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McKinstry M, Chung C, Truong H, Johnston BA, Snow JW.
The heat shock response and humoral immune response are mutually antagonistic in honey bees.
Sci Rep. 2017 Aug 18;7(1):8850.
PMID: 28821863

Corey

Regulation of protein function by *S*-nitrosation and *S*-glutathionylation: processes and targets in cardiovascular pathophysiology

Abstract

Decades of chemical, biochemical and pathophysiological research have established the relevance of post-translational protein modifications induced by processes related to oxidative stress, with critical reflections on cellular signal transduction pathways. A great deal of the so-called 'redox regulation' of cell function is in fact mediated through reactions promoted by reactive oxygen and nitrogen species on more or less specific aminoacid residues in proteins, at various levels within the cell machinery. Modifications involving cysteine residues have received most attention, due to the critical roles they play in determining the structure/function correlates in proteins. The peculiar reactivity of these residues results in two major classes of modifications, with incorporation of NO moieties (S-nitrosation, leading to formation of protein S-nitrosothiols) or binding of low molecular weight thiols (S- thionylation, *i.e.* in particular S-glutathionylation, S-cysteinylglycinylation and S- cysteinylation). A wide array of proteins have been thus analyzed in detail as far as their susceptibility to either modification or both, and the resulting functional changes have been described in a number of experimental settings. The present review aims to provide an update of available knowledge in the field, with a special focus on the respective (sometimes competing and antagonistic) roles played by protein S-nitrosations and S-thionylations in biochemical and cellular processes specifically pertaining to pathogenesis of cardiovascular diseases.

Patrick

1.
A membrane-associated thioredoxin required for
plant growth moves from cell to cell, suggestive of a role in intercellular communication
Ling Meng, Joshua H. Wong, Lewis J. Feldman, Peggy G. Lemaux, and Bob B. Buchanan1
Department of Plant and Microbial Biology, University of California, Berkeley, CA 94720
www.pnas.org/cgi/doi/10.1073/pnas.0913759107

Thioredoxins (Trxs) are small ubiquitous regulatory disulfide pro- teins. Plants have an unusually complex complement of Trxs com- posed of six well-defined types (Trxs *f*, *m*, *x*, *y*, *h*, and *o*) that reside in different cell compartments and function in an array of processes. The extraplastidic *h* type consists of multiple members that in gen- eral have resisted isolation of a specific phenotype. In analyzing mutant lines in *Arabidopsis thaliana*, we identified a phenotype of dwarf plants with short roots and small yellowish leaves for AtTrx *h*9 (henceforth, Trx *h*9), a member of the *Arabidopsis* Trx *h* family. Trx *h*9 was found to be associated with the plasma membrane and to move from cell to cell. Controls conducted in conjunction with the local- ization of Trx *h*9 uncovered another *h*-type Trx in mitochondria (Trx *h*2) and a Trx in plastids earlier described as a cytosolic form in tomato. Analysis of Trx *h*9 revealed a 17-amino acid N-terminal extension in which the second Gly (Gly^2) and fourth cysteine (Cys^4) were highly conserved. Mutagenesis experiments demonstrated that Gly^2 was required for membrane binding, possibly via myristoyla- tion. Both Gly^2 and Cys^4 were needed for movement, the latter seem- ingly for protein structure and palmitoylation. A three-dimensional model was consistent with these predictions as well as with earlier evidence showing that a poplar ortholog is reduced by a glutare- doxin rather than NADP-thioredoxin reductase. In demonstrating the membrane location and intercellular mobility of Trx *h*9, the present results extend the known boundaries of Trx and suggest a role in cell-to-cell communication.

2.

S-nitrosylation/denitrosylation as a regulatory mechanism of salt stress sensing in sunflower seedlings

Prachi Jaina, Christine von Toernebb, Christian Lindermayrc and Satish C Bhatlaa*
a Laboratory of Plant Physiology and Biochemistry, Department of Botany, University of Delhi, Delhi-110007, India
b Research Unit Protein Science, Helmholtz Zentrum Muenchen, Heidemannstr. 1
D-80939 München, Germany
c Helmholtz Zentrum Muenchen, German Research Center for Environmental Health, Neuherberg,
Germany
doi: 10.1111/ppl.12641

Nitric oxide (NO) and various reactive nitrogen species (RNS) produced in cells in normal growth conditions and their enhanced production under stress conditions, are responsible for a variety of biochemical aberrations. Present findings demonstrate that sunflower seedling roots exhibit high sensitivity to salt stress in terms of nitrite accumulation. A significant reduction in S-nitrosoglutathione reductase (GSNOR) activity is evident in response to salt stress. Restoration of GSNOR activity with dithioerythritol (DTT) shows that the enzyme is reversibly inhibited under conditions of 120 m*M* NaCl. Salt stress

mediated S-nitrosylation of cytosolic proteins was analyzed in roots and cotyledons using biotin switch assay. LC-MS/MS analysis revealed opposite patterns of S-nitrosylation in seedling cotyledons and roots. Salt stress enhances S-nitrosylation of proteins in cotyledons whereas roots exhibit denitrosylation of proteins. Highest number of proteins having undergone S-nitrosylation belonged to the category of carbohydrate metabolism followed by other metabolic proteins. Of the total 61 proteins observed to be regulated by S-nitrosylation, 17 are unique to cotyledons, 4 are unique to roots whereas 40 are common to both. Eighteen S-nitrosylated proteins are being reported for the first time in plant systems, including pectinesterase, phospholipase D alpha and calmodulin. Further physiological analysis of glyceraldehyde-3-phosphate dehydrogenase and monodehydro-ascorbate reductase showed that salt stress leads to a reversible inhibition of both these enzymes in cotyledons. However, seedling roots exhibit enhanced enzyme activity under salinity stress. These observations implicate the role of S- nitrosylation and denitrosylation in NO signaling thereby regulating various enzyme activities under salinity stress in sunflower seedlings.

Minsoo

1. Biol Rev Camb Philos Soc. 2017 Sep 20. doi: 10.1111/brv.12373. [Epub ahead of print]

ATAD3 proteins: brokers of a mitochondria-endoplasmic reticulum connection in mammalian cells.

Baudier J(1)(2).

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In yeast, a sequence of physical and genetic interactions termed the endoplasmic reticulum (ER)-mitochondria organizing network (ERMIONE) controls mitochondria-ER interactions and mitochondrial biogenesis. Several functions that characterize ERMIONE complexes are conserved in mammalian cells, suggesting that a similar tethering complex must exist in metazoans. Recent studies have identified a new

family of nuclear-encoded ATPases associated with diverse cellular activities (AAA+-ATPase) mitochondrial membrane proteins specific to multicellular eukaryotes, called the ATPase family AAA domain-containing protein 3 (ATAD3) proteins (ATAD3A and ATAD3B). These proteins are crucial for normal mitochondrial-ER interactions and lie at the heart of processes underlying mitochondrial biogenesis. ATAD3A orthologues have been studied in flies, worms, and mammals, highlighting the widespread importance of this gene during embryonic development and in adulthood. ATAD3A is a downstream effector of target of rapamycin (TOR) signalling in Drosophila and exhibits typical features of proteins from the ERMIONE-like complex in metazoans. In humans, mutations in the ATAD3A gene represent a new link between altered mitochondrial-ER interaction and recognizable neurological syndromes. The primate-specific ATAD3B protein is a biomarker of pluripotent embryonic stem cells. Through negative regulation of ATAD3A function, ATAD3B supports mitochondrial stemness propert

Keith

Reversible protein aggregation is a protective mechanism to ensure cell cycle restart after stress.

Nat Cell Biol. 2017 Oct;19(10):1202-1213.

Saad S[1,2], Cereghetti G[1,3], Feng Y[1,3], Picotti P[1], Peter M[1], Dechant R[1].

1 Institute of Biochemistry, Department of Biology, ETH Zürich, Otto-Stern-Weg 3, 8093 Zürich, Switzerland.
2 Life Science Zürich, PhD Program for Molecular and Translational Biomedicine, CH-8044 Zürich, Switzerland.
3 Life Science Zürich, PhD Program for Molecular Life Sciences, 8057 Zürich, Switzerland.

Protein aggregation is mostly viewed as deleterious and irreversible causing several pathologies. However, reversible proteinaggregation has recently emerged as a novel concept for cellular regulation. Here, we characterize stress-induced, reversibleaggregation of yeast pyruvate kinase, Cdc19. Aggregation of Cdc19 is regulated by oligomerization and binding to allosteric regulators. We identify a region of low compositional complexity (LCR) within Cdc19 as necessary and sufficient for reversible aggregation. During exponential growth, shielding the LCR within tetrameric Cdc19 or phosphorylation of the LCR prevents unscheduled aggregation, while its dephosphorylation is necessary for reversible aggregation during stress.
Cdc19 aggregation triggers its localization to stress granules and modulates their formation and dissolution. Reversible aggregation protects Cdc19 from stress-induced degradation, thereby allowing cell cycle restart after stress. Several other enzymes necessary for G1 progression also contain LCRs and aggregate reversibly during stress, implying

that reversible aggregation represents a conserved mechanism regulating cell growth and survival.

Elizabeth
Oct 5

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Nature Methods Contents: October 2017 Volume 14 pp 929 - 1016 2017
Internally ratiometric fluorescent sensors for evaluation of intracellular GTP levels and distribution **pp1003 - 1009**
Anna Bianchi-Smiraglia, Mitra S Rana, Colleen E Foley, Leslie M Paul, Brittany C Lipchick *et al.*
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The genetically encoded GEVAL sensors allow ratiometric imaging of the spatiotemporal dynamics of cellular GTP levels in living cells.

Physiologia Plantarum Content Alert (New Articles)
A role for glutathione reductase and glutathione in the tolerance of *Chlamydomonas reinhardtii* to photo-oxidative stress
Tsen-Hung Lin, Meng-Yuan Rao, Hao-Wen Lu, Chih-Wen Chiou, Shu-Tseng Lin, Hung-Wei Chao, Zhao-Liang Zheng, Hao-Chien Cheng and Tse-Min Lee
Accepted manuscript online: 26 SEP 2017 09:45AM EST | DOI: 10.1111/ppl.12622

PLOS Biology Volume 15(9) September 2017

Genome-wide identification of bacterial plant colonization genes

Benjamin J. Cole, Meghan E. Feltcher, Robert J. Waters, Kelly M. Wetmore, Tatiana S. Mucyn, Elizabeth M. Ryan, Gaoyan Wang, Sabah Ul-Hasan, Meredith McDonald, Yasuo Yoshikuni, Rex R. Malmstrom, Adam M. Deutschbauer, Jeffery L. Dangl, Axel Visel

A genome-wide barcoded transposon mutagenesis study in a root-colonizing strain of the bacterium *Pseudomonas simiae* revealed over a hundred genes that significantly impacted the ability to competitively colonize roots of the plant *Arabidopsis thaliana*.

PLOS Genetics Volume 13(9) September 2017

Interference with plastome gene expression and Clp protease activity in Arabidopsis triggers a chloroplast unfolded protein response to restore protein homeostasis

Ernesto Llamas, Pablo Pulido, Manuel Rodriguez-Concepcion

The EMBO Journal Table of Contents for 02 October 2017; Vol. 36, No. 19
Redox regulation of plant stem cell fate
Jian Zeng, Zhicheng Dong, Haijun Wu, Zhaoxia Tian and Zhong Zhao
Published online 24.08.2017

http://EMBOJ.embopress.org/content/36/19/2844?etoc

Superoxide regulates plant stem cell fate, and the balance between superoxide and H2O2 serves as a key switch for stem cell maintenance versus differentiation by antagonistically regulating expression of stem cell fate transcription factor WUSCHEL.

Nature Protocols Contents: Volume 12 Number 10, pp 2029-2250
Genetically encoded releasable photo-cross-linking strategies for studying protein-protein interactions in living cells **pp2147 - 2168**
This protocol describes strategies for the characterization of transient protein-protein interactions and their interaction interfaces via genetically encoded releasable photo-cross-linkers.
Yi Yang *et al.*
Published online: 21 September 2017 | doi:10.1038/nprot.2017.090
Abstract | Full Text | PDF (1,607K)

Rapid immunopurification of mitochondria for metabolite profiling and absolute quantification of matrix metabolites **pp2215 - 2231**
High-affinity magnetic immunocapture is used to rapidly purify HA-tagged mitochondria from cells for metabolite profiling. Matrix concentrations of mitochondrial metabolites are determined through LC/MS, immunoblotting, confocal microscopy, and volumetric analysis.
Walter W Chen, Elizaveta Freinkman and David M Sabatini
Published online: 28 September 2017 | doi:10.1038/nprot.2017.104
Abstract | Full Text | PDF (675K)

Nature Cell Biology contents: October 2017 Volume 19 Number 10, pp 1131 - 1296
Reversible protein aggregation is a protective mechanism to ensure cell cycle restart after stress **pp1202 - 1213**
Shady Saad, Gea Cereghetti, Yuehan Feng, Paola Picotti, Matthias Peter *et al.*
doi:10.1038/ncb3600
Protein aggregation is mostly viewed as deleterious and irreversible causing several pathologies. However, reversible protein aggregation has recently emerged as a novel concept for cellular regulation. Here, we characterize stress-induced, reversible aggregation of yeast pyruvate kinase, Cdc19. Aggregation of Cdc19 is regulated by oligomerization and binding to allosteric regulators. We identify a region of low compositional complexity (LCR) within Cdc19 as necessary and sufficient for reversible aggregation. During exponential growth, shielding the LCR within tetrameric Cdc19 or phosphorylation of the LCR prevents unscheduled aggregation, while its dephosphorylation is necessary for reversible aggregation during stress. Cdc19

aggregation triggers its localization to stress granules and modulates their formation and dissolution. Reversible aggregation protects Cdc19 from stress-induced degradation, thereby allowing cell cycle restart after stress. Several other enzymes necessary for G1 progression also contain LCRs and aggregate reversibly during stress, implying that reversible aggregation represents a conserved mechanism regulating cell growth and survival.

Preserving protein function through reversible aggregation **pp1142 - 1144**

Jörg Höhfeld

doi:10.1038/ncb3620

It is generally accepted that protein function depends on a defined 3D structure, with unfolding and aggregation dealing a final blow to functionality. A study now shows that the regulated exposure of an unstructured region in yeast pyruvate kinase triggers reversible aggregation to preserve protein function under stress.