquitin transfer

Review Article
Pages 58-65
Rhesa Budhidarmo, Yoshio Nakatani, Catherine L. Day

Various Journals:

Wang L, Li S, Wang J, Cramer G, Dai Z, Duan W, Xu H, Wu B, Fan P.
Transcriptomic analysis of grape (Vitis vinifera L.) leaves during and after recovery from heat stress.
BMC Plant Biol. 2012 Sep 28;12(1):174. [Epub ahead of print]
PMID: 23016701 [PubMed - as supplied by publisher]

Blamowska M, Neupert W, Hell K.
Biogenesis of the mitochondrial Hsp70 chaperone.
J Cell Biol. 2012 Sep 24;. [Epub ahead of print]
PMID: 23007651 [PubMed - as supplied by publisher]

Kulig M, Ecroyd H.

The small heat shock protein Î±Bâ€‘crystallin uses different mechanisms of chaperone action to prevent the amorphous versus fibrillar aggregation of Î±-lactalbumin.
Biochem J. 2012 Sep 24;. [Epub ahead of print]
PMID: 23005341 [PubMed - as supplied by publisher]

Herzog F, Kahraman A, Boehringer D, Mak R, Bracher A, Walzthoeni T, Leitner A, Beck M, Hartl FU, Ban N, MalmstrÃ¶m L, Aebersold R.
Structural probing of a protein phosphatase 2A network by chemical cross-linking and mass spectrometry.
Science. 2012 Sep 14;337(6100):1348-52.
PMID: 22984071 [PubMed - indexed for MEDLINE]

Oliveira HC, Salgado I, Sodek L.
Involvement of nitrite in the nitrate-mediated modulation of fermentative metabolism and nitric oxide production of soybean roots during hypoxia.
Planta. 2012 Sep 26;. [Epub ahead of print]
PMID: 23011570 [PubMed - as supplied by publisher]

Plant Breeding Content Alert (New Articles)

Analysis of genotypic variation for normalized difference vegetation index and its relationship with grain yield in winter wheat under terminal heat stress
Shahnoza Hazratkulova, Ram C. Sharma, Safar Alikulov, Sarvar Islomov, Tulkin Yuldashev, Zafar Ziyaev, Zakir Khalikulov, Zokhid Ziyadullaev and Jozef Turok
Article first published online: 26 SEP 2012 | DOI: 10.1111/pbr.12003

Analytical Biochemistry: Alert 23 September-29 September

Dual-color system for simultaneously monitoring intracellular Ca2+ and ATP dynamics

Pages 45-47
Hyuck Joon Kwon, Yoshihiro Ohmiya, Kazunori Yasuda