Lit Lunch 12_4_14

Damian:

1) *S*-nitrosothiols regulate nitric oxide production and storage in plants through the nitrogen assimilation pathway

- **Lucas Frungillo Michael J. Skelly Gary J. Loake Steven H. Spoel & Ione Salgado**

Nature Communications **5**, 5401(2014)doi:10.1038/ncomms6401

Nitrogen assimilation plays a vital role in plant metabolism. Assimilation of nitrate, the primary source of nitrogen in soil, is linked to the generation of the redox signal nitric oxide (NO). An important mechanism by which NO regulates plant development and stress responses is through*S*-nitrosylation, that is, covalent attachment of NO to cysteine residues to form *S*-nitrosothiols (SNO). Despite the importance of nitrogen assimilation and NO signalling, it remains largely unknown how these pathways are interconnected. Here we show that SNO signalling suppresses both nitrate uptake and reduction by transporters and reductases, respectively, to fine tune nitratehomeostasis. Moreover, NO derived from nitrate assimilation suppresses the redox enzyme *S*-nitrosoglutathione Reductase 1 (GSNOR1) by *S*-nitrosylation, preventing scavenging of *S*-nitrosoglutathione, a major cellular bio-reservoir of NO. Hence, our data demonstrates that (S)NO controls its own generation and scavenging by modulating nitrate assimilation and GSNOR1 activity.

Indu:

1. Science. 2014 Nov 7;346(6210):748-51. doi: 10.1126/science.1257522.

Targeting and plasticity of mitochondrial proteins revealed by proximity-specific ribosome profiling.

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Comment in
Science. 2014 Nov 7;346(6210):701-2.

Nearly all mitochondrial proteins are nuclear-encoded and are targeted to their mitochondrial destination from the cytosol. Here, we used proximity-specific ribosome profiling to comprehensively measure translation at the mitochondrial surface in yeast. Most inner-membrane proteins were cotranslationally targeted to mitochondria, reminiscent of proteins entering the endoplasmic reticulum (ER). Comparison between mitochondrial and ER localization demonstrated that the vast majority of proteins were targeted to a specific organelle. A prominent exception was the fumarate reductase Osm1, known to reside in mitochondria. We identified a conserved ER isoform of Osm1, which contributes to the oxidative protein-folding capacity of the organelle. This dual localization was enabled by alternative

translation initiation sites encoding distinct targeting signals. These findings highlight the exquisite in vivo specificity of organellar targeting mechanisms.

PMID: 25378625 [PubMed - in process]

2. Science. 2014 Nov 7;346(6210):1257521. doi: 10.1126/science.1257521. Epub 2014 Nov 6.

Principles of ER cotranslational translocation revealed by proximity-specific ribosome profiling.

Jan CH(1), Williams CC(1), Weissman JS(2).

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Comment in
Science. 2014 Nov 7;346(6210):701-2.

Localized protein synthesis is a fundamental mechanism for creating distinct subcellular environments. Here we developed a generalizable proximity-specific ribosome profiling strategy that enables global analysis of translation in defined subcellular locations. We applied this approach to the endoplasmic reticulum (ER) in yeast and mammals. We observed the large majority of secretory proteins to be cotranslationally translocated, including substrates capable of posttranslational insertion in vitro. Distinct translocon complexes engaged nascent chains at different points during synthesis. Whereas most proteins engaged the ER immediately after or even before signal sequence (SS) emergence, a class of Sec66-dependent proteins entered with a looped SS conformation. Finally, we observed rapid ribosome exchange into the cytosol after translation termination. These data provide insights into how distinct translocation mechanisms act in concert to promote efficient cotranslational recruitment.

PMID: 25378630 [PubMed - in process]

3. Science. 2014 Nov 7;346(6210):751-5. doi: 10.1126/science.1255638. Epub 2014 Sep 18.

Quality control of inner nuclear membrane proteins by the Asi complex.

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Misfolded proteins in the endoplasmic reticulum (ER) are eliminated by a quality control system called ER-associated protein degradation (ERAD). However, it is unknown how misfolded proteins in the inner nuclear membrane (INM), a specialized ER subdomain, are degraded. We used a quantitative proteomics approach to reveal an ERAD branch required for INM protein quality control in yeast. This branch involved the integral membrane proteins Asi1, Asi2, and Asi3, which assembled into an Asi complex. Besides INM misfolded proteins, the Asi complex promoted the degradation of functional regulators of sterol biosynthesis. Asi-mediated ERAD was required for ER homeostasis, which suggests that spatial segregation of protein quality control systems contributes to ER function.

PMID: 25236469 [PubMed - in process]

Nathen:

Plant Cell. 2014 Nov 18. pii: tpc.114.130997. [Epub ahead of print]
Systems-Wide Analysis of Acclimation Responses to Long-Term Heat Stress and Recovery in the Photosynthetic Model Organism Chlamydomonas reinhardtii.
Abstract

We applied a top-down systems biology approach to understand how Chlamydomonas reinhardtii acclimates to long-term heat stress (HS) and recovers from it. For this, we shifted cells from 25 to 42°C for 24 h and back to 25°C for ≥8 h and monitored abundances of 1856 proteins/protein groups, 99 polar and 185 lipophilic metabolites, and cytological and photosynthesis parameters. Our data indicate that acclimation of Chlamydomonas to long-term HS consists of a temporally ordered, orchestrated implementation of response elements at various system levels. These comprise (1) cell cycle arrest; (2) catabolism of larger molecules to generate compounds with roles in stress protection; (3) accumulation of molecular chaperones to restore protein homeostasis together with compatible solutes; (4) redirection of photosynthetic energy and reducing power from the Calvin cycle to the de novo synthesis of saturated fatty acids to replace polyunsaturated ones in membrane lipids, which are deposited in lipid bodies; and (5) when sinks for photosynthetic energy and reducing power are depleted, resumption of Calvin cycle activity associated with increased photorespiration, accumulation of reactive oxygen species scavengers, and throttling of linear electron flow by antenna uncoupling. During recovery from HS, cells appear to focus on processes allowing rapid resumption of growth rather than restoring pre-HS conditions.

Stephanie:

Plant Molecular Biology
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ZmGRF, a GA regulatory factor from maize, promotes flowering and plant growth in *Arabidopsis*

Miaoyun Xu, Yunming Lu, Hongmei Yang, Jingcheng He, Zhiqiu Hu, Xiaolong Hu, Mingda Luan, Lan Zhang, Yunliu Fan, Lei Wang

Abstract

Transcription factors that act as positive regulators of gibberellin (GA) biosynthetic genes in plants are not well understood. A nuclear-localized basic leucine zipper transcription factor, ZmGRF, was isolated from maize. The core DNA sequence motif recognized for binding by ZmGRF was CCANNTGGC. ZmGRF overexpression in transgenic *Arabidopsis* plants promoted flowering, stem elongation, and cell expansion. Chromatin immunoprecipitation assays revealed that ZmGRF bound directly to the *cis*-element CCANNTGGC in the promoter of the *Arabidopsis ent*-kaurene oxidase (*AtKO1*) gene and promoted *AtKO1* expression. GA_4 content increased by 372–567 % in transgenic*Arabidopsis* plants overexpressing *ZmGRF* compared to wild-type control plants. The GIBBERELLIN-INSENSITIVE DWARF1 gene, which encodes a GA receptor, was also upregulated and the growth-repressing DELLA protein gene GA INSENSITIVE was downregulated. Our results showed ZmGRF functioned through the GA-signaling pathway.