

**Indu:**

1. Science. 2013 Aug 30;341(6149):1240104. doi: 10.1126/science.1240104.

Nuclear lamin-A scales with tissue stiffness and enhances matrix-directed differentiation.

Swift J, Ivanovska IL, Buxboim A, Harada T, Dingal PC, Pinter J, Pajeroski JD, Spinler KR, Shin JW, Tewari M, Rehfeldt F, Speicher DW, Discher DE.

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Comment in

Science. 2013 Aug 30;341(6149):965-6.

Tissues can be soft like fat, which bears little stress, or stiff like bone, which sustains high stress, but whether there is a systematic relationship between tissue mechanics and differentiation is unknown. Here, proteomics analyses revealed that levels of the nucleoskeletal protein lamin-A scaled with tissue elasticity, E, as did levels of collagens in the extracellular matrix that determine E. Stem cell differentiation into fat on soft matrix was enhanced by low lamin-A levels, whereas differentiation into bone on stiff matrix was enhanced by high lamin-A levels. Matrix stiffness directly influenced lamin-A protein levels, and, although lamin-A transcription was regulated by the vitamin A/retinoic acid (RA) pathway with broad roles in development, nuclear entry of RA receptors was modulated by lamin-A protein. Tissue stiffness and stress thus increase lamin-A levels, which stabilize the nucleus while also contributing to lineage determination.

PMID: 23990565 [PubMed - indexed for MEDLINE]

2. Science. 2013 Sep 6;341(6150):1103-6. doi: 10.1126/science.1241602. Epub 2013 Aug 15.

Caffeoyl shikimate esterase (CSE) is an enzyme in the lignin biosynthetic pathway in Arabidopsis.

Vanholme R, Cesarino I, Rataj K, Xiao Y, Sundin L, Goeminne G, Kim H, Cross J,

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Lignin is a major component of plant secondary cell walls. Here we describe caffeoyl shikimate esterase (CSE) as an enzyme central to the lignin biosynthetic pathway. *Arabidopsis thaliana* cse mutants deposit less lignin than do wild-type plants, and the remaining lignin is enriched in p-hydroxyphenyl units. Phenolic metabolite profiling identified accumulation of the lignin pathway intermediate caffeoyl shikimate in cse mutants as compared to caffeoyl shikimate levels in the wild type, suggesting caffeoyl shikimate as a substrate for CSE. Accordingly, recombinant CSE hydrolyzed caffeoyl shikimate into caffeate. Associated with the changes in lignin, the conversion of cellulose to glucose in cse mutants increased up to fourfold as compared to that in the wild type upon saccharification without pretreatment. Collectively, these data necessitate the revision of currently accepted models of the lignin biosynthetic pathway.

PMID: 23950498 [PubMed - in process]

3. Science. 2013 Sep 6;341(6150):1100-3. doi: 10.1126/science.1241706.

Achieving the convention on biological diversity's goals for plant conservation.

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Identifying which areas capture how many species is the first question in conservation planning. The Convention on Biological Diversity (CBD) aspires to formal protection of at least 17% of the terrestrial world and, through the Global Strategy for Plant Conservation, 60% of plant species. Are these targets of protecting area and species compatible? We show that 67% of plant species live entirely within regions that comprise 17% of the land surface. Moreover, these regions include most terrestrial vertebrates with small geographical ranges. However, the connections between the CBD targets of protecting area and species are complex. Achieving both targets will be difficult because regions with the most plant species have only slightly more land protected than do those with fewer.

PMID: 24009391 [PubMed - in process]

**Damian:**

[Plant J.](#) 2013 Sep;75(6):965-76. doi: 10.1111/tpj.12259. Epub 2013 Jul 19.

**ABA and the ubiquitin E3 ligase KEEP ON GOING affect proteolysis of the Arabidopsis thaliana transcription factors ABF1 and ABF3.**

[Chen YT](#), [Liu H](#), [Stone S](#), [Callis J](#).

**Source**

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**Abstract**

The ABA Binding Factor/ABA-Responsive Element Binding Proteins (ABF/AREB) subfamily of bZIP-type transcription factors are positive effectors of ABA responses. Here, we examine the proteolytic regulation of two members: Arabidopsis thaliana ABF1 and ABF3. Both transcription factors are unstable in seedlings, and their degradation is sensitive to proteasome inhibition. ABA treatment of seedlings leads to their rapid accumulation, the result of slowed proteolysis. Deletion of the conserved C-terminal region required for 14-3-3 interaction destabilizes the proteins. The degradation of ABF1 and ABF3 are slower in vivo in seedlings lacking the ubiquitin E3 ligase KEEP ON GOING (KEG), and in vitro in extracts from keg seedlings, implicating KEG in their degradation. ABF1 and ABF3 are ubiquitylation substrates of KEG in vitro, and in vitro pull-down assays document their direct interaction. In contrast to ABI5, another KEG substrate, the degradation of ABFs and proteolytic regulation of ABFs by ABA still occurs in keg seedlings, suggesting that additional E3s participate in ABF1 and ABF3 proteolysis. Loss of ABF1 or ABF3 in the keg background has a phenotypic effect similar to the loss of ABI5, and there is no additional rescue of the keg phenotype in abf1 abf3 abi5 keg seedlings. This result suggests that the abundance of other substrates is altered in keg seedlings, affecting growth. In conclusion, ABF1 and ABF3 abundance is affected by ABA and KEG, and the conserved C4 region serves as a stabilizing element.

[Plant Physiol.](#) 2013 Sep 9. [Epub ahead of print]

**Molecular steps in the immune signaling pathway evoked by plant elicitor peptides (Peps): CPKs, NO and ROS are downstream from the early Ca<sup>2+</sup> signal.**

[Ma Y](#), [Zhao Y](#), [Walker RK](#), [Berkowitz GA](#).

**Source**

University of Connecticut.

**Abstract**

Endogenous plant elicitor peptides (Peps) act as damage associated molecular patterns (DAMPs) to facilitate pathogen defense responses. Binding of these DAMP peptides to Arabidopsis thaliana plasma membrane localized Pep receptors (PEPRs) leads to cytosolic Ca<sup>2+</sup> elevation, an early event in a signaling cascade that activates immune responses. This immune response includes the amplification of signaling evoked by direct perception of pathogen associated molecular patterns (PAMPs) by plant cells under assault. Work included in this report further characterizes this plant immune response and identifies new molecular steps in the signal transduction cascade. The PEPR coreceptor

BAK1 contributes to generation of the Pep-activated Ca<sup>2+</sup> signal and, in doing so, leads to increased defense gene expression and resistance to a virulent bacterial pathogen. Ca<sup>2+</sup>-dependent protein kinases (CPKs) 'decode' the Ca<sup>2+</sup> signal, also facilitating defense gene expression and enhanced resistance to the pathogen. Nitric oxide (NO) and NADPH oxidase-dependent reactive oxygen species (ROS) generation are also involved downstream from the Ca<sup>2+</sup> signal in the Pep immune defense signal transduction cascade. We find a synergism between function of the PEPR DAMP receptor and the PAMP flagellin receptor FLS2 in terms of both NO and ROS generation. Presented results are also consistent with the involvement of the secondary messenger cGMP and a cGMP-activated Ca<sup>2+</sup>-conducting channel in the Pep immune signaling pathway.

[FEBS Lett.](#) 2013 Sep 10. pii: S0014-5793(13)00678-9. doi: 10.1016/j.febslet.2013.08.045. [Epub ahead of print]

**Functional conservation between mammalian MGRN1 and plant LOG2 ubiquitin ligases.**

[Guerra DD](#), [Pratelli R](#), [Kraft E](#), [Callis J](#), [Pilot G](#).

**Source**

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**Abstract**

Plant LOSS OF GDU 2 (LOG2) and mammalian MAHOGUNIN RING FINGER 1 (MGRN1) proteins are RING-type E3 ligases sharing similarity N-terminal to the RING domain. Deletion of this region disrupts the interaction of LOG2 with the plant membrane protein GLUTAMINE DUMPER 1 (GDU1). Phylogenetic analysis identified two clades of LOG2/MGRN1-like proteins in vertebrates and plants. The ability of MGRN1 to functionally replace LOG2 was tested. MGRN1 ubiquitylates GDU1 in vitro and can partially substitute for LOG2 in the plant, partially restoring amino acid resistance to a GDU1-myc over-expression, log2-1 background. Altogether, these results suggest a conserved function for the N-terminal domain in evolution.

**Mechanism and consequence of the autoactivation of p38 $\alpha$  mitogen-activated protein kinase promoted by TAB1**

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Affiliations: A variety of institutions in Oxford and London, UK.

p38 $\alpha$  mitogen-activated protein kinase (p38 $\alpha$ ) is activated by a variety of mechanisms, including autophosphorylation initiated by TGF $\beta$ -activated kinase 1 binding protein 1

(TAB1) during myocardial ischemia and other stresses. Chemical-genetic approaches and coexpression in mammalian, bacterial and cell-free systems revealed that mouse p38 $\alpha$  autophosphorylation occurs in *cis* by direct interaction with TAB1(371–416). In isolated rat cardiac myocytes and perfused mouse hearts, TAT-TAB1(371–416) rapidly activates p38 and profoundly perturbs function. Crystal structures and characterization in solution revealed a bipartite docking site for TAB1 in the p38 $\alpha$  C-terminal kinase lobe. TAB1 binding stabilizes active p38 $\alpha$  and induces rearrangements within the activation segment by helical extension of the Thr-Gly-Tyr motif, allowing autophosphorylation in *cis*. Interference with p38 $\alpha$  recognition by TAB1 abolishes its cardiac toxicity. Such intervention could potentially circumvent the drawbacks of clinical pharmacological inhibitors of p38 catalytic activity.

### **Identification of the Major Ubiquitin-binding Domain of the *Pseudomonas aeruginosa* ExoU A<sub>2</sub> Phospholipase**

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Numerous Gram-negative bacterial pathogens use type III secretion systems to deliver effector molecules into the cytoplasm of a host cell. Many of these effectors have evolved to manipulate the host ubiquitin system to alter host cell physiology or the location, stability, or function of the effector itself. ExoU is a potent A<sub>2</sub> phospholipase used by *Pseudomonas aeruginosa* to destroy membranes of infected cells. The enzyme is held in an inactive state inside of the bacterium due to the absence of a required eukaryotic activator, which was recently identified as ubiquitin. This study sought to identify the region of ExoU required to mediate this interaction and determine the properties of ubiquitin important for binding, ExoU activation, or both. Biochemical and biophysical approaches were used to map the ubiquitin-binding domain to a C-terminal four-helix bundle of ExoU. The hydrophobic patch of ubiquitin is required for full binding affinity and activation. Binding and activation were uncoupled by introducing an L8R substitution in ubiquitin. Purified L8R demonstrated a parental binding phenotype to ExoU but did not activate the phospholipase *in vitro*. Utilizing these new biochemical data and intermolecular distance measurements by double electron-electron resonance, we propose a model for an ExoU-monoubiquitin complex.

**Stephanie:**

## **Transcriptomics approaches in the early *Arabidopsis* embryo**

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Early plant embryogenesis condenses the fundamental processes underlying plant development into a short sequence of predictable steps. The main tissues, as well as stem cells for their post-embryonic maintenance, are specified through genetic control networks. A key question is how cell fates are instructed by unique cellular transcriptomes, and important insights have recently been gained through cell type-specific transcriptomics during post-embryonic development. However, the poor accessibility and small size of *Arabidopsis* (*Arabidopsis thaliana*) embryos have obstructed similar progress during embryogenesis. Here, we review the current situation in plant embryo transcriptomics, and discuss how the recent development of novel cell-specific analysis technologies will enable the identification of cellular transcriptomes in the early *Arabidopsis* embryo.

De novo transcriptome analysis of an imminent biofuel crop,  
Camelina sativa L. using Illumina GAII-X sequencing platform  
and identification of SSR markers – **PMB**

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**Abstract:** Camelina sativa L. is an emerging biofuel crop with potential applications in industry, medicine, cosmetics and human nutrition. The crop is unexploited owing to very limited availability of transcriptome and genomic data. In order to analyse the various metabolic pathways, we performed de novo assembly of the transcriptome on Illumina GAII-X platform with paired end sequencing for obtaining short reads. The sequencing output generated a FastQ file size of 2.97 GB with 10.83 million reads having a maximum read length of 101 nucleotides. The number of contigs generated was 53,854 with maximum and minimum lengths of 10,086 and 200 nucleotides respectively. These transcripts were annotated using BLAST search against the Aracyc, Swiss-Prot, TrEMBL, gene ontology and clusters of orthologous groups (KOG) databases. The genes involved in lipid metabolism were studied and the transcription factors were identified. Sequence similarity studies of Camelina with the other related organisms indicated the close relatedness of Camelina with Arabidopsis. In addition, bioinformatics analysis revealed the presence of a total of 19,379 simple sequence repeats. This is the first report on Camelina sativa L., where the transcriptome of the entire plant, including seedlings, seed, root,

leaves and stem was done. Our data established an excellent resource for gene discovery and provide useful information for functional and comparative genomic studies in this promising biofuel crop.

**Nathen:**

**Molecular Cell:**

**The Membrane Stress Response Buffers**

**Lethal Effects of Lipid Disequilibrium**

by Reprogramming the Protein Homeostasis Network

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