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De Gara, L and Foyer, CH orcid.org/0000-0001-5989-6989 (2017) Ying and Yang interplay between reactive oxygen and reactive nitrogen species controls cell functions. Plant, Cell & Environment, 40 (4). pp. 459-461. ISSN 0140-7791

https://doi.org/10.1111/pce.12936

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Editorial:

Ying and Yang interplay between reactive oxygen and reactive nitrogen species controls cell functions

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Introduction

Reactive oxygen species (ROS) and reactive nitrogen species (RNS) function together in a nexus of reduction/oxidation (redox) control that impact on nearly every aspect of plant biology. ROS generation leading to oxidative signalling and the production of nitric oxide (NO) and its associated signalling pathways are key components of integrated responses of plant to environmental, metabolic and developmental triggers. These biological messengers, function together in the signalling hub that regulates plant growth and metabolism in response to biotic threats and abiotic challenges through the mediation of redox metabolites, protein modifications, enzyme activities, and transcript levels. It is not surprising therefore that enormous interest has continued to focus on this topic, leading to an extensive literature that documents the unprecedented progress that has been made in recent years (Foyer and Noctor, 2016). The manuscripts in this Special Issue make a valuable addition to this literature because they summarise the current knowledge and concepts that lay the foundations of the contemporary vision for ROS/RNS functions, particularly through interrelated signalling hubs. They also provide enticing snapshots of key areas of current endeavor and interest.

Redox-mediated post-translational modifications come of age

The important emerging topic of the complex interplay of ROS and NO signaling in developmental and stress-induced hypoxia has been comprehensively reviewed by Pucciariello and Perata (ref). Redox signaling not only plays a key role in the metabolic readjustments that are required for survival of low oxygen availability but the crosstalk between ROS and NO signaling pathways is also crucial to the regulation of group VII ethylene response factors that is pivotal in driving the metabolic and molecular acclimation to low oxygen conditions. These authors also discuss the experimental evidence that demonstrates the pivotal role of the physiological regulation of hypoxia in specific tissues such as seeds

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and buds and highlighting that the developmental regulation of hypoxia is a crucial strategy that plants use in the control of dormancy and quiescence, with release to the metabolically-active state upon germination and growth. ROS and RNS trigger a wide range of redox-based, post-translational modifications such as protein S-nitrosylation that are used in signal transduction to regulate gene expression. Keech and co-workers (ref) provide a competent and insightful overview of the role of post translational modifications in the redox-regulation of photorespiration. Highlighting the redox control of the glycerate kinase and glycine cleavage systems, the complexity of the redox control of this metabolic pathway is discussed together with control of the fluxes of reducants and oxidants between the different compartments involved in photorespiration. These authors provide evidence based on redox proteome data that almost all of the enzymes of the photorespiratory enzymes might be regulated by oxidative modifications, pointing out that it is timely to investigate the post-translational regulation of these proteins in more detail (Keech and co-workers (ref). Sulphenomics, which is an essential component of redox proteomics, has been effectively used to analyze ROS- and RNS-mediated post-translational modifications. This topic has been comprehensively discussed within the wider context of redox signaling in the review by Trost and coworkers (ref), who describe the kinetic and thermodynamic factors influencing the hydrogen peroxide-dependent oxidation rate of protein cysteines with a particularly focus on glyceraldehyde-3-phosphate dehydrogenases, which have been intensively studied in animals as well as plants. These authors highlight the key role of the protein micro-environment in determining cysteine residue reactivity, sulphenic acid stability and ability to generate secondary modifications (Trost et al., ref). The important topic of S-nitrosoproteomics is addressed in the paper by Loake and co-workers (ref), who provide a comprehensive overview of the role of nitric oxide in abiotic stress tolerance, with particular emphasis on the role of protein S-nitrosylation as a major control point for NO-dependent metabolic rearrangements underpining abiotic stress responses and tolerance.

Plant immunity responses

The elicitor cryptogenin was used to explore the specific roles of NO and ROS-dependent steps in the signaling pathways leading to plant immunity in the tobacco Bright Yellow-2 (TBY-2) cell model system in two studies reported in this Special Issue. Rosnoblet and coworkers (Ref) present evidence showing that the ATPase molecular chaperon Cdc48 is an important component in cryptogeninin-induced hypersensitive-like cell death. Using mass spectrometry, these authors present compelling evidence that dc48 interacts with about hundred proteins, demonstrating the involvement of this molecular chaperone in a number of key cellular processes, particularly ubiquitin-proteasome dependent protein degradation, sub-cellular trafficking and redox regulation. In contrast to previously suggestions, only a low level of protein S-nitrosylation was observed in the Cdc48 population, the authors concluding that this PTM may not be particularly relevant in cryptogenin-triggered responses (Rosnoblet and coworkers, Ref). Using radioactive [33P]-orthophosphate labeling together with a range of biochemical, pharmacological and reverse genetic approaches, Ruelland and co-workers (ref) provide evidence that cryptogenin also activates an early lipid-mediated signaling pathway leading to positive regulation the plasmamembrane NADPH oxidase called RBOHD.

Enhanced abiotic stress tolerance

Environmental abiotic stresses such as soil water deficits and salinity currently limit plant growth in many parts of the world. Abiotic stresses are predicted to become even more severe as desertification covers increasing areas of the terrestrial environment and the faster-than-predicted changes in the global climate, suggest an increase in aridity for the semiarid regions of the globe. Hence, low water supply (drought) and accompanying restrictions on water uptake by roots have been identified as the single most common abiotic threat to the growth of crops worldwide. One way that the impact of drought on plant productivity might be limited is through the improved control of stomata and hence reduced leaf water loss leading to enhancing drought tolerance. A novel factor modulating NOS-like activity in Arabidopsis guard cells is described in the study reported by Zhai and coworkers (ref) in this Special Issue, who provide evidence that a homolog of the human WD40-REPEAT 5 protein, is involved in H₂O₂-induced NO accumulation in stomatal guard cells. This leads to the improved control of stomatal closure and enhanced drought tolerance.

Iron is an essential plant nutrient that is required for a wide variety of functions in proteins that play crucial roles in accepting or donating electrons for example in the photosynthetic and respiratory electron transport chains. Iron homeostasis is essential in plants because iron accumulation is toxic. Functional genomic approaches have shown that plants respond to a deficiency or an excess of iron by inducing the expression of different gene sets. However, two rice genotypes that were derived from a QTL mapping population and differ in iron tolerance showed similar tissue iron concentrations, iron distribution between plant organs and the expression of genes associated with sub-cellular partitioning (Wu et al. ref). However, ascorbate oxidase was increased in the iron-tolerant plants and dehydroascorbate reductase was lowered (Wu et al. ref). These data strongly implicate ascorbate as an essential metabolite for the reduction of Fe³⁺ into Fe²⁺⁺, Therefore, in situations of excess iron excess reduced ascorbate could have more a pro-oxidant action by promoting iron-induced oxidation via Fenton chemistry (Wu et al. ref).

NADPH oxidases (RBOH) play important, but often poorly understood, roles in the complex interplay of signals that trigger a wide range of responses to abiotic and biotic stresses. For example, the differential expression of RBOHs in different plant organs and tissues contributes to the regulation of cellular and whole plant responses to heavy metals and xenobiotics, including nutrient translocation and homeostasis in shoots (Sandalio et al, ref). The roles of different isoforms of NADPH oxidase in short-term and long term exposures to cadmium were studied in a range of Arabidopsis rboh mutants by Sandalio et al, (ref). Evidence is provided for the influence of different RBOHs on ROS and NO accumulation, lipid peroxidation and ion accumulation in roots and shoots, together with effects on the activities of ROS scavenging enzymes, and ascorbate and glutathione metabolism (Sandalio et al, ref). In addition to NAPDH oxidases, other enzymes such as polyamine oxidases, are involved in stress-induced ROS production. Salt tolerance was increased in Arabidopsis atpao5-2 and atpao5-3 mutants with impaired spermine or thermospermine conversion to spermidine. Transcript and metabolite profiling analysis of these two independent loss-of-function mutants (Ruben and coworkers, ref) demonstrate that the higher thermospermine content which characterizes these mutants is important in salt stress tolerance. Accumulation of this polyamine resulted in an accumulation of compatible soluble and TCA cycle intermediates, and altered the biosynthesis of abscisic acid and jasmonates (Ruben and coworkers, ref). Loss of AtPAO5 functions also led to the altered expression of genes involved in Na⁺ fluxes between intracellular compartments. These data implicate thermospermine, but not its isomer spermine, in the specific reprogramming of metabolic pathways that underpin salt stress tolerance in Arabidopsis (Ruben and coworkers, ref).

Future perspectives

The papers in this Special Issue not only highlight the complex Ying and Yang interplay of ROS and RNS signalling that is a key control of most if not all major processes in plant biology but they also demonstrate that rapid progress that is being made in understanding the plethora of post translational controls of plant proteins that underpins these ROS and RNS functions. While many questions remain to be addressed regarding the precise functions of redox mediated PTMs in the control metabolic and signalling pathways, several papers in this special issue demonstrate the underpinning importance of new

and emerging technologies, particularly redox proteomics and sulphenomics in driving fundamental research and hence knowledge generation forwards in plant redox biology. The concept that **e**pigenetic mechanisms are important in the intergenerational control of plant growth, development and defense responses is now widely accepted not least because epigenetic marks area major mechanism of memorizing past stress experiences. Trans-generational inheritance of epigenetic information confers adaptive advantages to a wide range of environmental challenges. Moreover, epigenetic marks such as histone modifications and DNA methylation are a major driving force for plant and animal evolution. While little is as yet known about the role of ROS and RNS signalling in the regulation of histone modifications and DNA methylation, we consider that future studies are likely to focus on gaining a deeper understanding of how cellular redox homeostasis and signaling influence chromatin and epigenetic dynamics, since such approaches have the potential to lead to the discovery of novel markers for improved plant growth, defense and sustainability in the face of climate change.

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Other references are manuscripts in the Special Issue