Lit Lunch – October 17, 2012

Various journals:

Mazur MJ, van den Burg HA.
Global SUMO Proteome Responses Guide Gene Regulation, mRNA Biogenesis, and Plant Stress Responses.
Front Plant Sci. 2012;3:215.
PMID: 23060889 [PubMed - in process]

Aurelian L, Laing JM, Lee KS.
H11/HspB8 and Its Herpes Simplex Virus Type 2 Homologue ICP10PK Share Functions That Regulate Cell Life/Death Decisions and Human Disease.
Autoimmune Dis. 2012;2012:395329.
PMID: 23056924 [PubMed]

Zhou Q, Sun S, Tai P, Sui SF.
Structural Characterization of the Complex of SecB and Metallothionein-Labeled proOmpA by Cryo-Electron Microscopy.
PLoS One. 2012;7(10):e47015.
PMID: 23056562 [PubMed - in process]

Altieri DC.
Hsp90 regulation of mitochondrial protein folding: from organelle integrity to cellular homeostasis.
Cell Mol Life Sci. 2012 Sep 30;. [Epub ahead of print]
PMID: 23052217 [PubMed - as supplied by publisher]

Firon N, Pressman E, Meir S, Khoury R, Altahan L.
Ethylene is involved in maintaining tomato (Solanum lycopersicum) pollen quality under heat-stress conditions.
AoB Plants. 2012;2012:pls024.
PMID: 23050072 [PubMed]

Takei Y, Iizuka R, Ueno T, Funatsu T.
Single-molecule observation of protein folding in symmetric GroEL-(GroES)2 complexes.
J Biol Chem. 2012 Oct 9;. [Epub ahead of print]
PMID: 23048033 [PubMed - as supplied by publisher]

Kiktev DA, Patterson JC, MÃ¼ller S, Bariar B, Pan T, Chernoff YO.
Regulation of the chaperone effects on a yeast prion by the cochaperone Sgt2.
Mol Cell Biol. 2012 Oct 8;. [Epub ahead of print]
PMID: 23045389 [PubMed - as supplied by publisher]

Mosbech A, Gibbs-Seymour I, Kagias K, Thorslund T, Beli P, Povlsen L, Nielsen SV, Smedegaard S, Sedgwick G, Lukas C, Hartmann-Petersen R, Lukas J, Choudhary C, Pocock R, Bekker-Jensen S, Mailand N.
DVC1 (C1orf124) is a DNA damage-targeting p97 adaptor that promotes ubiquitin-dependent responses to replication blocks.
Nat Struct Mol Biol. 2012 Oct 7;. [Epub ahead of print]
PMID: 23042605 [PubMed - as supplied by publisher]

Ducett JK, Peterson FC, Hoover LA, Prunuske AJ, Volkman BF, Craig EA.
Unfolding of the C-terminal Domain of the J-protein Zuo1 Releases Autoinhibition and Activates Pdr1-dependent Transcription.
J Mol Biol. 2012 Oct 1;. [Epub ahead of print]
PMID: 23036859 [PubMed - as supplied by publisher]

Filippou P, Antoniou C, Fotopoulos V.
The nitric oxide donor sodium nitroprusside regulates polyamine and proline metabolism in leaves of Medicago truncatula plants.

Free Radic Biol Med. 2012 Oct 3;. [Epub ahead of print]
PMID: 23041351 [PubMed - as supplied by publisher]

Gupta KJ, Igamberdiev AU, Mur LA.
NO and ROS homeostasis in mitochondria: a central role for alternative oxidase.
New Phytol. 2012 Jul;195(1):1-3.
PMID: 22626260 [PubMed - indexed for MEDLINE]

Lounifi I, Arc E, Molasiotis A, Job D, Rajjou L, Tanou G.
Interplay between protein carbonylation and nitrosylation in plants.
Proteomics. 2012 Oct 4;. [Epub ahead of print]
PMID: 23034931 [PubMed - as supplied by publisher]

Huang S, Taylor NL, StrÃ¶her E, Fenske R, Harvey Millar A.
Succinate dehydrogenase assembly factor 2 is needed for assembly and activity of mitochondrial complex II and for normal root elongation in Arabidopsis.
Plant J. 2012 Oct 4;. [Epub ahead of print]
PMID: 23036115 [PubMed - as supplied by publisher]

Chang F, Gu Y, Ma H, Yang Z.
AtPRK2 promotes ROP1 activation via RopGEFs in the control of polarized pollen tube growth.
Mol Plant. 2012 Sep 30;. [Epub ahead of print]
PMID: 23024212 [PubMed - as supplied by publisher]

Burmann BM, Knauer SH, Sevostyanova A, Schweimer K, Mooney RA, Landick R, Artsimovitch I, RÃ¶sch P.
An Î± helix to Î² barrel domain switch transforms the transcription factor RfaH into a translation factor.
Cell. 2012 Jul 20;150(2):291-303.
PMID: 22817892 [PubMed - indexed for MEDLINE]

Journal of Agronomy and Crop Sci... Content Alert (New Articles)
Soybean Pollen Anatomy, Viability and Pod Set under High Temperature Stress
M. Djanaguiraman, P. V. V. Prasad, D. L. Boyle and W. T. Schapaugh
Article first published online: 12 OCT 2012 | DOI: 10.1111/jac.12005

Plant, Cell & Environment Content Alert (New Articles)
Review
Light acclimation, retrograde signalling, cell death, and immune defences in plants
Stanisław Karpiński, Magdalena Szechyńska-Hebda, Weronika Wituszyńska and Paweł Burdiak
Accepted manuscript online: 9 OCT 2012 10:01AM EST | DOI: 10.1111/pce.12018

The Plant Journal Content Alert (New Articles)

Selective recruitment of mRNAs and miRNAs to polyribosomes in response to rhizobia infection in *Medicago truncatula*
Mauricio Alberto Reynoso, Flavio Antonio Blanco, Julia Bailey-Serres, Martín Crespi and María Eugenia Zanetti
Accepted manuscript online: 11 OCT 2012 03:25AM EST | DOI: 10.1111/tpj.12033

Nature Oct 4

A transcriptomic hourglass in plant embryogenesis Nature490,98–101
Marcel Quint, Hajk-Georg Drost, Alexander Gabel, Kristian Karsten Ullrich, Markus Bönn & Ivo Grosse

Animal and plant development starts with a constituting phase called embryogenesis, which evolved independently in both lineages[1]. Comparative anatomy of vertebrate development—based on the Meckel-Serrès law[2] and von Baer's laws of embryology[3] from the early nineteenth century—shows that embryos from various taxa appear different in early stages, converge to a similar form during mid-embryogenesis, and again diverge in later stages. This morphogenetic series is known as the embryonic 'hourglass'[4, 5], and its bottleneck of high conservation in mid-embryogenesis is referred to as the phylotypic stage[6]. Recent analyses in zebrafish and *Drosophila* embryos provided convincing molecular support for the hourglass model, because during the phylotypic stage the transcriptome was dominated by ancient genes[7] and global gene expression profiles were reported to be most conserved[8]. Although extensively explored in animals, an embryonic hourglass has not been reported in plants, which represent the second major kingdom in the tree of life that evolved embryogenesis. Here we provide phylotranscriptomic evidence for a molecular embryonic hourglass in *Arabidopsis thaliana*, using two complementary approaches. This is particularly significant because the possible absence of an hourglass based on morphological features in plants suggests that morphological and molecular patterns might be uncoupled. Together with the reported developmental hourglass patterns in animals, these findings indicate convergent evolution of the molecular hourglass and a conserved logic of embryogenesis across kingdoms.

Nature Oct 11

Small heat-shock proteins protect from heat-stroke-associated neurodegeneration

Nikos Kourtis, Vassiliki Nikoletopoulou & Nektarios Tavernarakis

Nature 490, 213–218

Heat stroke is a life-threatening condition, characterized by catastrophic collapse of thermoregulation and extreme hyperthermia. In recent years, intensification of heat waves has caused a surge of heat-stroke fatalities. The mechanisms underlying heat-related pathology are poorly understood. Here we show that heat stroke triggers pervasive necrotic cell death and neurodegeneration in *Caenorhabditis elegans*. Preconditioning of animals at a mildly elevated temperature strongly protects from heat-induced necrosis. The heat-shock transcription factor HSF-1 and the small heat-shock protein HSP-16.1 mediate cytoprotection by preconditioning. HSP-16.1 localizes to the Golgi, where it functions with the Ca^{2+}- and Mn^{2+}-transporting ATPase PMR-1 to maintain Ca^{2+} homeostasis under heat stroke. Preconditioning also suppresses cell death inflicted by diverse insults, and protects mammalian neurons from heat cytotoxicity. These findings reveal an evolutionarily conserved mechanism that defends against diverse necrotic stimuli, and may be relevant to heat stroke and other pathological conditions involving necrosis in humans.

Nature Online

A map of rice genome variation reveals the origin of cultivated rice

Xuehui Huang, Nori Kurata, et al.

Nature (2012) doi:10.1038/nature11532 03 October 2012

Crop domestications are long-term selection experiments that have greatly advanced human civilization. The domestication of cultivated rice (*Oryza sativa* L.) ranks as one of the most important developments in history. However, its origins and domestication processes are controversial and have long been debated. Here we generate genome sequences from 446 geographically diverse accessions of the wild rice species *Oryza rufipogon*, the immediate ancestral progenitor of cultivated rice, and from 1,083 cultivated *indica* and *japonica* varieties to construct a comprehensive map of rice genome variation. In the search for signatures of selection, we identify 55 selective sweeps that have occurred during domestication. In-depth analyses of the domestication

sweeps and genome-wide patterns reveal that *Oryza sativa japonica* rice was first domesticated from a specific population of *O. rufipogon* around the middle area of the Pearl River in southern China, and that *Oryza sativa indica* rice was subsequently developed from crosses between *japonica* rice and local wild rice as the initial cultivars spread into South East and South Asia. The domestication-associated traits are analysed through high-resolution genetic mapping. This study provides an important resource for rice breeding and an effective genomics approach for crop domestication research.

Journal of Plant Physiology: Alert 28 September-4 October

Role of microRNAs and other sRNAs of plants in their changing environments Original Research Article

Pages 1664-1672

Katarzyna Kruszka, Marcin Pieczynski, David Windels, Dawid Bielewicz, Artur Jarmolowski, Zofia Szweykowska-Kulinska, Franck Vazquez

Cell: Alert 27 September-3 October

Reprogramming of DNA Methylation in Pollen Guides Epigenetic Inheritance via Small RNA Original Research Article

Pages 194-205

Joseph P. Calarco, Filipe Borges, Mark T.A. Donoghue, Frédéric Van Ex, Pauline E. Jullien, Telma Lopes, Rui Gardner, Frédéric Berger, José A. Feijó, Jörg D. Becker, Robert A. Martienssen

Nature Cell Biology contents: October 2012 Volume 14 Number 10, pp 977 – 1112

Auxin regulates aquaporin function to facilitate lateral root emergence pp991 - 998

Benjamin Péret, Guowei Li, Jin Zhao, Leah R. Band, Ute Voß, Olivier Postaire, Doan-Trung Luu, Olivier Da Ines, Ilda Casimiro, Mikaël Lucas, Darren M. Wells, Laure Lazzerini, Philippe Nacry, John R. King, Oliver E. Jensen, Anton R. Schäffner, Christophe Maurel and Malcolm J. Bennett

doi:10.1038/ncb2573

Bennett and colleagues find that auxin modulates water uptake in *Arabidopsis* roots by negatively regulating the expression of water channel aquaporins to allow lateral root emergence. The functional importance of aquaporins is supported by a mathematical model that shows delayed lateral root emergence when aquaporin levels are perturbed, as well as by the effects observed after aquaporin overexpression or mutation.

Endocytosis of the seven-transmembrane RGS1 protein activates G-protein-coupled signalling in *Arabidopsis* pp1079 - 1088

Daisuke Urano, Nguyen Phan, Janice C. Jones, Jing Yang, Jirong Huang, Jeffrey Grigston, J. Philip Taylor and Alan M. Jones

doi:10.1038/ncb2568

In plants, the heterotrimeric G-protein α subunit is kept inactive by binding to the regulator of G protein signalling 1 (RGS1) protein. Jones and colleagues show that G-protein β and γ subunits recruit the WNK8 kinase to the plasma membrane, where WNK8 phosphorylates RGS1 and facilitates its internalization. This effect de-represses Gα signalling and is required for sugar signalling and cell proliferation.

Current Biology

JAGGED Controls Growth Anisotropy and Coordination between Cell Size and Cell Cycle during Plant Organogenesis

Katharina Schiessl, Swathi Kausika, Paul Southam, Max Bush, Robert Sablowski

- Highlights
- *JAGGED (JAG*) is required for growth of initiating floral organs in *Arabidopsis*
- *JAG* decouples cell cycle from cell growth during organ emergence
- *JAG* promotes fast, anisotropic growth when floral organs emerge from the meristem
- *JAG* directly represses meristem identity genes

Summary

Background

In all multicellular organisms, the links between patterning genes, cell growth, cell cycle, cell size homeostasis, and organ growth are poorly understood, partly due to the difficulty of dynamic, 3D analysis of cell behavior in growing organs. A crucial step in plant organogenesis is the emergence of organ primordia from the apical meristems. Here, we combined quantitative, 3D analysis of cell geometry and DNA synthesis to study the role of the transcription factor JAGGED (JAG), which functions at the interface between patterning and primordium growth in *Arabidopsis* flowers.

Results

The floral meristem showed isotropic growth and tight coordination between cell volume and DNA synthesis. Sepal primordia had accelerated cell division, cell enlargement, anisotropic growth, and decoupling of DNA synthesis from cell volume, with a concomitant increase in cell size heterogeneity. All these changes in growth parameters required *JAG* and were genetically separable from primordium emergence. Ectopic JAG activity in the meristem promoted entry into S phase at inappropriately small cell volumes, suggesting that JAG can override a cell size checkpoint that operates in the meristem. Consistent with a role in the transition from meristem to primordium identity, JAG directly repressed the meristem regulatory genes *BREVIPEDICELLUS* and *BELL 1* in developing flowers.

Conclusions

We define the cellular basis for the transition from meristem to organ identity and identify *JAG* as a key regulator of this transition. *JAG* promotes anisotropic growth and is required for changes in cell size homeostasis associated with accelerated growth and the onset of differentiation in organ primordia.

Nature Biotechnology

Selective enrichment of newly synthesized proteins for quantitative secretome analysis

- Katrin Eichelbaum,
- Markus Winter,
- Mauricio Berriel Diaz,
- Stephan Herzig
- & Jeroen Krijgsveld

Secreted proteins constitute a large and biologically important subset of proteins that are involved in cellular communication, adhesion and migration. Yet secretomes are understudied because of technical limitations in the detection of low-abundance proteins against a background of serum-containing media. Here we introduce a method that combines click chemistry and pulsed stable isotope labeling with amino acids in cell culture to selectively enrich and quantify secreted proteins. The combination of these two labeling approaches allows cells to be studied irrespective of the complexity of the background proteins. We provide an in-depth and differential secretome analysis of various cell lines and primary cells, quantifying secreted factors, including cytokines, chemokines and growth factors. In addition, we reveal that serum starvation has a marked effect on secretome composition. We also analyze the kinetics of protein secretion by macrophages in response to lipopolysaccharides.

The Plant Cell

In Vivo Function of Tryptophans in the Arabidopsis UV-B Photoreceptor UVR8

Andrew O'Hara and Gareth I. Jenkins[1]

rabidopsis thaliana UV RESISTANCE LOCUS8 (UVR8) is a photoreceptor specifically for UV-B light that initiates photomorphogenic responses in plants. UV-B exposure causes rapid conversion of UVR8 from dimer to monomer, accumulation in the nucleus, and interaction with CONSTITUTIVELY PHOTOMORPHOGENIC1 (COP1), which functions with UVR8 in UV-B responses. Studies in yeast and with purified UVR8 implicate several tryptophan amino acids in UV-B photoreception. However, their roles in UV-B responses in plants, and the functional significance of all 14 UVR8 tryptophans, are not known. Here we report the functions of the UVR8 tryptophans in vivo. Three tryptophans in the β-propeller core are important in maintaining structural stability and function of UVR8. However, mutation of three other core tryptophans and four at the dimeric interface has no apparent effect on function in vivo. Mutation of three tryptophans implicated in UV-B photoreception, W233, W285, and W337, impairs photomorphogenic responses to different extents. W285 is essential for UVR8 function in plants, whereas W233 is important but not essential for function, and W337 has a lesser role. Ala mutants of these tryptophans appear monomeric and constitutively bind COP1 in plants, but their responses indicate that monomer formation and COP1 binding are not sufficient for UVR8 function.

Journal of Molecular Biology

The Structure of Human GALNS Reveals the Molecular Basis for Mucopolysaccharidosis IV A

Yadilette Rivera-Colón, Emily K. Schutsky, Adriana Z. Kita, Scott C. Garman

Lysosomal enzymes catalyze the breakdown of macromolecules in the cell. In humans, loss of activity of a lysosomal enzyme leads to an inherited metabolic defect known as a lysosomal storage disorder. The human lysosomal enzyme galactosamine-6-sulfatase (GALNS, also known as *N*-acetylgalactosamine-6-sulfatase and GalN6S; E.C. 3.1.6.4) is

deficient in patients with the lysosomal storage disease mucopolysaccharidosis IV A (also known as MPS IV A and Morquio A). Here, we report the three-dimensional structure of human GALNS, determined by X-ray crystallography at 2.2 Å resolution. The structure reveals a catalytic gem diol nucleophile derived from modification of a cysteine side chain. The active site of GALNS is a large, positively charged trench suitable for binding polyanionic substrates such as keratan sulfate and chondroitin-6-sulfate. Enzymatic assays on the insect-cell-expressed human GALNS indicate activity against synthetic substrates and inhibition by both substrate and product. Mapping 120 MPS IV A missense mutations onto the structure reveals that a majority of mutations affect the hydrophobic core of the structure, indicating that most MPS IV A cases result from misfolding of GALNS. Comparison of the structure of GALNS to paralogous sulfatases shows a wide variety of active-site geometries in the family but strict conservation of the catalytic machinery. Overall, the structure and the known mutations establish the molecular basis for MPS IV A and for the larger MPS family of diseases.

Impaired Folding of the Mitochondrial Small TIM Chaperones Induces Clearance by the *i*-AAA Protease

Michael J. Baker, Ved P. Mooga, Bernard Guiard, Thomas Langer, Michael T. Ryan, Diana Stojanovski

The intermembrane space of mitochondria contains a dedicated chaperone network—the small translocase of the inner membrane (TIM) family—for the sorting of hydrophobic precursors. All small TIMs are defined by the presence of a twin CX_3C motif and the monomeric proteins are stabilized by two intramolecular disulfide bonds formed between the cysteines of these motifs. The conserved cysteine residues within small TIM members have also been shown to participate in early biogenesis events, with the most N-terminal cysteine residue important for import and retention within the intermembrane space via the receptor and disulfide oxidase, Mia40. In this study, we have analyzed the *in vivo* consequences of improper folding of small TIM chaperones by generating site-specific cysteine mutants and assessed the fate of the incompletely oxidized proteins within mitochondria. We show that no individual cysteine residue is required for the function of Tim9 or Tim10 in yeast and that defective assembly of the small TIMs induces their proteolytic clearance from mitochondria. We delineate a clearance mechanism for the mutant proteins and their unassembled wild-type partner protein by the mitochondrial ATP-dependent protease, Yme1 (yeast mitochondrial escape 1).

These are two abstracts of articles published in plant physiology:
Title: The Effect of TRANSPARENT TESTA2 on Seed FattyAcid Biosynthesis and Tolerance to EnvironmentalStresses during Young Seedling Establishmentin Arabidopsis
Abstract: In plants, fatty acids (FAs) and FA-derived complex lipids are major carbon and energy reserves in seeds. They are essentialcomponents of cellular membranes and cellular signal or hormone molecules. Although TRANSPARENT TESTA2 (TT2) is wellstudied for its function in regulating proanthocyanidin biosynthesis in the seed coat, little attention has been given to its role inaffecting seed FA accumulation and tolerance to environmental stresses. We demonstrate that the tt2 mutation remarkablyincreased the seed FA content, decreased seed weight, and altered the FA composition. The increase in FA content in the tt2seeds was due to the relative decrease of seed coat proportion as well as the more efficient FA synthesis in the tt2

embryo.Microarray analysis revealed that tt2 mutation up-regulated a group of genes critical to FA biosynthesis and embryonicdevelopment. The mutation also altered the gene expressions that respond to stress. The microarray analysis discovered thatthe increase in FA accumulation of the tt2 seeds were accompanied by the significant up-regulation of FUSCA3, a transcriptionalfactor for embryonic development and FATTY ACID ELONGASE1, which catalyzes the elongation of FA chains. Moreover,lower seed protein accumulation during seed maturation also contributed to the increased seed FA accumulation i n tt2 mutants.This study advances the understanding of the TT2 gene in seed FA accumulation and abiotic stresses during seed germinationand seedling establishment

Title:RNA Silencing Induced by an Artificial Sequence That Prevents Proper Transcription Termination in Rice

Abstract: Posttranscriptional gene silencing (PTGS) is a sequence-specific mRNA degradation caused by small RNA, such as microRNA(miRNA) and small interfering RNA (siRNA). miRNAs are generated from MIRNA loci, whereas siRNAs originate from varioussources of double-stranded RNA. In this study, an artificial RNA silencing inducible sequence (RSIS) was identified in rice (Oryzasativa). This sequence causes PTGS of 59 or 39 flanking-sequence-containing genes. Interestingly, two target genes can besimultaneously suppressed by linking a unique target sequence to either the 59 or 39 end of RSIS. Multiple gene suppressioncan be also achieved though a single transformation event by incorporating the multisite gateway system. Moreover, RSISmediatedPTGS occurs in nuclei. Deep sequencing of small RNAs reveals that siRNAs are produced from RSIS-expressingcassettes and transitive siRNAs are produced from endogenous target genes. Furthermore, siRNAs are typically generated fromuntranscribed transgene terminator regions. The read-through transcripts from the RSIS-expression cassette were consistentlyobserved, and most of these sequences were not polyadenylated. Collectively, this data indicates that RSIS inhibits propertranscription termination. The resulting transcripts are not polyadenylated. These transcripts containing RSIS become templatesfor double-stranded RNA synthesis in nuclei. This is followed by siRNA production and target degradation of target genes.