

Indu:

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Stephanie:

Annals of Botany:

The effects of induced production of reactive oxygen species in organelles on endoplasmic reticulum stress and on the unfolded protein response in arabidopsis

Rengin Ozgur, Baris Uzilday, A. Hediye Sekmen and Ismail Turkan*

Background and Aims Accumulation of unfolded proteins caused by inefficient chaperone activity in the endoplasmic reticulum (ER) is termed 'ER stress', and it is perceived by a complex gene network. Induction of these genes triggers a response termed the 'unfolded protein response' (UPR). If a cell cannot overcome the accumulation of unfolded proteins, the ER-associated degradation (ERAD) system is induced to degrade those proteins. In addition to other factors, reactive oxygen species (ROS) are also produced during oxidative

protein-folding in the ER. It has been shown in animal systems that there is a tight association between mitochondrial ROS and ER stress. However, in plants there are no reports concerning how induced ROS production in mitochondria and chloroplasts affects ER stress and if there is a possible role of organelle-originated ROS as a messenger molecule in the unfolded protein response. To address this issue, electron transport in chloroplasts and mitochondria and carnitine acetyl transferase (CAT) activity in peroxisomes were inhibited in wild-type *Arabidopsis thaliana* to induce ROS production. Expression of UPR genes was then investigated.

Keith:

Effects of C-terminal Truncation of Chaperonin GroEL on the Yield of In-cage Folding of the Green Fluorescent Protein

June 12, 2015 The Journal of Biological Chemistry, 290, 15042-15051.

So Ishino[‡], Yasushi Kawata[§], Hideki Taguchi[¶], Naoko Kajimura^{||}, Katsumi Matsuzaki[‡] and Masaru Hoshino^{‡1}

[‡]Graduate School of Pharmaceutical Sciences, Kyoto University, 46-29 Yoshida-Shimoadachi, Sakyo-ku, Kyoto 606-8501, Japan,

[§]Department of Biotechnology, Graduate School of Engineering, Tottori University, 4-101 Koyama-Minami, Tottori 680-8552, Japan, [¶]Graduate School of Bioscience and Biotechnology, Tokyo Institute of Technology, B-56, 4259 Nagatsuta, Midori-ku, Yokohama 226-8501, Japan, and ^{||}Graduate School of Frontier Biosciences, Osaka University, 1-3 Yamadaoka, Suita, Osaka 565-0871, Japan

Chaperonin GroEL from *Escherichia coli* consists of two heptameric rings stacked back-to-back to form a cage-like structure. It assists in the folding of substrate proteins in concert with the co-chaperonin GroES by incorporating them into its large cavity. The mechanism underlying the incorporation of substrate proteins currently remains unclear. The flexible C-terminal residues of GroEL, which are invisible in the x-ray crystal structure, have recently been suggested to play a key role in the efficient encapsulation of substrates. These C-terminal regions have also been suggested to separate the double rings of GroEL at the bottom of the cavity. To elucidate the role of the C-terminal regions of GroEL on the efficient encapsulation of substrate proteins, we herein investigated the effects of C-terminal truncation on GroE-mediated folding using the green fluorescent protein (GFP) as a substrate. We demonstrated that the yield of in-cage folding mediated by a single ring GroEL (SR1) was markedly decreased by truncation, whereas that mediated by a double ring football-shaped complex was not affected. These results suggest that the C-terminal region of GroEL functions as a barrier between rings, preventing the leakage

of GFP through the bottom space of the cage. We also found that once GFP folded into its native conformation within the cavity of SR1 it never escaped even in the absence of the C-terminal tails. This suggests that GFP molecules escaped through the pore only when they adopted a denatured conformation. Therefore, the folding and escape of GFP from C-terminally truncated SR1·GroES appeared to be competing with each other.

Mary:

PLoS Genetics

Multilayered Organization of Jasmonate Signalling in the Regulation of Root Growth

Debora Gasperini, Aurore Chételat, [...], and Edward E. Farmer

Physical damage can strongly affect plant growth, reducing the biomass of developing organs situated at a distance from wounds. These effects, previously studied in leaves, require the activation of jasmonate (JA) signalling. Using a novel assay involving repetitive cotyledon wounding in *Arabidopsis* seedlings, we uncovered a function of JA in suppressing cell division and elongation in roots. Regulatory JA signalling components were then manipulated to delineate their relative impacts on root growth. The new transcription factor mutant *myc2-322B* was isolated. In vitro transcription assays and whole-plant approaches revealed that *myc2-322B* is a dosage-dependent gain-of-function mutant that can amplify JA growth responses. Moreover, *myc2-322B* displayed extreme hypersensitivity to JA that totally suppressed root elongation. The mutation weakly reduced root growth in undamaged plants but, when the upstream negative regulator NINJA was genetically removed, *myc2-322B* powerfully repressed root growth through its effects on cell division and cell elongation. Furthermore, in a JA-deficient mutant background, *ninja1 myc2-322B* still repressed root elongation, indicating that it is possible to generate JA-responses in the absence of JA. We show that NINJA forms a broadly expressed regulatory layer that is required to inhibit JA signalling in the apex of roots grown under basal conditions. By contrast, MYC2, MYC3 and MYC4 displayed cell layer-specific localisations and MYC3 and MYC4 were expressed in mutually exclusive regions. In nature, growing roots are likely subjected to constant mechanical stress during

soil penetration that could lead to JA production and subsequent detrimental effects on growth. Our data reveal how distinct negative regulatory layers, including both NINJA-dependent and -independent mechanisms, restrain JA responses to allow normal root growth. Mechanistic insights from this work underline the importance of mapping JA signalling components to specific cell types in order to understand and potentially engineer the growth reduction that follows physical damage.

Elizabeth:

June 14 2015

Ariosa A, Lee JH, Wang S, Saraogi I, Shan SO.

Regulation by a chaperone improves substrate selectivity during cotranslational protein targeting.

Proc Natl Acad Sci U S A. 2015 Jun 8;. [Epub ahead of print] PMID: 26056263 [PubMed - as supplied by publisher]

Jevtov I, Zacharogianni M, van Oorschot MM, van Zadelhoff G, Aguilera-Gomez A, Vuillez I, Braakman I, Hafen E, Stocker H, Rabouille C.

TORC2 mediates the heat stress response in Drosophila by promoting the formation of stress granules.

J Cell Sci. 2015 Jun 8; [Epub ahead of print] PMID: 26054799 [PubMed - as supplied by publisher]

Li C, Yeh FL, Cheung AY, Duan Q, Kita D, Liu MC, Maman J, Luu EJ, Wu BW, Gates L, Jalal M, Kwong A, Carpenter H, Wu HM.

Glycosylphosphatidylinositol-anchored proteins as chaperones and co-receptors for FERONIA receptor kinase signaling in Arabidopsis.

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Peptide signalling during the pollen tube journey and double fertilization.

J Exp Bot. 2015 Jun 11;. [Epub ahead of print] PMID: 26068467 [PubMed - as supplied by publisher]

Gasperini D, ChÃ©telat A, Acosta IF, Goossens J, Pauwels L, Goossens A, Dreos R, Alfonso E, Farmer EE.

Multilayered Organization of Jasmonate Signalling in the Regulation of Root Growth.

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Response to Comment on "Principles of ER cotranslational translocation revealed by proximity-specific ribosome profiling".

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

Science. 2015 Jun 12;348(6240):1217. PMID: 26068841 [PubMed - as supplied by publisher]

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Protein synthesis during cellular quiescence is inhibited by phosphorylation of a translational elongation factor.

Proc Natl Acad Sci U S A. 2015 Jun 8;. [Epub ahead of print] PMID: 26056311 [PubMed - as supplied by publisher]

Nedialkova DD, Leidel SA.

Optimization of Codon Translation Rates via tRNA Modifications Maintains Proteome Integrity.

Cell. 2015 Jun 3;. [Epub ahead of print] PMID: 26052047 [PubMed - as supplied by publisher]

The Plant Journal Content Alert (New Articles)

PAYI improves plant architecture and enhances grain yield in rice

Lei Zhao, Lubin Tan, Zuofeng Zhu, Langtao Xiao, Daoxin Xie and Chuanqing Sun

Accepted manuscript online: 10 JUN 2015 09:59PM EST | DOI: 10.1111/tpj.12905

Plant architecture, a complex of the important agronomic traits that determine grain yield, is a primary target of artificial selection of rice domestication and improvement. Some important genes affecting plant architecture and grain yield have been isolated and characterized in recent decades; however, their underlying mechanism remains to be elucidated. Here, we report genetic identification and functional analysis of the *PLANT ARCHITECTURE AND YIELD 1 (PAYI)* gene in rice, which affects plant architecture and grain yield in rice. Transgenic plants over-expressing *PAYI* had twice the number of grains per panicle and consequently produced nearly 38% more grain yield per plant than control plants. Mechanistically, *PAYI* could improve plant architecture via affecting polar auxin transport activity and altering endogenous indole-3-acetic acid distribution. Furthermore, introgression of *PAYI* into elite rice cultivars, using marker-assisted background selection, dramatically increased grain yield compared with the recipient parents. Overall, these results demonstrated that *PAYI* could be a new beneficial genetic resource for shaping ideal plant architecture and breeding high-yielding rice varieties.

Arabidopsis ACT11 Modifies Actin Turnover to Promote Pollen Germination and Maintain the Normal Rate of Tube Growth

Ming Chang and Shanjin Huang Accepted manuscript online: 10 JUN 2015 08:52PM EST | DOI: 10.1111/tpj.12910

Cell Host & Microbe: Alert 5 June-11 June

[The Oxidative Stress Network of *Mycobacterium tuberculosis* Reveals Coordination between Radical Detoxification Systems](#) Pages 829-837

Subhalaxmi Nambi, Jarukit E. Long, Bibhuti B. Mishra, Richard Baker, Kenan C. Murphy, Andrew J. Olive, Hien P. Nguyen, Scott A. Shaffer, Christopher M. Sassetti

M. tuberculosis (Mtb) survives a hostile environment within the host that is shaped in part by oxidative stress. The mechanisms used by *Mtb* to resist these stresses remain ill-defined because the complex combination of oxidants generated by host immunity is difficult to accurately recapitulate in vitro. We performed a genome-wide genetic interaction screen to comprehensively delineate oxidative stress resistance pathways necessary for *Mtb* to resist oxidation during infection. Our analysis predicted functional relationships between the superoxide-detoxifying enzyme (SodA), an integral membrane protein (DoxX), and a predicted thiol-oxidoreductase (SseA). Consistent with that, SodA, DoxX, and SseA form a membrane-associated oxidoreductase complex (MRC) that physically links radical detoxification with cytosolic thiol homeostasis. Loss of any MRC component correlated with defective recycling of mycothiol and accumulation of cellular oxidative damage. This previously uncharacterized coordination between oxygen radical detoxification and thiol homeostasis is required to overcome the oxidative environment *Mtb* encounters in the host.

Analytical Biochemistry: Alert 29 May-4 June

[Fluorimetric screening assay for protein carbonyl evaluation in biological samples](#) Original Research Article

Pages 55-61

P. Stocker, E. Ricquebourg, N. Vidal, C. Villard, D. Lafitte, L. Sellami, S. Pietri

Franco MC, Ricart KC, Gonzalez AS, Dennys CN, Nelson PA, Janes MS, Mehl RA, Landar A, Estevez AG.

Nitration of Hsp90 on tyrosine 33 regulates mitochondrial metabolism.

J Biol Chem. 2015 Jun 17;. [Epub ahead of print] PMID: 26085096

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Interaction of $\hat{I}\pm$ -crystallin with some small molecules and its effect on its structure function.

Biochim Biophys Acta. 2015 Jun 12;. [Epub ahead of print] PMID: 26073614

Mulaudzi-Masuku T, Mutepe RD, Mukhoro OC, Faro A, Ndimba B.

Identification and characterization of a heat-inducible Hsp70 gene from Sorghum bicolor which confers tolerance to thermal stress.

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Andley UP, Goldman JW.

Autophagy and UPR in alpha-crystallin mutant knock-in mouse models of hereditary cataracts.

Biochim Biophys Acta. 2015 Jun 11;. PMID: 26071686 [PubMed - as supplied by publisher]

Bharti N, Bhatla SC.

Nitric oxide mediates strigolactone signaling in auxin and ethylene-sensitive lateral root formation in sunflower seedlings.

Plant Signal Behav. 2015 Jun 15;:0. PMID: 26076049 [PubMed - as supplied by publisher]

A novel multiple-stage antimalarial agent that inhibits protein synthesis.

Nature. 2015 Jun 18;522(7556):315-20. PMID: 26085270 [PubMed - in process]

Adio S, Senyushkina T, Peske F, Fischer N, Wintermeyer W, Rodnina MV.

Fluctuations between multiple EF-G-induced chimeric tRNA states during translocation on the ribosome.

Nat Commun. 2015 Jun 15;6:7442. PMID: 26072700 [PubMed - in process]

Spitale RC, Flynn RA, Zhang QC, Crisalli P, Lee B, Jung JW, Kuchelmeister HY, Batista PJ, Torre EA, Kool ET, Chang HY.

Structural imprints in vivo decode RNA regulatory mechanisms.

Nature. 2015 Mar 26;519(7544):486-90. PMID: 25799993 [PubMed - indexed for MEDLINE]

Stress physiology functions of the Arabidopsis histidine kinase cytokinin receptors (pages 369–380)

M. Nagaraj Kumar and Paul E. Verslues

Article first published online: 3 NOV 2014 | DOI: 10.1111/ppl.12290

Methods in Enzymology

Volume 559 , Pages 2-148, 2015

Purification of His-Tagged Proteins

Pages 1-15

Anne Priestersbach, Jan Kubicek, Frank Schafer, Helena Block, Barbara Maertens

[Affinity Purification of a Recombinant Protein Expressed as a Fusion with the Maltose-Binding Protein \(MBP\) Tag](#)

Pages 17-26 Krisna C. Duong-Ly, Sandra B. Gabelli

[Immunoaffinity Purification of Proteins](#)

Pages 27-36 Jennifer M. Kavran, Daniel J. Leahy

[Affinity Purification of Protein Complexes Using TAP Tags](#)

Pages 37-52 Erica Gerace, Danesh Moazed

[Strep-Tagged Protein Purification](#)

Pages 53-69 Barbara Maertens, Anne Spriestersbach, Jan Kubicek, Frank Schafer

[Proteolytic Affinity Tag Cleavage](#)

Pages 71-97 Helena Block, Barbara Maertens, Anne Spriestersbach, Jan Kubicek, Frank Schafer

[Affinity Pull-Down of Proteins Using Anti-FLAG M2 Agarose Beads](#)

Pages 99-110 Erica Gerace, Danesh Moazed

[Protein Affinity Purification using Intein/Chitin Binding Protein Tags](#)

Pages 111-125 Sarah F. Mitchell, Jon R. Lorsch

[Purification of GST-Tagged Proteins](#)

Pages 127-139 Frank Schafer, Nicole Seip, Barbara Maertens, Helena Block, Jan Kubicek

Molecular Cell: Alert 13 June-19 June

[Autophagic Degradation of the 26S Proteasome Is Mediated by the Dual ATG8/Ubiquitin Receptor RPN10 in Arabidopsis](#) Original Research Article

Pages 1053-1066 Richard S. Marshall, Faqiang Li, David C. Gemperline, Adam J. Book, Richard D. Vierstra

Cell: Alert 13 June-19 June

[Optimization of Codon Translation Rates via tRNA Modifications Maintains Proteome Integrity](#) Original Research Article

Pages 1606-1618 Danny D. Nedialkova, Sebastian A. Leidel

Current Opinion in Structural Biology: Alert 12 June-18 June

[The importance of dynamics in integrative modeling of supramolecular assemblies](#) Review Article

Pages 28-34 Giorgio E Tamo, Luciano A Abriata, Matteo Dal Peraro

Plant, Cell & Environment Content Alert (New Articles)

[Seed set, pollen morphology and pollen surface composition response to heat stress in field pea](#)

YUNFEI JIANG, RACHID LAHLALI, CHITHRA KARUNAKARAN, SAROJ KUMAR, ARTHUR R. DAVIS and ROSALIND A. BUECKERT

Accepted manuscript online: 17 JUN 2015 03:48AM EST | DOI: 10.1111/pce.12589

From NATURE: Christopher Mason, a computational geneticist at Weill Cornell Medical College in New York City, told the conference how a baseline survey of genetic material from surfaces in the city's subway system had uncovered DNA from almost 1,700 known taxa, mostly harmless bacteria. But 48% of the genetic material did not match anything yet identified. "Half the world under our fingertips is unknown," said Mason. Still, trends are emerging from the global Metagenomics and Metadesign of Subways and Urban Biomes initiative (MetaSUB), which aims to characterize the genetic material found on public-transport systems in 16 world cities to elucidate the microscopic riders that share the commute.

Storms leave a mark: months after New York City's South Ferry Station was flooded in 2012's Hurricane Sandy, it still harboured DNA from bacteria associated with cold marine environments and fish, Mason said. However, most of the bacteria in the subway were harmless *Acinetobacter* species and others associated with human skin.

Convergence of biological nitration and nitrosation via symmetrical nitrous anhydride pp504 - 510

Dario A Vitturi, Lucia Minarrieta, Sonia R Salvatore, Edward M Postlethwait, Marco Fazzari *et al.*
doi:10.1038/nchembio.1814 NO₂⁻ has been viewed primarily as a reservoir for NO and NO-modified species, activated by acids or metal catalysis. Isotopic labeling of NO and NO₂⁻ modifications *in vitro* and *in vivo* now demonstrates that NO₂⁻ also participates directly in these reactions through a symmetric N₂O₃ intermediate.

Miliara X, Garnett JA, Tatsuta T, Ali FA, Baldie H, PÃ©rez-Dorado I, Simpson P, Yague E, Langer T, Matthews S.

Structural insight into the TRIAP1/PRELI-like domain family of mitochondrial phospholipid transfer complexes.

EMBO Rep. 2015 Jun 12;. PMID: 26071602 [PubMed - as supplied by publisher]

Ozgur R, Uzilday B, Sekmen AH, Turkan I.

The effects of induced production of reactive oxygen species in organelles on endoplasmic reticulum stress and on the unfolded protein response in arabidopsis.

Ann Bot. 2015 Jun 12;. PMID: 26070642 [PubMed - as supplied by publisher]

Sandalio LM, Romero-Puertas MC.

Peroxisomes sense and respond to environmental cues by regulating ROS and RNS signalling networks.

Ann Bot. 2015 Jun 12;. PMID: 26070643 [PubMed - as supplied by publisher]

Plant, Cell & Environment Content Alert: 38, 7 (July 2015)

Conserved and novel heat stress-responsive microRNAs were identified by deep sequencing in *Saccharina japonica* (Laminariales, Phaeophyta) (pages 1357–1367)

FULI LIU, WENJUN WANG, XIUTAO SUN, ZHOURUI LIANG and FEIJU WANG

Article first published online: 23 JAN 2015 | DOI: 10.1111/pce.12484

Studying the heat stress response and resistance mechanism of *Saccharina* is of great significance for understanding the acclimation to heat stress under domestication as well as for breeding new cultivars with heat stress resistance. Forty-nine known miRNAs and 75 novel miRNAs were identified, of which seven known and 25 novel miRNAs were expressed differentially under heat stress. Thirty nine and 712 genes were predicted to be targeted by the seven known miRNAs and 25 novel miRNAs, respectively. Gene function and pathway analyses showed that these genes probably play important roles in *S. japonica* heat stress tolerance.

Cellular Incorporation of Unnatural Amino Acids and Bioorthogonal Labeling of Proteins

[Kathrin Lang](#) * and [Jason W. Chin](#) *

Medical Research Council Laboratory of Molecular Biology, Francis Crick Avenue, Cambridge CB2 0QH, United Kingdom

Chem. Rev., 2014, 114 (9), pp 4764–4806

[Cell 161, 858–867, 2015](#)

The AAA+ unfoldase ClpX contributes to bacterial proteostasis. In eukaryotes ClpX is found only in mitochondria (mtClpX), and its function has so far remained elusive. Baker and colleagues now report that mtClpX plays a part in heme biosynthesis by facilitating synthesis of the precursor 5-aminolevulinic acid (ALA). Searching large-scale genetic- and chemical-interaction data in *Saccharomyces cerevisiae*, they found that the interaction profile of the gene encoding the yeast mtClpX homolog Mcx1 is strongly correlated with those of the genes involved in the initial steps of heme biosynthesis, including *HEM1*, which encodes the ALA synthase Hem1. Deletion or function-impairing mutation of Mcx1 reduces cellular heme levels, but the phenotype is rescued by supplementation with ALA, thus suggesting a direct role of Mcx1 in ALA synthesis. ALA synthases, including Hem1, require the cofactor pyridoxal phosphate (PLP) for enzymatic activity. Baker and colleagues found that Mcx1 directly interacts with Hem1 and increases PLP binding to the apo-Hem1 by eight-fold, thus facilitating its activation. Although PLP binding requires Hem1 to maintain at least a partially folded state, Hem1 activation is nevertheless dependent on the unfoldase function of Mcx1. These observations led the authors to propose that upon interacting with the apoenzyme, mtClpX may locally unfold ALA synthase, thus exposing its buried active site to facilitate PLP binding. Consistently with the high sequence conservation of mtClpX and ALA synthase in yeast and mammals, mouse mtClpX also stimulates PLP activation of a human ALA synthase apoenzyme *in vitro*; this suggests that the mechanism identified in yeast is conserved across eukaryotes. Finally, Baker and colleagues found that knockdown of mtClpX in zebrafish embryos impairs erythropoiesis, consistently with the high requirement for heme to form hemoglobin during this process. These findings shed light on the role of ClpX in mitochondria and indicate an unexpected function for AAA+ unfoldases.

Current Opinion in Biotechnology: Alert 28 May-3 June

[Mathematical modeling of unicellular microalgae and cyanobacteria metabolism for biofuel production](#) Review Article

Pages 198-205

Caroline Baroukh, Rafael Munoz-Tamayo, Olivier Bernard, Jean-Philippe Steyer

[Engineering cyanobacteria for direct biofuel production from CO₂](#) Review Article

Pages 8-14

Philipp Savakis, Klaas J Hellingwerf

[Enzyme activities of Arabidopsis inositol polyphosphate kinases AtIPK2 and AtIPK2 \$\beta\$ are involved in pollen development, pollen tube guidance and embryogenesis \(pages 758–771\)](#)

Huadong Zhan, Yujiao Zhong, Zhongnan Yang and Huijun Xia

Article first published online: 11 MAY 2015 | DOI: 10.1111/tpj.12846

Significance Statement

Our results in this study demonstrate that AtIPK2 and AtIPK2 β play an essential role in pollen development, pollen tube guidance and embryogenesis in a kinase activity-dependent manner. Our data provides insights into the underlying molecular mechanism of pollen tube guidance.

[Expression of the tetrahydrofolate-dependent nitric oxide synthase from the green alga *Ostreococcus tauri* increases tolerance to abiotic stresses and influences stomatal development in Arabidopsis \(pages 806–821\)](#)

Noelia Foresi, Martín L. Mayta, Anabella F. Lodeyro, Denise Scuffi, Natalia Correa-Aragunde, Carlos García-Mata, Claudia Casalongué, Néstor Carrillo and Lorenzo Lamattina

Article first published online: 27 MAY 2015 | DOI: 10.1111/tpj.12852

Significance Statement

Transgenic *Arabidopsis* plants expressing nitric oxide synthase from *Ostreococcus tauri* (OtNOS) accumulate high NO concentration and show increased tolerance to salt, drought and oxidative stress. Transgenic *OtNOS* lines exhibited increased stomatal index and survival rate to desiccation. OtNOS, unlike mammalian NOS, can efficiently use tetrahydrofolate (THF) as cofactor in *Arabidopsis* plants. This finding identifies THF as the cofactor employed by the enzymatic system responsible for the arginine-dependent NO synthesis in higher plants.

[Sugars as hydroxyl radical scavengers: proof-of-concept by studying the fate of sucralose in *Arabidopsis* \(pages 822–839\)](#)

Andrea Matros, Darin Peshev, Manuela Peukert, Hans-Peter Mock and Wim Van den Ende
Article first published online: 27 MAY 2015 | DOI: 10.1111/tpj.12853

Significance Statement

Plant sugars represent an integral part of antioxidant mechanisms contributing to cellular ROS homeostasis. In this study we showed the *in vivo* formation of recombination and oxidation products by non-enzymatic reactions with hydroxyl radicals using sucralose, an artificial analogue of sucrose. Oxidation products of endogenous sugars have also been elucidated *in planta* for *Arabidopsis* and barley.

[HSP33 in eukaryotes – an evolutionary tale of a chaperone adapted to photosynthetic organisms \(pages 850–860\)](#)

Na'ama Segal and Michal Shapira

Article first published online: 27 MAY 2015 | DOI: 10.1111/tpj.12855

Significance Statement

Hsp33 is the only known chaperone which is activated under oxidizing conditions, and was well characterized in bacteria. Since the natural physiology of photosynthetic organisms involves light-induced oxidative stress, we were interested to see whether the algal ortholog, HSP33, is expressed in the chloroplast and if it possesses a similar activation mode. Our results highlight a significant evolutionary variability of the algal protein and we also discuss its biotechnological value.