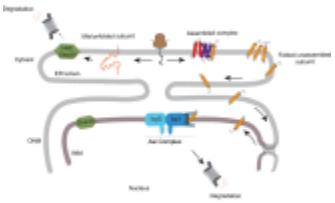
January 2020
Molecular Cell : Volume 77, Issue 1

Quality Control of Protein Complex Assembly by a Transmembrane Recognition Factor

Pages 108-119.e9

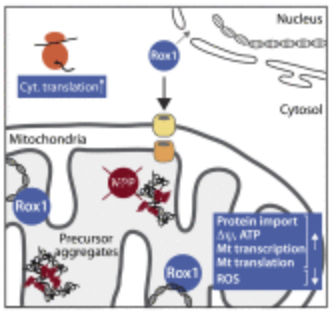
Nivedita Natarajan, Ombretta Foresti, Kim Wendrich, Alexander Stein, Pedro Carvalho



An Early mtUPR: Redistribution of the Nuclear Transcription Factor Rox1 to Mitochondria Protects against Intramitochondrial Proteotoxic Aggregates

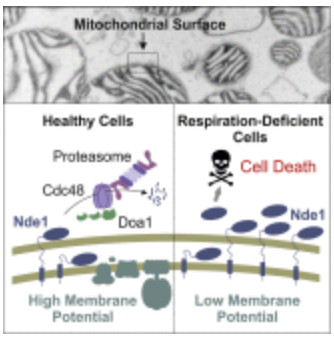
Pages 180-188.e9

Daniel Poveda-Huertes, Stanka Matic, Adinarayana Marada, Lukas Habernig, ... F.-Nora Vögtle



The NADH Dehydrogenase Nde1 Executes Cell Death after Integrating Signals from Metabolism and Proteostasis on the Mitochondrial Surface ***Pages 189-202.e6***

SreeDivya Saladi, Felix Boos, Michael Poglitsch, Hadar Meyer, ... Johannes M. Herrmann



Nature

The water lily genome and the early evolution of flowering plants

The genome of the tropical blue-petal water lily *Nymphaea colorata* and the transcriptomes from 19 other Nymphaeales species provide insights into the early evolution of angiosperms.

Liangsheng Zhang, Fei Chen & Haibao Tang

Abstract

Water lilies belong to the angiosperm order Nymphaeales. Amborellales, Nymphaeales and Austrobaileyales together form the so-called ANA-grade of angiosperms, which are extant representatives of lineages that diverged the earliest from the lineage leading to the extant mesangiosperms[1,2,3]. Here we report the 409-megabase genome sequence of the blue-petal water lily (*Nymphaea colorata*). Our phylogenomic analyses support Amborellales and Nymphaeales as successive sister

lineages to all other extant angiosperms. The *N. colorata* genome and 19 other water lily transcriptomes reveal a Nymphaealean whole-genome duplication event, which is shared by Nymphaeaceae and possibly Cabombaceae. Among the genes retained from this whole-genome duplication are homologues of genes that regulate flowering transition and flower development. The broad expression of homologues of floral ABCE genes in *N. colorata* might support a similarly broadly active ancestral ABCE model of floral organ determination in early angiosperms. Water lilies have evolved attractive floral scents and colours, which are features shared with mesangiosperms, and we identified their putative biosynthetic genes in *N. colorata*. The chemical compounds and biosynthetic genes behind floral scents suggest that they have evolved in parallel to those in mesangiosperms. Because of its unique phylogenetic position, the *N. colorata* genome sheds light on the early evolution of angiosperms.

 Article | 04 December 2019
RGF1 controls root meristem size through ROS signalling
RITF1, a newly identified plant transcription factor, links signalling through the peptide hormone RGF1 to the balance of reactive oxygen species and thereby enhances the stability of another transcription factor, PLETHORA2, a master regulator of root stem cells.
Masashi Yamada, , Xinwei Han & Philip N. Benfey

The stem cell niche and the size of the root meristem in plants are maintained by intercellular interactions and signalling networks involving a peptide hormone, root meristem growth factor 1 (RGF1)[1]. Understanding how RGF1 regulates the development of the root meristem is essential for understanding stem cell function. Although five receptors for RGF1 have been identified[2,3,4], the downstream signalling mechanism remains unknown. Here we report a series of signalling events that follow RGF1 activity. We find that the RGF1-receptor pathway controls the distribution of reactive oxygen species (ROS) along the developmental zones of the *Arabidopsis* root. We identify a previously uncharacterized transcription factor, *RGF1-INDUCIBLE TRANSCRIPTION FACTOR 1* (*RITF1*), that has a central role in mediating RGF1 signalling. Manipulating *RITF1* expression leads to the redistribution of ROS along the root developmental zones. Changes in ROS distribution in turn enhance the stability of the PLETHORA2 protein, a master regulator of root stem cells. Our results thus clearly depict a signalling cascade that is initiated by RGF1, linking this peptide to mechanisms that regulate ROS.

Burke JM, Lester ET, Tauber D, Parker R.
RNase L promotes the formation of unique ribonucleoprotein granules distinct from stress granules.
J Biol Chem. 2020 Jan 2;. [Epub ahead of print] PMID: 31896577 [PubMed - as supplied by publisher]

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Peroxisomal fission is modulated by the mitochondrial Rho-GTPases, Miro1 and Miro2.
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Vecchi G, Sormanni P, Mannini B, Vandelli A, Tartaglia GG, Dobson CM, Hartl FU, Vendruscolo M.
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Structural and mechanistic insights into Hsp104 function revealed by synchrotron x-ray footprinting.
J Biol Chem. 2019 Dec 27;. [Epub ahead of print] PMID: 31882541 [PubMed - as supplied by publisher]

Khan M, Imran QM, Shahid M, Mun BG, Lee SU, Khan MA, Hussain A, Lee IJ, Yun BW.
Nitric oxide- induced AtAO3 differentially regulates plant defense and drought tolerance in Arabidopsis thaliana.
BMC Plant Biol. 2019 Dec 30;19(1):602. PMID: 31888479 [PubMed - in process]

Zhao Y, Ma W, Wei X, Long Y, Zhao Y, Su M, Luo Q.
Identification of Exogenous Nitric Oxide-Responsive miRNAs from Alfalfa (<i>Medicago sativa</i> L.) under Drought Stress by High-Throughput Sequencing.
Genes (Basel). 2019 Dec 26;11(1). PMID: 31888061 [PubMed - in process]

Kustatscher, G. et al. Co-regulation map of the human proteome enables identification of protein functions. ***Nat. Biotechnol.*** **37**, 1361–1371 (2019).
A protein co-regulation database facilitates proteome-wide functional annotations.
Gene co-expression profiling is a well-established method to predict protein function. These analyses are often carried out at the transcript level, but this may lead to inaccurate results when mRNA and protein levels do not correlate.
Juri Rappsilber and colleagues at the University of Edinburgh used quantitative proteomics to perform large-scale co-expression screens directly at the protein level and built a database of co-regulated proteins. These data reveal protein associations and functional connections independent of mRNA co-expression, physical protein interactions or colocalization.

The researchers combined their own and published isotope labeling mass spectrometry data to quantify the cellular proteome response to 294 biological conditions. To identify proteins with similar quantitative trends across these conditions, Rappsilber and co-workers used unsupervised machine learning, which is shown to be more robust and selective than Pearson correlation analysis or related metrics. They also provided evidence that machine-learning-derived protein co-regulation scores are more informative than mRNA co-expression analysis, although transcriptomics still has distinct advantages with regard to gene coverage.

The protein co-regulation scores form the basis of the ProteomeHD resource, which complements existing protein association databases such as STRING and BioGRID. The Rappsilber team shows that ProteomeHD can reveal proteins with dual cellular functions and provide functional insights that are difficult to obtain by other proteomics approaches. For example, they find the peroxisomal protein PEX11β is co-regulated with several mitochondrial proteins, and confirm in follow-up experiments that PEX11β contributes to peroxisome-mitochondria contacts. ProteomeHD is available as an interactive and functionally annotated map at www.proteomeHD.net, bringing functional genomics one step closer to the protein level.

Science

Computational design of a modular protein sense-response system
Anum A. Glasgow[…],Tanja Kortemme[1,2,3,4,6,7,#]
Science 22 Nov 2019:
Vol. 366, Issue 6468, pp. 1024-1028
DOI: 10.1126/science.aax8780
Sense and respond
Many signaling pathways start with cellular proteins sensing and responding to small molecules. Despite advances in protein design, creating a protein-based sense-and-respond system remains challenging. Glasgow *et al.* designed binding sites at the interface of protein heterodimers (see the Perspective by Chica). By fusing each monomer to one half of a split reporter, they linked ligand-driven dimerization to the reporter output. The computational design strategy provides a generalizable approach to create synthetic sensing systems with different outputs.
Science, this issue p. 1024; see also p. 952
Abstract
Sensing and responding to signals is a fundamental ability of living systems, but despite substantial progress in the computational design of new protein structures, there is no general approach for engineering arbitrary new protein sensors. Here, we describe a generalizable computational strategy for designing sensor-actuator proteins by building binding sites de novo into heterodimeric protein-protein interfaces and coupling ligand sensing to modular actuation through split reporters. Using this approach, we designed protein sensors that respond to farnesyl pyrophosphate, a metabolic intermediate in the production of valuable compounds. The sensors are functional in vitro and in cells, and the crystal structure of the engineered binding site closely matches the design model. Our computational design strategy opens broad avenues to link biological outputs to new signals.

Nature Methods
Article | 25 November 2019
Bottom-up structural proteomics: cryoEM of protein complexes enriched from the cellular milieu
An approach combining cryo-electron microscopy and mass spectrometry analysis of protein complexes enriched directly from cells enables structure determination of unknown complexes at atomic resolution.
Chi-Min Ho, Xiaorun Li[…] & Z. Hong Zhou

E-life

GC content shapes mRNA storage and decay in human cells
Maïté Courel, Yves Clément ... Dominique Weil
The GC content of human mRNAs is key to P-body localization and protein yield, and has a major impact on their post-transcriptional control.

The GTPase Nog1 co-ordinates assembly, maturation and quality control of distant ribosomal functional centers
Purnima Klingauf-Nerurkar, Ludovic C Gillet ... Vikram G Panse

Misfolded proteins bind and activate death receptor 5 to induce apoptosis during unresolved endoplasmic reticulum stress
Mable Lam, Scot A Marsters ... Peter Walter

Plant Cell

Matrix Redox Physiology Governs the Regulation of Plant Mitochondrial Metabolism through Post-Translational Protein Modifications
Ian Max Møller, Abir U Igamberdiev, Natalia V. Bykova, Iris Finkemeier, Allan G. Rasmusson and Markus Schwarzländer
Plant Cell 2020 tpc.19.00535; Advance Publication January 6, 2020; doi:10.1105/tpc.19.00535
http://www.plantcell.org/content/early/2020/01/06/tpc.19.00535.abstract

Plant Journal

Overexpression of BUNDLE SHEATH DEFECTIVE 2 improves the efficiency of photosynthesis and growth in *Arabidopsis*
Florian A. Busch, Jun Tominaga, Masato Muroya, Norihiko Shirakami, Shunichi Takahashi, Wataru Yamori, Takuya Kitaoka, Sara E. Milward, Kohji Nishimura, Erika Matsunami, Yosuke Toda, Chikako Higuchi, Atsuko Muranaka, Tsuneaki Takami, Shunsuke Watanabe, Toshinori Kinoshita, Wataru Sakamoto, Atsushi Sakamoto, Hiroshi Shimada
Version of Record online: 26 December 2019

Significance Statement

Catalytic properties of RuBisCO are susceptible to oxidation of its thiols, but the underlying process resulting in a change in RuBisCO activation has been largely elusive. Here we identify BSD2, known as a chaperone for RuBisCO assembly, as a protein that takes an essential role in the redox homeostasis of mature RuBisCO. We show that overexpression of BSD2 improves RuBisCO carboxylation efficiency through manipulating the redox potential.

Topologies of *N6*-adenosine methylation (m6A) in land plant mitochondria and their putative effects on organellar gene expression
Omer Murik, Sam Aldrin Chandran, Keren Nevo-Dinur, Laure D. Sultan, Corinne Best, Yuval Stein, Carina Hazan, Oren Ostersetzer-Biran
Version of Record online: 22 December 2019

Significance Statement

Our study focuses on *N6*-methyladenosine (m6A) in plant mitochondria. The significance of m^6A-RNA modifications is under investigation, but it is widely accepted that m^6A mediates structural switches that affect RNA stability or activity. Biochemical and RNA-seq analyses indicate that m^6A targets all types of mtRNAs, including coding regions, introns, untranslated regions (UTRs), as well as transcribed intergenic species. While non-coding-RNAs undergo multiple modifications along the transcripts, in coding-genes m^6A is predominantly positioned around start codons and may modulate mitochondrial RNA translatability.

Cell

Every Breath You Take: New Insights into Plant and Animal Oxygen Sensing
Pages 22-24

Daniel J. Gibbs, Michael J. Holdsworth

A Pathogen-Responsive Gene Cluster for Highly Modified Fatty Acids in Tomato
Pages 176-187.e19
Ju Eun Jeon, Jung-Gun Kim, Curt R. Fischer, Niraj Mehta, ... Elizabeth Sattely

PLANT CELL

Advanced Cataloging of Lysine-63 Polyubiquitin Networks by Genomic, Interactome, and Sensor-Based Proteomic Analyses
Natali Romero-Barrios, Dario Monachello, Ulla Dolde, Aloysius Wong, Hélène San Clemente, Anne Cayrel, Alexander Johnson, Claire Lurin and Grégory Vert
Plant Cell 2020 32: 123-138. First Published on November 11, 2019; doi:10.1105/tpc.19.00568

An Improved Recombineering Toolset for Plants
Javier Brumos, Chengsong Zhao, Yan Gong, David Soriano, Arjun P. Patel, Miguel A. Perez-Amador, Anna N. Stepanova and Jose M. Alonso
Plant Cell 2020 32: 100-122. First Published on October 30, 2019; doi:10.1105/tpc.19.00431
http://www.plantcell.org/content/32/1/100.abstract

A scalable recombineering procedure for whole-gene editing in plants via homologous recombination in bacteria was used to tag 62 auxin-related genes in 123 transgenic Arabidopsis lines.
Erhardt S, Stoecklin G.
The heat's on: nuclear stress bodies signal intron retention.
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Rampelt H, Sucec I, Bersch B, Horten P, Perschil I, Martinou JC, van der Laan M, Wiedemann N, Schanda P, Pfanner N.
The mitochondrial carrier pathway transports non-canonical substrates with an odd number of transmembrane segments.
BMC Biol. 2020 Jan 6;18(1):2. PMID: 31907035 [PubMed - in process]

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Stress Responsive Gene Regulation in Relation to Hydrogen Sulfide in Plants under Abiotic Stress.
Physiol Plant. 2020 Jan 9;. [Epub ahead of print] PMID: 31916586 [PubMed - as supplied by publisher]

Rudler DL, Hughes LA, Perks KL, Richman TR, Kuznetsova I, Ermer JA, Abudulai LN, Shearwood AJ, Viola HM, Hool LC, Siira SJ, Rackham O, Filipovska A.
Fidelity of translation initiation is required for coordinated respiratory complex assembly.
Sci Adv. 2019 Dec;5(12):eaay2118. PMID: 31903419 [PubMed - in process]
Abstract
Mammalian mitochondrial ribosomes are unique molecular machines that translate 11 leaderless mRNAs; however, it is not clear how mitoribosomes initiate translation, since mitochondrial mRNAs lack untranslated regions. Mitochondrial translation initiation shares similarities with prokaryotes, such as the formation of a ternary complex of fMet-tRNA^{Met}, mRNA and the 28*S* subunit, but differs in the requirements for initiation factors. Mitochondria have two initiation factors: MTIF2, which closes the decoding center and stabilizes the binding of the fMet-tRNA^{Met} to the leaderless mRNAs, and MTIF3, whose role is not clear. We show that MTIF3 is essential for survival and that heart- and skeletal muscle–specific loss of MTIF3 causes cardiomyopathy. We identify increased but uncoordinated mitochondrial protein synthesis in mice lacking MTIF3, resulting in loss of specific respiratory complexes. Ribosome profiling shows that MTIF3 is required for recognition and regulation of translation initiation of mitochondrial mRNAs and for coordinated assembly of OXPHOS complexes in vivo.