Indu

1.Plant scientists: GM technology is safe
BY NOAH FAHLGREN, REBECCA BART, LUIS HERRERA-ESTRELLA, RUBÉN RELLÁN-ÁLVAREZ, DANIEL H. CHITWOOD, JOSÉ R. DINNENY
SCIENCE19 FEB 2016 : 824

2. Calling all failed replication experiments
BY JOCELYN KAISER

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3.Structures of a CRISPR-Cas9 R-loop complex primed for DNA cleavage
Fuguo Jiang1,*, David W. Taylor1,2,*, Janice S. Chen1, Jack E. Kornfeld3, Kaihong Zhou3, Aubri J. Thompson4, Eva Nogales1,2,3,5,†, Jennifer A. Doudna1,2,3,4,5,†
Science 19 Feb 2016:Vol. 351, Issue 6275, pp. 867-871

4.RPN1 PROVIDES ADJACENT RECEPTOR SITES FOR SUBSTRATE BINDING AND DEUBIQUITINATION BY THE PROTEASOME
Yuan Shi1,*, Xiang Chen2,*, Suzanne Elsasser1,*, Bradley B. Stocks3,*, Geng Tian1, Byung-Hoon Lee1,Yanhong Shi2,4, Naixia Zhang4, Stefanie A. H. de Poot1, Fabian Tuebing1, Shuangwu Sun1, Jacob Vannoy2, 5, Sergey G. Tarasov6, John R. Engen3,†, Daniel Finley1,†, Kylie J. Walters
Science 19 Feb 2016:Vol. 351, Issue 6275, pp.

5.Using decoys to expand the recognition specificity of a plant disease resistance protein
Sang Hee Kim*, Dong Qi†, Tom Ashfield, Matthew Helm, Roger W. Innes‡
Science 12 Feb 2016: Vol. 351, Issue 6274, pp. 684-687

Minsoo

1. Plant synthetic biology for molecular engineering of signalling and development
Jennifer L. Nemhauser & Keiko U. Torii
Nature Plants 2, Article number: 16010 (2016)
Published online:
02 March 2016
Molecular genetic studies of model plants in the past few decades have identified many key genes and pathways controlling development, metabolism and environmental responses. Recent technological and informatics advances have led to unprecedented volumes of data that may uncover underlying principles of plants as biological systems. The newly emerged discipline of synthetic biology and related

molecular engineering approaches is built on this strong foundation. Today, plant regulatory pathways can be reconstituted in heterologous organisms to identify and manipulate parameters influencing signalling outputs. Moreover, regulatory circuits that include receptors, ligands, signal transduction components, epigenetic machinery and molecular motors can be engineered and introduced into plants to create novel traits in a predictive manner. Here, we provide a brief history of plant synthetic biology and significant recent examples of this approach, focusing on how knowledge generated by the reference plant Arabidopsis thaliana has contributed to the rapid rise of this new discipline, and discuss potential future directions.

2. Molecular cell special issue. The mighty mitochondria.

3. Mol Cell. 2016 Mar 3;61(5):705-19.
Mitochondria-Translocated PGK1 Functions as a Protein Kinase to Coordinate Glycolysis and the TCA Cycle in Tumorigenesis.

Li X(1), Jiang Y(2), Meisenhelder J(3), Yang W(1), Hawke DH(4), Zheng Y(1), Xia Y(2), Aldape K(4), He J(5), Hunter T(3), Wang L(6), Lu Z(7).

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It is unclear how the Warburg effect that exemplifies enhanced glycolysis in the cytosol is coordinated with suppressed mitochondrial pyruvate metabolism. We demonstrate here that hypoxia, EGFR activation, and expression of K-Ras G12V and B-Raf V600E induce mitochondrial translocation of phosphoglycerate kinase 1 (PGK1); this is mediated by ERK-dependent PGK1 S203 phosphorylation and

subsequent PIN1-mediated cis-trans isomerization. Mitochondrial PGK1 acts as a protein kinase to phosphorylate pyruvate dehydrogenase kinase 1 (PDHK1) at T338,
which activates PDHK1 to phosphorylate and inhibit the pyruvate dehydrogenase (PDH) complex. This reduces mitochondrial pyruvate utilization, suppresses reactive oxygen species production, increases lactate production, and promotes brain tumorigenesis. Furthermore, PGK1 S203 and PDHK1 T338 phosphorylation levels
correlate with PDH S293 inactivating phosphorylation levels and poor prognosis in glioblastoma patients. This work highlights that PGK1 acts as a protein kinase in coordinating glycolysis and the tricarboxylic acid (TCA) cycle, which is instrumental in cancer metabolism and tumorigenesis.

Jarrett

1)
Identification of Interactions in the NMD Complex Using Proximity-Dependent Biotinylation (BioID)
Christoph Schweingruber , Paolo Soffientini , Marc-David Ruepp , Angela Bachi , Oliver Mühlemann
Published: March 2, 2016 PLOS One
http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0150239

2)
Nitric Oxide in the Offensive Strategy of Fungal and Oomycete Plant Pathogens
Magdalena Arasimowicz-Jelonek1* and Jolanta Floryszak-Wieczorek2
Front. Plant Sci., 04 March 2016 | http://dx.doi.org/10.3389/fpls.2016.00252

Keith

The dynamic N^1-methyladenosine methylome in eukaryotic messenger RNA

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Nature **530**, 441–446 (25 February 2016)

Gene expression can be regulated post-transcriptionally through dynamic and reversible RNA modifications. A recent noteworthy example is N^6-methyladenosine (m^6A), which affects messenger RNA (mRNA) localization, stability, translation and splicing. Here we report on a new mRNA modification, N^1-methyladenosine (m^1A), that occurs on thousands of different gene transcripts in eukaryotic cells, from yeast to mammals, at an estimated average transcript stoichiometry of 20% in humans. Employing newly developed sequencing approaches, we show that m^1A is enriched around the start codon upstream of the first splice site: it preferentially decorates more structured regions around canonical and alternative translation initiation sites, is dynamic in response to physiological conditions, and correlates positively with protein production. These unique features are highly conserved in mouse and human cells, strongly indicating a functional role for m^1A in promoting translation of methylated mRNA.

Late acquisition of mitochondria by a host with chimaeric prokaryotic ancestry

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The origin of eukaryotes stands as a major conundrum in biology[1]. Current evidence indicates that the last eukaryotic common ancestor already possessed many eukaryotic hallmarks, including a complex subcellular organization[1, 2, 3]. In addition, the lack of evolutionary intermediates challenges the elucidation of the relative order of emergence of eukaryotic traits. Mitochondria are ubiquitous organelles derived from an alphaproteobacterial endosymbiont[4]. Different hypotheses disagree on whether mitochondria were acquired early or late during eukaryogenesis[5]. Similarly, the nature and complexity of the receiving host are debated, with models ranging from a simple prokaryotic host to an already complex proto-eukaryote[1, 3, 6, 7]. Most competing scenarios can be roughly grouped into either mito-early, which consider the driving force of eukaryogenesis to be mitochondrial endosymbiosis into a simple host, or mito-late, which postulate that a significant complexity predated mitochondrial endosymbiosis[3]. Here we provide evidence for late

mitochondrial endosymbiosis. We use phylogenomics to directly test whether proto-mitochondrial proteins were acquired earlier or later than other proteins of the last eukaryotic common ancestor. We find that last eukaryotic common ancestor protein families of alphaproteobacterial ancestry and of mitochondrial localization show the shortest phylogenetic distances to their closest prokaryotic relatives, compared with proteins of different prokaryotic origin or cellular localization. Altogether, our results shed new light on a long-standing question and provide compelling support for the late acquisition of mitochondria into a host that already had a proteome of chimaeric phylogenetic origin. We argue that mitochondrial endosymbiosis was one of the ultimate steps in eukaryogenesis and that it provided the definitive selective advantage to mitochondria-bearing eukaryotes over less complex forms.

Crystal structure of eukaryotic translation initiation factor 2B

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Eukaryotic cells restrict protein synthesis under various stress conditions, by inhibiting the eukaryotic translation initiation factor 2B (eIF2B)[1, 2]. eIF2B is the guanine nucleotide exchange factor for eIF2, a heterotrimeric G protein consisting of α-, β- and γ-subunits. eIF2B exchanges GDP for GTP on the γ-subunit of eIF2 (eIF2γ), and is inhibited by stress-induced phosphorylation of eIF2α. eIF2B is a heterodecameric complex of two copies each of the α-, β-, γ-, δ- and ε-subunits[3]; its α-, β- and δ-subunits constitute the regulatory subcomplex[4], while the γ- and ε-subunits form the catalytic subcomplex[5]. The three-dimensional structure of the entire eIF2B complex has not been determined. Here we present the crystal structure of *Schizosaccharomyces pombe* eIF2B with an unprecedented subunit arrangement, in which the α2β2δ2 hexameric regulatory subcomplex binds two γε dimeric catalytic subcomplexes on its opposite sides. A structure-based *in vitro* analysis by a surface-scanning site-directed photo-cross-linking method identified the eIF2α-binding and eIF2γ-binding interfaces, located far apart on the regulatory and catalytic subcomplexes, respectively. The eIF2γ-binding interface is located close to the conserved 'NF motif', which is important for nucleotide exchange. A structural model was constructed for the complex of eIF2B with phosphorylated

eIF2α, which binds to eIF2B more strongly than the unphosphorylated form. These results indicate that the eIF2α phosphorylation generates the 'nonproductive' eIF2–eIF2B complex[5], which prevents nucleotide exchange on eIF2γ, and thus provide a structural framework for the eIF2B-mediated mechanism of stress-induced translational control.