

Early View Alert: Plant, Cell & Environment

REVIEWS

Present knowledge and controversies, deficiencies, and misconceptions on nitric oxide synthesis, sensing, and signaling in plants

José León, Álvaro Costa-Broseta

Research on nitric oxide (NO) in plants has relied largely on the use of pharmacological approaches, which suffers from low specificity, and analytical techniques that do not allow the precise and quantitative determination of endogenous NO. Better tools, including specific sensors and improved proteomics of posttranslational modifications, as well as genetic approaches will help to identify the components, processes, and mechanisms involved in NO-triggered regulation of plant biology.

The Plant Journal

An ‘eFP-Seq Browser’ for visualizing and exploring RNA sequencing data

Alexander Sullivan, Priyank K. Purohit, Nowlan H. Freese, Asher Pasha, Eddi Esteban, Jamie Waese, Alison Wu, Michelle Chen, Chih Y. Chin, Richard Song, Sneha R. Watharkar, Agnes P. Chan, Vivek Krishnakumar, Matthew W. Vaughn, Chris Town, Ann E. Loraine, Nicholas J. Provart

Version of Record online: 23 August 2019

Significance Statement

We present a tool, the eFP-Seq Browser, for rapidly identifying RNA sequencing samples with strong expression levels of a given gene, or where the read maps for a given gene/sample best match a particular gene model. Details can be called up with convenient links to the Integrated Genome Browser.

Reactive oxygen species and reactive carbonyl species constitute a feed-forward loop in auxin signaling for lateral root formation

Md. Sanaullah Biswas, Hidehiro Fukaki, Izumi C. Mori, Kazuha Nakahara, Jun'ichi Mano

Version of Record online: 21 August 2019

Significance Statement

Auxin induces the formation of reactive oxygen species (ROS), which promote lateral root (LR) formation. We show that ROS and lipid peroxide-derived reactive carbonyl species (RCS), signal mediators downstream of ROS, facilitate the degradation of the auxin/indole-3-acetic acid repressor, and thereby enforce the auxin signal for LR formation. Specifically, ROS and RCS constitute a feed-forward pathway to modulate the auxin signaling for LR formation. The RCS provide a connection between the ROS signal and auxin signaling pathways.

Determination of protein-only RNase P interactome in *Arabidopsis* mitochondria and chloroplasts identifies a complex between PRORP1 and another NYN domain nuclease

Ayoub Bouchouha, Florent Waltz, Géraldine Bonnard, Mathilde Arrivé, Philippe Hammann, Lauriane Kuhn, Cédric Schelcher, Hélène Zuber, Anthony Gobert, Philippe Giegé

Significance Statement

RNase P is a key enzyme in tRNA maturation that removes the 5' leader sequences of tRNA precursors. In this study, the interaction network of the protein-only RNase P enzyme PRORP1 was identified in *Arabidopsis* mitochondria and chloroplasts. In particular, an RNA maturation complex was characterized. Results provided insights into the integration of PRORP1 functions with other gene expression processes and helped to understand the diversity of RNase P enzymes in evolution.

Current Opinion in Cell Biology : Volume 59 Membrane Trafficking

The enigma of an interconnected mitochondrial reticulum: new insights into mitochondrial fusion

Pages 159-166

Sevan Mattie, Michiel Krols, Heidi M McBride

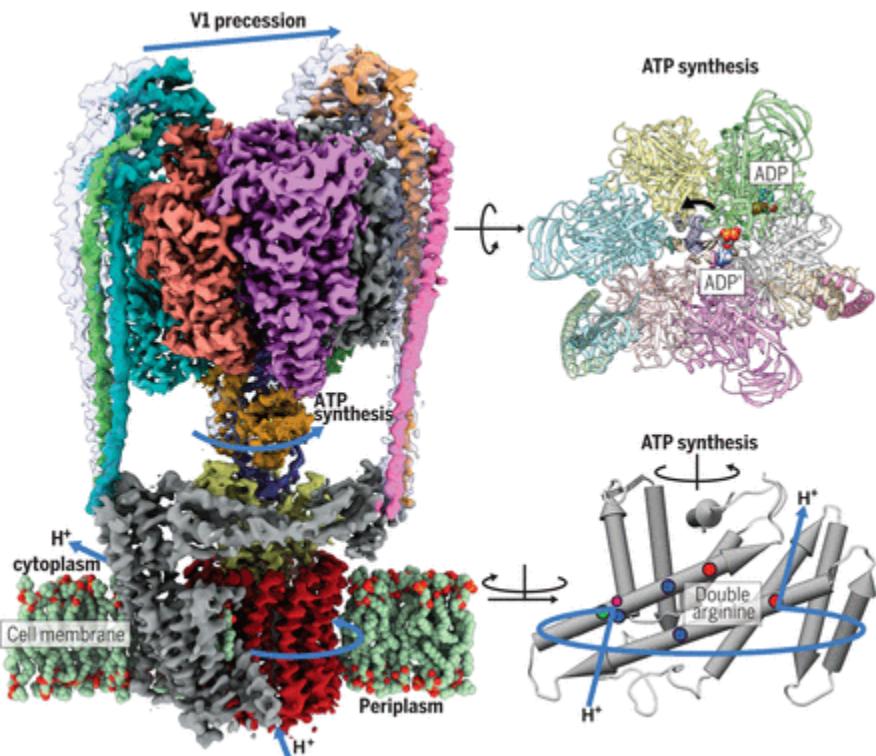
Molecular Machines

Innovations in an ATPase/ATP synthase

1. Michael A. Funk

Enzymes that couple the chemical energy of adenosine triphosphate (ATP) to movement of ions across a membrane are present in all domains of life. Like their F-type cousins in mitochondria, chloroplasts, and most bacteria, vacuolar/archaeal (V/A-type) ATPases couple synthesis or hydrolysis of ATP to movement of protons across the membrane. To uncover mechanistic differences in energy coupling between F- and V/A-type enzymes, Zhou and Sazanov determined structures of a V/A-type ATP synthase from the bacterium *Thermus thermophilus*. With structures of multiple substates visible, the domain interfaces are made clear and a role for the elastic peripheral stalks is apparent in coupling rotational energy from V_o into the ATP-synthesizing V_i domain.

Science, this issue p. eaaw9144



Nat Struct Mol Biol. 2019 Aug;26(8):671-678. doi: 10.1038/s41594-019-0257-3. Epub 2019 Jul 8.

An allosteric network in spastin couples multiple activities required for microtubule severing.

Sandate CR¹, Szyk A², Zehr EA², Lander GC³, Roll-Mecak A^{4,5}.

Abstract

The AAA+ ATPase spastin remodels microtubule arrays through severing and its mutation is the most common cause of hereditary spastic paraplegias (HSP). Polyglutamylation of the tubulin C-terminal tail recruits spastin to microtubules and modulates severing activity. Here, we present a ~3.2 Å resolution cryo-EM structure of the *Drosophila melanogaster* spastin hexamer with a polyglutamate peptide bound in its central pore. Two electropositive loops arranged in a double-helical staircase coordinate the substrate sidechains. The structure reveals how concurrent nucleotide and substrate binding organizes the conserved spastin pore loops into an ordered network that is allosterically coupled to oligomerization, and suggests how tubulin tail engagement activates spastin for microtubule disassembly. This allosteric coupling may apply generally in organizing AAA+ protein translocases into their active conformations. We show that this allosteric network is essential for severing and is a hotspot for HSP mutations.

[Cryo-EM structures reveal coordinated domain motions that govern DNA cleavage by Cas9](#)

Cryo-EM structures of the active Cas9–sgRNA–DNA complex in the presence of Mg²⁺ capture Cas9 in the pre- and postcatalytic states as well as in the product-bound state, and reveal coupled domain motions and interactions between the enzyme and nucleic acids.

The structure of the stress-induced photosystem I–IsiA antenna supercomplex

Cyanobacteria express IsiA, a photosystem I antenna, in response to stress. The structure of the photosystem I–IsiA complex reveals flexibility of the interactions within the complex and suggests the mechanism of energy transfer.

CAT tails drive degradation of stalled polypeptides on and off the ribosome

Alanine and threonine residues added to the C terminus of stalled nascent chains (CAT tails) increase degradation of such polypeptides by promoting their ubiquitylation by Ltn1 or by acting as degrons off the ribosome.

- Cole S. Sitron
- & Onn Brandman

Stalled translation produces incomplete, ribosome-tethered polypeptides that the ribosome-associated quality control (RQC) pathway targets for degradation via the E3 ubiquitin ligase Ltn1. During this process, the protein Rqc2 and the large ribosomal subunit elongate stalled polypeptides with carboxy-terminal alanine and threonine residues (CAT tails). Failure to degrade CAT-tailed proteins disrupts global protein homeostasis, as CAT-tailed proteins can aggregate and sequester chaperones. Why cells employ such a potentially toxic process during RQC is unclear. Here, we developed quantitative techniques to assess how CAT tails affect stalled polypeptide degradation in *Saccharomyces cerevisiae*. We found that CAT tails enhance the efficiency of Ltn1 in targeting structured polypeptides, which are otherwise poor Ltn1 substrates. If Ltn1 fails to ubiquitylate those stalled polypeptides or becomes limiting, CAT tails act as degrons, marking proteins for proteasomal degradation off the ribosome. Thus, CAT tails functionalize the carboxy termini of stalled polypeptides to drive their degradation on and off the ribosome.

NAD depletion as pathogen response

One way that plants respond to pathogen infection is by sacrificing the infected cells. The nucleotide-binding leucine-rich repeat immune receptors responsible for this hypersensitive response carry Toll/interleukin-1 receptor (TIR) domains. In two papers, Horsefield *et al.* and Wan *et al.* report that these TIR domains cleave the metabolic cofactor nicotinamide adenine dinucleotide (NAD⁺) as part of their cell-death signaling in response to pathogens. Similar signaling links mammalian TIR-containing proteins to NAD⁺ depletion during Wallerian degeneration of neurons.

Science, this issue p. 793, p. 799

NAD⁺ cleavage activity by animal and plant TIR domains in cell death pathways

Shane Horsefield, ...Bostjan Kobe

Science 23 Aug 2019 : 793-799 Full Access

A plant immune receptor enzymatically transduces pathogen recognition into cell death.

TIR domains of plant immune receptors are NAD⁺-cleaving enzymes that promote cell death

By Li Wan, Kow Essuman, Ryan G. Anderson, Yo Sasaki, Freddy Monteiro, Eui-Hwan Chung, Erin Osborne Nishimura, Aaron DiAntonio, Jeffrey Milbrandt, Jeffery L. Dangl, Marc T. Nishimura

Science 23 Aug 2019 : 799-803 Full Access

A plant immune receptor enzymatically transduces pathogen recognition into cell death.

[Hydrogen Sulfide: A New Warrior against Abiotic Stress](#)

Available Online 04 September 2019

Francisco J. Corpas

Molecular Cell : Volume 75, Issue 5

[Early Scanning of Nascent Polypeptides inside the Ribosomal Tunnel by NAC](#)

Pages 996-1006.e8

Martin Gämmerdinger, Kan Kobayashi, Annalena Wallisch, Stefan G. Kreft, Carolin Sailer, Renate Schlömer, Nadine Sachs, Ahmad Jomaa, Florian Stengel, Nenad Ban, Elke Deuerling

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[Signaling interactions between mitochondria and chloroplasts in *Nicotiana tabacum* leaf](#)

Nicole A. Alber, Greg C. Vanlerberghe

Pages: 188-204 | First Published: 22 November 2018

Zhou H, Wang X, Huo C, Wang H, An Z, Sun D, Liu J, Tang W, Zhang B.

A Quantitative Proteomics Study of Early Heat-Regulated Proteins by Two-Dimensional Difference Gel Electrophoresis Identified OsUBP21 as a Negative Regulator of Heat Stress Responses in Rice.

Proteomics. 2019 Sep 6;:e1900153. [Epub ahead of print]

PMID: 31491808 [PubMed - as supplied by publisher]

Tran DM, Ishiwata-Kimata Y, Mai TC, Kubo M, Kimata Y.

The unfolded protein response alongside the diauxic shift of yeast cells and its involvement in mitochondria enlargement.

Sci Rep. 2019 Sep 4;9(1):12780.

PMID: 31484935 [PubMed - in process]

Gal J, Chen J, Na DY, Tichacek L, Barnett KR, Zhu H.

The Acetylation of Lysine-376 of G3BP1 Regulates RNA Binding and Stress Granule Dynamics.

Mol Cell Biol. 2019 Sep 3;. [Epub ahead of print]

PMID: 31481451 [PubMed - as supplied by publisher]

Guo J, Li X, Zhang W, Chen Y, Zhu S, Chen L, Xu R, Lv Y, Wu D, Guo M, Liu X, Lu W, Deng H.

HSP60-regulated Mitochondrial Proteostasis and Protein Translation Promote Tumor Growth of Ovarian Cancer.

Sci Rep. 2019 Sep 2;9(1):12628.

PMID: 31477750 [PubMed - in process]

Hartman S, Liu Z, van Veen H, Vicente J, Reinen E, Martopawiro S, Zhang H, van Dongen N, Bosman F, Bassel GW, Visser EJW, Bailey-Serres J, Theodoulou FL, Hebelstrup KH, Gibbs DJ, Holdsworth MJ, Sasidharan R, Voesenek LACJ. Ethylene-mediated nitric oxide depletion pre-adapts plants to hypoxia stress.

Nat Commun. 2019 Sep 5;10(1):4020.

PMID: 31488841 [PubMed - in process]

Rodríguez-Ruiz M, González-Gordo S, Cañas A, Campos MJ, Paradela A, Corpas FJ, Palma JM.

Sweet Pepper (*Capsicum annuum*) Fruits Contain an Atypical Peroxisomal Catalase That is Modulated by Reactive Oxygen and Nitrogen Species.

Antioxidants (Basel). 2019 Sep 4;8(9).

PMID: 31487955 [PubMed]

Kapuganti JG, Hancock JT, Petivalsky M, Kolbert Z, Lindermayr C, Durner J, Barroso JB, Palma JM, Brouquisse R, Wendehenne D, Corpas FJ, Loake GJ.

Recommendations on terminology and experimental best practice associated with plant nitric oxide research.

New Phytol. 2019 Sep 3;. [Epub ahead of print]

PMID: 31479520 [PubMed - as supplied by publisher]

Paul S, Roychoudhury A.

Regulation of physiological aspects in plants by hydrogen sulfide and nitric oxide under challenging environment.

Physiol Plant. 2019 Sep 3;. [Epub ahead of print]

PMID: 31479515 [PubMed - as supplied by publisher]